```
 **********************************************
 *                                            *
 *    M P S R C H                        (TM)  *
 *                                            *
 **********************************************

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MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:          Wed Jul  8 01:11:48 1998;   MasPar time 948.80 Seconds
                                       874.266 Million cell updates/sec

Tabular output not generated.

Title:            >US-08-554-424-7
Description:      (1-6513) from US08554424.seq
Perfect Score:    6513
N.A. Sequence:    6513   1 TCTAGACGTTGGCCGCATAG.........ACGGGAGTATTAGCTCTAGA 6513
                          AGATCTGCAACCGGCGTATC.........TGCGCTCATAATCGAGATCT
N.A. Comp:

Scoring table:    TABLE default
                  Gap 6

Nmatch   STD :    Dbase 0;  Query 0

Searched:         176886 seqs, 63680241 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        n-geneseq31-2
                  1:part1  2:part2  3:part3  4:part4  5:part5  6:part6  7:part7
                  8:part8  9:part9  10:part10 11:part11 12:part12 13:part13
                 14:part14 15:part15 16:part16 17:part17 18:part18
                 19:part19 20:part20 21:part21 22:part22 23:part23
                 24:part24 25:part25 26:part26 27:part27 28:part28
                 29:part29 30:part30 31:part31 32:part32 33:part33
                 34:part34 35:part35 36:part36 37:part37

Statistics:      Mean 10.618;  Variance 6.276;  scale 1.692

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| | 6513 | 100.0 | 6513 | 22 | T18986 | Drosophila para volta | 0.00e+00 |
| ~13 | 100.0 | 6513 | 22 | T33238 | Drosophila para volta | 0.00e+00 |
| | 5.4 | 7555 | 13 | Q81328 | Cardiac sodium channe | 3.19e-221 |
| | 5.3 | 7555 | 1 | Q05831 | Cardiac sodium channe | 1.63e-215 |
| | .8 | 3033 | 22 | T30192 | Peripheral nervous sy | 1.01e-192 |
| | | 6452 | 22 | T30193 | Peripheral nervous sy | 1.01e-192 |
| | | 6371 | 22 | T30194 | Peripheral nervous sy | 7.08e-190 |
| | 04 | 22 | T30195 | Peripheral nervous sy | 7.08e-190 |
| | 32 | | | T77806 | cDNA encoding wild ty | 2.37e-181 |
| | | | | T77803 | cDNA encoding variant | 2.37e-181 |
| | | | | T77805 | cDNA encoding variant | 2.37e-181 |
| | | | | T77804 | cDNA encoding variant | 2.04e-135 |
| | | | | scd131, a subclone of | 1.07e-97 |
| | | | | scd61, a subclone of | 1.14e-42 |

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15  50  0.8   204    1   N81164   Base substituted E.co   1.25e-13
16  44  0.7    91    9   Q51746   Oligonucleotide probe   3.78e-10
17  45  0.7    91    9   Q51746   Oligonucleotide probe   1.01e-10
18  48  0.7   204    1   N81164   Base substituted E.co   1.86e-12
19  43  0.7  6725   15   Q87834   Human neuronal calciu   1.40e-09
20  38  0.6   114   12   Q70465   Generic DNA sequence    8.42e-07
21  37  0.6   114   12   Q70469   Generic DNA sequence    2.93e-06
22  36  0.6   114   12   Q70468   Generic DNA sequence    1.01e-05
23  36  0.6   114   12   Q70467   Generic DNA sequence    1.01e-05
24  39  0.6   114   12   Q70469   Generic DNA sequence    1.01e-05
25  38  0.6   114   12   Q70467   Generic DNA sequence    2.39e-07
26  38  0.6   114   12   Q70466   Generic DNA sequence    8.42e-07
27  38  0.6   114   12   Q70468   Generic DNA sequence    8.42e-07
28  38  0.6   114   12   Q70465   Generic DNA sequence    8.42e-07
29  36  0.6   114   12   Q70470   Generic DNA sequence    8.42e-07
30  41  0.6   178   31   T76405   Human endothelin-1 an   1.01e-05
31  40  0.6   190   35   T76452   Chymase antisense oli   1.86e-08
32  42  0.6   811    5   Q29261   Human calcium channel   6.70e-08
33  36  0.6  1028    0   Q27091   XrY26 probe.            5.12e-09
34  39  0.6  1089    4   N92576   Sequence of the 1.1kd   1.01e-05
35  41  0.6  1809   19   T15008   Mouse Elf-1 cDNA.       2.39e-07
36  36  0.6  2050    5   Q29265   Human calcium channel   1.01e-05
37  36  0.6  3109    5   Q24982   DNA induced in human    1.86e-08
38  37  0.6  3765    5   Q31890   FMR-1 gene for detect   1.01e-05
39  37  0.6  5904    5   Q37813   Sequence encoding the   2.39e-06
40  37  0.6  5975   36   T96811   Rabbit skeletal calci   2.39e-07
41  37  0.6  5975    1   N91778   Rabbit calcium channe   2.93e-06
42  37  0.6  5975   30   T70228   Rabbit seletal muscle   2.93e-06
43  37  0.6  5975   14   Q87978   Rabbit skeletal calci   2.93e-06
44  39  0.6  6575   15   Q84655   Human neuronal calcu    2.93e-06
45  35  0.5  6407   23   T36035   rchd528 gene differen   3.44e-05
```

ALIGNMENTS

```
RESULT
  1
ID   T18986 standard; cDNA; 6513 BP.
AC   T18986.
DT   15-OCT-1996 (first entry)
DE   Drosophila para voltage-activated sodium channel cDNA.
KW   Para voltage-activated sodium channel; cation channel; tipE;
KW   antisense: ss.
OS   Drosophila melanogaster.
PN   WO9615220-A1.
PD   23-MAY-1996.
PF   08-NOV-1995; U14378.
PR   10-NOV-1994; US-337339.
PA   (MERI ) MERCK & CO INC.
PA   (UVNY ) UNIV NEW YORK STATE.
PI   Arena JP, Feng G, Hall LM, Liu K, Van Der Ploeg LHT;
PI   Wang P, Warmke JW;
DR   WPI; 96-259828/26.
PT   Co-expression of voltage-activated cation channel alpha and beta
PT   sub-units - esp. para and tip E sub-units of Drosophila voltage
PS   activated sodium channel protein in biologically active form
CC   Claim 19; Page 36-40; 52pp; English.
CC   A full-length cDNA clone (T18986) codes for the Drosophila para
CC   voltage-activated sodium channel (VASC), a protein responsible for
CC   the fast depolarising phase of the action potential that underlies
CC   electrical signaling in neurons, muscles, etc. Functional expression
CC   of the para VASC requires the co-expression of the para alpha subunit
CC   with tipE, a putative Drosophila VASC beta subunit. The para VASC
CC   cDNA clone was obtd. from 3 overlapping regions of para cDNA isolated
CC   by PCR amplification using primers (see also T18987-92) based on a
CC   published para sequence. Recombinant host cells (E.coli, yeast
CC   mammalian or insect) expressing the Drosophila para VASC can be used
CC   to isolate para VASC in biologically active form. Antisense
CC   constructs can block expression of the gene.
SQ   Sequence 6513 BP;   1681 A;   1548 C;   1702 G;   1582 T;

Query Match          100.0%;  Score 6513;  DB 22;  Length 6513;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 6513;  Conservative    0;  Mismatches    0;  Indels    0,  Gaps    0,
```

1998

Left column (positions 1–1080):

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b     1 tctagacgttggcgcgatagacaatgacagaagattccgactcgatatctgaggaagaac  60
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Qy    1 TCTAGACGTTGGCGCGGATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC  60

Db   61 gcagttgttccgtcccttacccgcgaatcattggtgtcaaatcgaacaacgcattgccg  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 GCAGTTGTTCCGTCCCTTACCCGCGAATCATTGGTGTCAAATCGAACAACGCATTGCCG   120

Db  121 ctgaacatgaaaagcagaagagctggaaagaagagagccgagggagaggtgccgcgat   180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121 CTGAACATGAAAAGCAGAAGAGCTGGAAAGAAGAGAGCCGAGGGAGAGGTGCCGCGAT    180

Db  181 atggtcgcaagaaaaacaaaaagaaatccgataccttgccaataacctgttgaggcagtc   240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 ATGGTCGCAAGAAAAACAAAAAGAAATCCGATAACCTGTTGAGGCAGTC             240

Db  241 cacaaccggatccttacaacaggtgtgccaataacctgttgattgcaggcagct        300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241 CACAACCGGATCCTACACTTGACTTGCGATTGCAGGGGCAGCT                   300

Db  301 tcccgcgcgaattggcctcactcctctcgaggatatcgatccctactacacagtgtac    360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301 TCCCGCGGAATTGGCCTCCTCTCCGAGGATAATCGATCCCTACTACACAGCAATGTAC    360

Db  361 tgacattcgtagttgtaagcaaagagaaagatattttcgctttttctgatcaaaagcaa   420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  361 TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAA   420

Db  421 tgtggatgtcgatccattcaatccgatacgtcgtgtggccattacattcctagtgcatc    480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTCTTAGTGCATC  480

Db  481 cattatttccctattcatcatcaccacaattctgtcaactgcatcctgatgataatgc    540
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Qy  481 CATTATTTCCCTATTCATCATCATCACCACAATTCTCGTCAACTGCATCCTGATGATAATGC  540

Db  541 cgacaacgcccacggttgagtccactgagtgatattcaccggaatctacacatttgaat   600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  541 CGACAACGCCCACGGTTGAGTCCACTGAGTGATAATTCACCGGAATCTACACATTTGAAT  600

Db  601 cagctgttaaagtgatggcacgaggttcattttatgccgtttacgtgataggg tatagatg   660
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Qy  601 CAGCTGTTAAAGTGATGGCACGAGGTTCATTTTATGCCGTTTACGTTAGGAGATG      660

Db  661 catggaattgctggacttcggtagtaatagcttagctttagttagttagtgtag atagatt   720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  661 CATGGAATTGGCTGGACTTCGTACTTCCTAGTAATAGCTTTAGTTGACCATGGGTATAGATT  720

Db  721 taggtaatctagcagccctcgaacgtttaggggtgctgcgagcgctttaaaacctagcca   780
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Qy  721 TAGGTAATCTAGCAGCCCTCGAACGTTTAGGGTGCTGCGAGCGCTTAAAAACCTAGCCA   780

Db  781 ttgtgccaggcttgaagaccatcgtcggcggccgtcatcgaatcggtgaagaatctcggcg   840
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Qy  781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGGCCGTCATCGAATCGGTGAAGAATCTCGCGCG   840

Db  841 atgtgattatccgacatgttctccgcgttgatggtgcgttgatggtgggcctacagatc   900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  841 ATGTGATTATCCGACCATGTTCTCCCCGTGTTCATTTTATGCCGTTTCGGTTGGGGGCA  900

Db  901 atatgggcgttcaccggaagtgcatcaagaagtgcatcaagaagttccccgtggggca   960
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Qy  901 ATATGGGCGTTCACCGGAAGTGCATCAAGAAGTGCATCAAGAAGTTCCCGGTGGGGGCA   960

Db  961 atctgaccgacgagaagtggactggaatatcacaatcgcaatgactcoaattggtattccgagg 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  961 ATCTGACCGACGAGAAGTGGACTGGAATATCACAATCGCAATAGCTCCAATTGGTATTCCGAGG 1020

Db 1021 acgagggcatctcatttccgttatgcggcaatatatccgttcgggcgggggcgcgcgacg 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1021 ACGAGGGCATCTCATTTCCGTTATGCGGCAATATATCCGTTCGGGCGGGGGCAATGCCGACGACG 1080
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Right column (positions 1081–2220):

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Db 1081 attacgtgtgcctgcagggggttggtcgaatccgaattatggctacaccagcttcgatt 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1081 ATTACGTGTGCCTGCAGGGGTTTGGTCCGAATTCCGAATTATGGCTACACCAGCTTCGATT 1140

Db 1141 cgttcggatgggcttttcctgtccgcctccggctgatgacacaggactcttggggggatc 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1141 CGTTCGGATGGGCTTTTCCTGTCCGCCTTCCGGCTGATGCACAGGACTTCTGGGAGGATC 1200

Db 1201 tgtaccagctggtgttgcggcgccgaccatgcacatgtgctgttctttatagtcatca 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1201 TGTACCAGCTGGTGTTGCGGCGCCGGACCATGCACATGTGCTGTTCTTTATAGTCATCA 1260

Db 1261 tcttcctagttcattcatctgtgaatttgattttggccattgttgccatgtcgtatg 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1261 TCTTCCTAGTTCATTCATTCTTGTGAATTTGATTTGGCCATTGTTGCCCATGTCGTATG 1320

Db 1321 acgaattgcaaagaaggccgaagaagaaggcgtgccgaagaggcgatacgtgaag 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1321 ACGAATTGCAAAGAAGGAAGGCCGAAGAAGAAGGCCTGCCGAAGAGAGGCCGATAACTGAAG 1380

Db 1381 cggaagaagctgccgcccgccaagaccgccaagctggaggaggcgggggcgccaatgccaggcctc 1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1381 CGGAAGAAGCTGCCGCCCCCAAAGACCGCCAAGCTGGAGGAGGCGGGGGCCAATGCCAGGCTC 1440

Db 1441 aggcagcacgcggatgcgcggctgccgcccgccgaagaggctgcactgcactgcatcccggaaatggccaaga 1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1441 AGGCAGCACCAGCGGATGCCGGCGCTGCCCGCCGAAGAGGCTGCACTGCACTGCATCCCGGAAATGGCCAAGA 1500

Db 1501 gtccgacgtattcttgcatcagctatgagctatggcgtatttgttggcgcggagaagggcaacgatg 1560
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Qy 1501 GTCCGACGTATTCTTGCATCAGCTATGAGCTATGTTGGCGGCGGAGAAGGGCAACGATG 1560

Db 1561 acaacacaaagagaagatgtccattcgagcgtcgagtggagtcggagtcggagtcgggtgagcg 1620
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1561 ACAACACAAAGAGAAGATGTCCATTCGGAGCGTCGAGTGGAGTCGGAGTCGGAGTCGGGTGAGCG 1620

Db 1621 ttataacaagacaacacaacagcaacaccaccaccaccaccagcacagtgaagttcgtaaagtga 1680
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Qy 1621 TTATACAAAGACAACAACAACAGCAACAACACCACCACCAGCACCAAGCTTCGTAAAGTTCGTAAAGTGA 1680

Db 1681 gcacgacatcctatcctcctgttcacggcgtttaaacatacgacaggggatcacgtagtt 1740
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Qy 1681 GCACGACAATCCTTATCCTTACCTGGTTCACCGTTTAACATACGCAGGGGATTCACGTAGTT 1740

Db 1741 ctcaaagtacacgatacggaacgacgtggcgtttggatataccggtagcggatcgta 1800
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Qy 1741 CTCAAAGTACACGATACACGATACGGAACGACGTGGCCCGCTTTGGTATACCCGGTAGCGGATCGTA 1800

Db 1801 agccattggtattgtcaacatatcaggatgccagcagcccagcgccagcgcgacgact 1860
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Qy 1801 AGCCATTGGTATTGTCAACATATCAGGATGCCAGCAGCCCAGCCAGCAGCACTTGCCCCTATGCCCGACGACT 1860

Db 1861 cgaatgccgtcaccccgatcgtccgaagagaatggggccatcatagtgccgtgtactatg 1920
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Qy 1861 CGAATGCCGTCACCCCGATGTCCGAAGGAGAATGGGCCCATCATAGTGCCCGTGTACTATG 1920

Db 1921 gcaatctaggctcccgacactcatcctataccttcgtatctgtcagtccggaatatcgtatacct 1980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1921 GCAATCTAGGCTCCCGACACTCACTTCATCTCCGAATATCGTATATCCT 1980

Db 1981 cacatggcgatctactcggcggcatggcgtcatggcgcgatcagcacacaacaccaagaggaga 2040
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Qy 1981 CACATGGCGATCTACTCGCCGGCATGGCGTCATCAGCACACAACAACACCAAGGAGA 2040

Db 2041 gcaaattgcgcaaccgcaatcacacggctcgatcatcgcgatcatcaatcaatggcgcacca 2100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2041 GCAAATTGCGCAACCGCAATCACACGGCTCGATCATCGCGATCATCAATCAATGGCGCACCA 2100

Db 2101 cctgtctggacaccaatcacaagctcgatcatcgcgatcatcggcgacgacg 2160
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Qy 2101 CCTGTCTGGACACCAATCACAAGCTCGATCATCGGCGATCATCGGCGACTACGTGGAGTGCA 2160

Db 2161 cggacgaagctggcaagaatggcaagtaaacatcatgacaatcctttatcgagcccgtccagacac 2220
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Qy 2161 CGGACGAAGCTGGCAAGAATGGCAAGTAAACATCAACATCACCAAGCTCTGGAGTGCA 2220
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Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||        2220
Db  2161   CGACGAAGCTGCAAGATTAAACATGATGACAATCCTTTATCGAGCCCGTCCAGACAC        2220

Qy  2221   aacggtggttgatatgaaagatgtgatggtcctgaatgacatcatcgaacaggccgctg     2280
Db         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     2280
Qy  2221   AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTG     2280

Db  2281   gtcggcacagtcggcaagcggatcgcggtctccgttcactatttcccaacagaggacg      2340
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||      2340
Db  2281   GTCGGCACAGTCGGCAAGCGGATCGCGGTGTCCGTTCACTATTTCCCAACAGAGGACG      2340

Db  2341   atgacgaggagcagacgccagcgttcaaagacaaggcactcgaagtgatcctcaaaggcatcg   2400
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     2400
Db  2341   ATGACGAGGAGCAGACGCCAGCGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCG   2400

Db  2401   atgtgttgtgtgggactgttgcgggtttggtgaaatttcaggagtgggtatcgc         2460
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||         2460
Db  2401   ATGTGTTTGTGTGGGACTGTTGCTGGGTTTGGTGAAATTTCAGGAGTGGGTATCGC        2460

Db  2461   tcatcgcttcgatccttcgtcgagctcttcatcacgctgtgcattgtggtcaacacga     2520
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     2520
Db  2461   TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGA    2520

Db  2521   tgttcatgcaatggatcaccacgatatagaacaaggagatggaacgcgtgctcaagagtg    2580
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     2580
Db  2521   TGTTCATGCAATGGATCACCACGATATGAACAAGGAGATGGAACGCGTGCTCAAGAGTG     2580

Db  2581   gcaactattttcttcacgccacctttgccatgagctgaacatctcgacttcattatggccatga   2640
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     2640
Db  2581   GCAACTATTTTCTTCACCGCCACCTTTGCCGATGAGCTGAACATCTTCATTATGGCCATGA     2640

Db  2641   gcccaagtactatttcaggagggctgaaacatctggcccacacttaattactactcgatta    2700
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||      2700
Db  2641   GCCCCAAGTACTATTTCAGGAGGGCTGGAAACATCTTGGCCCACACTTAATTACTATTCGATTA   2700

Db  2701   cgctattggaactggactgagggtgtccaggtctgccgtattgcttccttttcgat        2760
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||        2760
Db  2701   CGCTATTGGAACTGGACTGAGGGTGTCCGAGGGTCTGCCGTATTGCGTTCCTTTTCGAT     2760

Db  2761   tgtgcggtgtattcaagctgttggcccaacttaatttactcatttcgatta            2820
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||             2820
Db  2761   TGCTGCGGTGTATTCAAACTGCTTGGCCCAACTTAATTTACTCATTTCGATTA           2820

Db  2821   tgggacgaccatgggcgcttggtatctggtacttgcattatcatcatcttca            2880
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||            2880
Db  2821   TGGGACGCCACCATGGGCGCTTTGGTATCTGGTAATCATTGTACTTGCATTATCATCTTCA    2880

Db  2881   tctttgcggtgatgggaatgcgacctgttcggaagaattcatgatcatgatcacaaggaccggct   2940
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||      2940
Db  2881   TCTTTGCGGTGATGGGAATGCGGCAACTGTTTCGGAAGAATTATCATGATCACAAGGACCGGCT    2940

Db  2941   ttccggatggcgacctgccgcgcgacttcaccgacttgtgggacgttatgatcg         3000
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||         3000
Db  2941   TTCCGGATGGCGACCTGCCGCGCGACTTCACCGACTTCATGATCG                  3000

Db  3001   tgttccgggtgctctgcgagaatggacggactgggactgcatgtgggcg             3060
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||             3060
Db  3001   TGTTCCCGGGTGCTCTGCGGAGAATGGAATGGGGACTCCATGTGGGCG              3060

Db  3061   atgtctgctgcaataatagccgaggcccttcaatcgaattggccgatttaaaagtt        3120
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||         3120
Db  3061   ATGTCTGCTGCAATATAGCCGAGGCCCTTCAATCGAATTGGCCGATTTAAAAGTT         3120

Db  3121   ccgataacgatacgaataaaatagccggacttaatcgaattgtttcaagttactt         3180
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||         3180
Db  3121   CCGATAACGATACGAATAAAATAGCCGGACTTAATCGAATTGTTTCAGCGCCGACTG      3180

Db  3181   gggttaagcgtaatattgctgattgtttcaagttaatacgtaacaaatgacaaatcaaa     3300
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     3300
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Qy  3241   GGGTTAAGCGCTAATATTGCTGATTGTTTCAAGTTAATACGTAACAAATGACAAATCAA     3300

Db  3301   taagtgatcaacctcagtgagcggaccaaccagtcagttgattggagcgaagagc        3360
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||        3360
Qy  3301   TAAGTGATCAACCATCAGTGAGCGGACCAACCAACCAGATCAGTTGATTTGGAGCGAAGAGC   3360

Db  3361   atggtgcaacgaactggagctggccacgacagatcctcgccgacggcctcatcaaga      3420
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||      3420
Qy  3361   ATGGTGACAACGAACTGGAGCTGGCCACGACGACAGATCCTCGCCGACGCCCTCATCAAGA   3420

Db  3421   agggatcaaggagcagacgcaactggagtggccatcggagtggatcggatggaattcacga   3480
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    3480
Qy  3421   AGGGGATCAAGGAGCAGGCAGACGCAACTGGAGTGGCCATCGGAGTGGATCGGATGGAATTCACGA  3480

Db  3481   tacacggcacatgaagaacaacagccgaagaaatccaaatatctaataacgcaacga      3540
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||      3540
Qy  3481   TACACGGCGACATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAAATAACGCAACGA   3540

Db  3541   tgattggcaactcaattaaccaccaagacaatagactggaacacgagctaaaccatagag   3600
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    3600
Qy  3541   TGATTGGCACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAG    3600

Db  3601   gtttgtccttacaggacgacgacactgccagcattaactcatatggtagccataagaatc   3660
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    3660
Qy  3601   GTTTGTCCTTACAGGACGACGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATC    3660

Db  3661   gaccattcaaggacgacgcccacagggcagcgcccgacggaacgcgaggaggagaagc     3720
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     3720
Qy  3661   GCGACGCCAGCAAGGACGAGAGCAGCGCCCAGACGGAACGCGGAGGGCGGAGGAGAAGC    3720

Db  3721   gcgacgccagcaggagatttagtctcgacaggaactggacgagggcgaatcgy           3780
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||           3780
Qy  3721   GCGACGCCGCCGCTCGGCAGGATTTAGTCTCGCAGGAGGAGGACTGGACGAGGGAATGCG    3780

Db  3781   aggagggcccgctcgacggtgtatcattattcatgcacgacgaggataactactcgatg    3840
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    3840
Qy  3781   AGGAGGGCGCCGCTCGACGGTGATATCATTCATGCACACGACGAGGATATACTCGATG     3840

Db  3841   aatatccagctgattgctgcccccgattcgtactataagaaatttccgatcttagccggtg   3900
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    3900
Qy  3841   AATATCCAGCTGATTGCTGCGCCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG  3900

Db  3901   acatgatccgccgttcgcaaggatgggcaatttacgactgaaaacttttcaattaa        3960
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||        3960
Qy  3901   ACGATGACCTGCCCGTTCGCAAGGATGGGCAATTTACGACTGAAAACTTTCAATTAA      3960

Db  3961   ttgaaaataaatatttgaaacagctgttatcactgatgatttaatgagtagctagctt    4020
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     4020
Qy  3961   TTGAAAATAAATATTTGAAACAGCTGTTATCACTGATGATTTAATGAGTAGCTTAGCTT   4020

Db  4021   tggcattagaagtgtacatctgccacaaagacccatactgcaggatatttatactata     4080
Qy         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     4080
Qy  4021   TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTATACTATA    4080

Db  4081   tggacagaatatttacggttatattcttcttgaaaatgttaateaagtgttggcgctcg    4140
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     4140
Qy  4081   TGGACAGAATATTTACGGTTATATTCTTCTTGAAATGTTAATCAGTGTTGGCGCTCG     4140

Db  4141   gcttcaaagtgtacttcaccttcgttgctcaacttgttggagccttcaagcctttcaagc   4200
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    4200
Qy  4141   GCTTCAAAGTGTACTTCACCTTCGTTGCTTCACTTGTTGGAGCCTTCAAGCCTTCAAGACTA  4200

Db  4201   cgcttatcaacttcgttgctcacttgttgctattcaagatggttgtattcgtcgcgctcg   4260
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    4260
Qy  4201   CGCTTATCATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTGTATTCAAGCCTTCAAGACTA  4260

Db  4261   tgcgaacgttaagagcactgagaccactacgtgccatgtcccgtatgcagggcatgaggg   4320
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    4320
Qy  4261   TGCGAACGTTAAGAGCACTGAGAACCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGG  4320

Db  4321   tcgtcgttaatgcgctggtacaagctatacgtccatcttcaatgtgcattggtgtgtc     4380
Qy         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||     4380
Qy  4321   TCGTCGTTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCATTGGTGTGTC    4380
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Db  4381 taatattttggctaattttgtgccataatgggtgtacagctttttgctgtgaaaatatttta 4440
         |||||||| ||||| ||||||||||||||||||||||||||| ||||||||||||||||||
Qy  4381 TAATATTTTGGCTAATTTTGGCCATAATGGGTGTACAGCTTTTGCTGTGAAAATATTTTA  4440

Db  4441 agtgcgaggacatgaatgcacgaagctcagccagccacgagatcatacccacgagatcgcaatgcct 4500
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Qy  4441 AGTGCGGAGACATGAATGCACGAGCTCAGCCAGCCACGAGATCATACCCACGAAATCGCAATGCCT  4500

Db  4501 gcgagaggcagaactacacgtgggtgaattcagcaatgaattcgatcatcgtagtaacg 4560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4501 GCGAGAGGCAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATCGTAGTAACG  4560

Db  4561 cgtatctgccttttccaagtggccaccttcaaaggctggatacaaatcatgaacgatg 4620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4561 CGTATCTGCCTTTTCCAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG  4620

Db  4621 ctatcgattcacgagaggtggacaagcaaccaattcgtgaaacgaacatctacatgtatt 4680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4621 CTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT  4680

Db  4681 tatatttcgtattcttcatcatattggatccttttcacactcaatctgttcattggtg 4740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4681 TATATTTCGTATTCTTCATCATATTGGATCCTTTTCACACTCAATCTGTTCATTGGTG  4740

Db  4741 ttatcattgataatttaatgagcaaagaaaaagcaggtgatcattagaaatgttca 4800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4741 TTATCATTGATAATTTAATGAGCAAAGAAAAAGCAGGTGGATCATTAGAAATGTTCA  4800

Db  4801 tgacgaagatcagaaaaagtactatatatgctatgaaaagatggcctaaaaaccat 4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4801 TGACGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGCTCTAAAAAACCAT  4860

Db  4861 taaaagccattccagaccaaggtggcgaccacaagcaatagtctttgaaatagtaaccg 4920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCAATAGTCTTTGAAATAGTAACCG  4920

Db  4921 ataagaaattcgatataatcattatgttattccgtcctagactatctcaatgcgatat 4980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4921 ATAAGAAATTCGATATAATCATTATGTTATTCATTGTCGAACATGTTCAACCATGACCC  4980

Db  4981 tcgatcttacgatgctgctcagttccgaatgctctagactatctcaatgcgatat 5040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4981 TCGATCGTTACGATGCCTCGGACACGTATAAACGCGTATAACGTAGACTATCGCGATAT  5040

Db  5041 tcgtagttatttcagttccgaatgtctattaaatattcgctttacgatatcactatt 5100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5041 TCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAATATTCGCTTTACGATATCACTATT  5100

Db  5101 ttattgagcactggaatttatttgatgtagttagttcgtcattttatccatccttagttcttg 5160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5101 TTATTGAGCCATGGAATTTATTTGATGTAGTTAGTTGTCATTTTATCCATCCTTAGGTCTTG  5160

Db  5161 tacttagcgatattatcgagaagtacttcgtcgtgtccgaccccgcttccgagttccgagtgtgtg 5220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5161 TACTTAGCGATATTATCGAGAAGTACTTCGTCGTGTCCGACCCCGCTTCCGAGTTCCGAGTGTG  5220

Db  5221 tggcgaaagtgggccgtgtccttcgactggtgaagggagccaaggccattccggacactgc 5280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5221 TGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGGAGCCAAGGCCATTCCGGACACTGC  5280

Db  5281 tcttcggttggccatgtgggccatgtccgcggcccctgttcaacatctgcctgttcctgg 5340
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Qy  5281 TCTTCGGTTGGCCATGTGGGCCATGTCCGCGGCCCGTGTTCAACATCTGCCTGTTCCTGG  5340

Db  5341 tcatgttcatctttgcccattttggcgattttcggacatgtcgttcttcatgcacgtgaagagagcg 5400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5341 TCTTCATGTTCATCTTTGCCCATTTTGGCCATGTCGTTCTTCATGCACGTGAAGAGAGGACG  5400

Db  5401 gcattaacgacgtctcacaactttggccagagcaatgatcctgctcttcca  5460
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5401 GCATTAACGACGTCTACAACTTCAAGAACCTTTGGCCAGCAATGATCCTGCTCTTCAGA  5460
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Db  5461 tgtcgacgtcagccggttgggatggtgtactgacgacgccattatcaatgagaggaagcatgcg 5520
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Qy  5461 TGTCGACGTCAGCCGGTTGGGATGGTGTACTGACGACGCCATTATCAATGAGGAGCATGCG  5520

Db  5521 atccaccgacagcgacaaaggctatccggcaattggttcagcgaacttggaataa 5580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5521 ATCCACCGACAGCGACAAAGGCTATCCGGCAATTGGTTCAGCGACCGGTTGGAATAA  5580

Db  5581 cgtttctcctcacctagttataagcttcttttgatagttattaaatagtacattgctg 5640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5581 CGTTTCTCCTCATACCTAGTTATATAAGCTTTTGATAGTTATTAAATAGTACATTGCTG  5640

Db  5641 tcattctgagaactatatcaggccaccgagacgtgcaagagggtcaaccgacacg 5700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5641 TCATTCTGAGAACTATAGTCAGGCCACCGAGACGTGCAAGAGGGTCTAACCGACACG  5700

Db  5701 actacgacatgtactatgagatctggcagcaattcgatctggaggcgcacccagtacatac 5760
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Qy  5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATAC  5760

Db  5761 gctatgatcagctgtccgaattcctggacgtactggaccccccgctgcagatccacaaac 5820
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Qy  5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCGCTGCAGATCCACAAAC  5820

Db  5821 cgaacaagtacaagatcatatcgatggacataccatctgtcgcggtgacctcatgtact 5880
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Qy  5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT  5880

Db  5881 gcgtcgacatcctcgacgccttacgaaagacttcttgcgcccgatacggagggcaatcgatag 5940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5881 GGGTCGACATCCTCGACGCCCTTACGAAAGACTTCTTGCGCCGGAAGGGCAATCGGATAG  5940

Db  5941 aggacaggtgagattggtgagatagcggcccgcccccgatacggagggctacgagcccg 6000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5941 AGGAGACGGGTGAGATTGGTGAGATGGCGGCCCGCCCCCGGATACGGAGGGCTACGAGCCCG  6000

Db  6001 tctcatcaacgctgtggcgtcagcgtgaggagtactgcgcccgcgctaatccagcacgcgcct 6060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6001 TCTCATCAACGCTGTGGCGTCAGCGTGAGGAGTACTGCGCCCGCGCTAATCCAGCACGCGCCT  6060

Db  6061 ggcgaaagcacaaggcgcgcggcggcggcccgccgagggagtggggcggatcatg 6120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6061 GGCGAAAGCACAAGGCGCGCGGCGGCGGCCCGCCGAGGGAGGTGGGTCCTTTGAGCCGGATACGGATCATG  6120

Db  6121 gcgatggcggtgatccgatgcgcccggcgggaccccgcggccgccccgatggcggcgatg 6180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6121 GCGATGGCGGTGATCCGATGCGGCCCGGCGGGACCCCGGCGGCCGCCCGATGGCGGCGATG  6180

Db  6181 cgccccgctcggtggagatggtagtggtgttaacggtactgcgcgatgcgcccgatgccgatg 6240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6181 CGCCCCGCTGGTGGTGGAGATGGTAGTGGTGTTAACGGTTAACGGTACTGCGGGCGATGTGGCCGATG  6240

Db  6241 agagtaatgtaaatagtccgggatggcggcgccagcagcagcagcagcagcagcag 6300
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Qy  6241 AGAGTAATGTAAATAGTAAATAGTCCGGGATGGCGGCGCTGCCAGCAGCAGCAGCAGCAG  6300

Db  6301 cggcggcggcggcggcggcggccccgaggcgccggagtccgggagcgccgggggcgacaga 6360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6301 CGGCGGCGGCGGCGGCGGCGGCCCCGAGGCGCCGGAGTCCCGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGACAGA  6360

Db  6361 ccgccgttctcgttggagacgacgggttcgtgacgaagaaggtgtcatcc 6420
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6361 CCGCCGTTCTCGTTGGAGAGCGACGACGGGGTTCTGACGAAGAACGGCCACAAGGTGGTCATCC  6420

Db  6421 actcgcgatcgccgagcatcacgtcgcggcacgtcgccgatgtctgagcaccaggagcgc 6480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6421 ACTCGCGATCGCCGAGCATCACGTCGCGGCACGTCGCCGATGTCTGCGCACCAGGCCTCGCCCCC  6480

Db  6481 ccctccaagatgcacgcgagttattagctctcaga 6513
         |||||||||||||||||||||||||||||||||
Qy  6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTTCAGA  6513
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RESULT  2
ID   T33238 standard; cDNA; 6513 BP.
AC   T33238;
DT   15-OCT-1996  (first entry)
DE   Drosophila para voltage-activated sodium channel cDNA.
KW   Para voltage-activated sodium channel; cation channel; insecticide;
KW   arachnicide; pesticide; neuroprotective; ischaemia; antagonist;
KW   therapy; monoclonal antibody; ss.
OS   Drosophila melanogaster.
PN   WO9614860-A1.
PD   23-MAY-1996.
PF   06-NOV-1995; U14262.
PR   10-NOV-1994; US-338702.
PA   (MERI ) MERCK & CO INC.
PI   Van Der Ploeg LHT, Warmke JW;
DR   WPI; 96-259563/26.
PT   Mono-specific antibodies to voltage-activated cation channel - also
PT   new cation channel DNA, useful for identifying channel modulators,
PT   potentially useful partic. as insecticide and neuroprotective
PT   agents
PS   Claim 17; Page 39-43; 55pp; English.
CC   A full-length cDNA clone (T33238) codes for the Drosophila para
CC   voltage-activated sodium channel (VASC), a protein responsible for
CC   the fast depolarising phase of the action potential that underlies
CC   electrical signaling in neurons, muscles, etc.  The cDNA clone was
CC   obtd. from 3 overlapping regions of para cDNA isolated by PCR
CC   amplification using primers (see also T33239-44) based on a
CC   published para sequence.  Recombinant host cells (E.coli, yeast
CC   mammalian or insect) expressing the Drosophila para VASC can be
CC   used to identify modulators of insect VASCs, useful as insecticides
CC   and arachnicides.  VASC antagonists can be used as neuroprotective
CC   agents for treatment of ischaemia in humans.
SQ   Sequence 6513 BP;    1681 A;    1548 C;    1702 G;    1582 T;

Query Match             100.0%;  Score 6513;  DB 22;  Length 6513;
Best Local Similarity  100.0%;  Pred. No. 0.00e+00;
Matches 6513; Conservative    0; Mismatches   0; Indels   0; Gaps   0;

Db         1 tctagagcttggccgcatagacaatgacagaagattccgactcgatatctgaggaagaac    60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy         1 TCTAGAGCTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC    60

Db        61 gcagtttgttcgtccctttacccgcgaatcattggtgcaaatcgaacaacgcattgccg   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        61 GCAGTTTGTTCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCATTGCCG   120

Db       121 ctgaacatgaaaagcagaaggaggtggaaaagaagagagagccgagggagagttgccgcat   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       121 CTGAACATGAAAAGCAGAAGGAGGTGGAAAAGAAGAGAGAGCCGAGGGAGAGTTGCCGCAT   180

Db       181 atggtcgcaagaagaaacaaaagaaatccgatatgatgacgagagacgaggatgaaggtc   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       181 ATGGTCGCAAGAAGAAACAAAAGAAATCCGATATGATGACGAGAGACGAGGATGAAGGTC   240

Db       241 cacaaccgatcctcacacttgacacagggtgtgccaataacctgttcgaggcagggcagct   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       241 CACAACCGATCCTCACACTTGACACAGGGTGTGCCAATAACCTGTTCGATTGCAGGGCAGCT   300

Db       301 tccggccggaattggcctccactcctcgaggatatcgatccctactacagcaatgtac   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       301 TCCCGGCCGGAATTGGCCTCCACTCCTCGAGGATATCGATCCCTACTACAGCAATGTAC   360

Db       361 tgcattcgtagttgtaagcaaaggaaaagatatttttcggcttttctgcatcaaaagcaa   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       361 TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTTCGGCTTTTACATTTACATTCGCATC   420

Db       421 tgtgatgctcgatccatcaatccgatacgtcgtgtggccatttacattctagtcgatc   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       421 TGTGGATGCTCGATCCATCAATCCGATACGTCGTGTGGCCCATTTACATTTACATTCTAGTGTCATC   480

Db        81 cattatttcctattcatcatcaccacaattctcgtcaactgacgatcctgatgataatgc   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        81 TTTTCCCTATTCATCATCATCATCACCACAATTCTCGTCAACTGACGATCCTCGATGATAATGC   540
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Db  1621  ttatacaagacaaccagctaccaccacacaccagcagcaccaagctaccaagttcgtaaagtga  1680
          |||||||||  ||||||||||||||||||| ||||||||||||||||| |||||||||||||||
Qy  1621  TTATACAAAGACAACCAGCTACCACCAGCACCACCAAAGTTCGTAAAGTGA              1680

Db  1681  gacgacatccttatccttacctgttcacgttaacatacgcaggggatcacgtagtt        1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681  GCACGACACCTTATCCTTACCTGTTCACCGTTTAACATACGCCAGGGATCACGTAGTT      1740

Db  1741  ctacaagtacacgatacggaacggacgtggccgcctttggtatacccgtagcgatcgta     1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741  CTCACAAGTACACGATACGGAACGGACGTGGCCGCCTTTGACATTTGTACTTGTCATTGTCATTCTCA  1800

Db  1801  agccattggtattgtcaacatatcaggatgccagcagcaacttgccctatgccgacgact     1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801  AGCCATTGGTATTGTCAACATATCAGGATGCCCAGCAGCAACTTGCCCTATGCCGACGACT   1860

Db  1861  cgaattccgtcaccccgatgtccgaagagaatgggcatccatcagtcccgtgtactatg     1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861  CGAATGCCGTCACCCCGATGTCCGGAAGAGAATGGGCCATCATCAGTCCCGTGTACTATG   1920

Db  1921  gcaatcaggtcccgacactcatcgtatacctcgcatcagtcccgaatatcgtatacct     1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921  GCAATCTAGGTCCCGACATCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT     1980

Db  1981  cacatggcgatctactggcgcgtcatgggcatggggccgccaccaatggcggcacca     2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981  CACATGGCGATCTACTGGCGCGTCATGGGCCATGGGGCCGCCACCAATGGCGGCACCA     2040

Db  2041  gcaaattgcgcaaccgaatcacacgcaatcatcagtgggcgccaatggcgcacca      2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041  GCAAATTGCGCAACCGAATCACACGCAATCAATCAGTGGGCGCCAATGGCGCACCA       2100

Db  2101  cctgtctggacacaccatcacacaagtcgatcgcgactacggaagttgggctggagtgca    2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2101  CCTGTCTGGACACCACCAATCACAAGCTCGATCGCGACTACGGAAATTGGGCTGGAGTGCA  2160

Db  2161  cggacgaagctgcaagataaacatcatgacaatcctttatcgagcccgtccagacac      2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161  CGGACGAAGCTGGCAAGATTAAACATCCTTTATCGAGCCCCGTCCAGACAC            2220

Db  2221  aaacggttgatatgaagatgtgatggtcctgaatgacatcatcgaacatgggcgctg      2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221  AAACGGTGGTTGATATGAAGATGTGATGGTCCTGAATGACATGACATCGAACATGGGCCGCTG  2280

Db  2281  gtcggcacagtcgggcaagcgatcgcgggcgtgtctcgttctctattccaacagaggacg    2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281  GTCGGCACAGTCGGGCAAGCGATCGCGGCGTGTCCGTTTTTACTATTTCCCCAACAGAGGACG  2340

Db  2341  atgacgaggatgggccgacgttcaaagacaaggcactcgaagtgatcctcgaaggcatcg     2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341  ATGACGAGGATGGGCCGACGTTCAAAGACACAGGCACTCGAAGTCGTCATCGTTGGTCAACACGA   2400

Db  2401  atgtgtttgtgtgtggactgtcgcgggtgtctcgttcgttgttgttcaggagtgggtatcgc    2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401  ATGTGTTTTGTGTCGTCGTGGACTGCGTGTGTCGGTTTGGTTTTGGTTTGGTTTGTTGAAATTTCGC 2460

Db  2461  tcatcgtcttcgatccctcgtcgagctcttcatcacgctgtcattggtggtcaacacga      2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461  TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCATCACGCTGTCGCATTGGTTGGTCAACACGA  2520

Db  2521  tgttcatggcaatggatcacccacgatcaatgaacaaggagatagggccaccatggccatga    2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521  TGTTCATGGCAATGGATCACCCACGATCATCGAGGCCCATGAGGCCACCATGGCCCATGA    2580

Db  2581  gcaactatttcttcaccgcacctttgccatcgaggacatcttcgacttcattatcgtggccctat     2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581  GCAACTATTTCTTCACCGCCACCTTTGCCATCTTCGAGGACTTAATGGCCATGA         2640

Db  2641  gcccaagtacatttccaggagggttggaacatcttcgacttcattatcgtgggcccctat     2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2641  GCCCAAGTACACTATTTCAGGGAGGGGCTTGGGAGGGGGCTTGGACTTCATTATCGTGGGCCCTAT  2700

Db  2701  cgctattggaactgggactcgagggtgtcgagggtctgtccgtattgcgttccttttcgat  2760
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Qy  2701  CGCTATTGGAACTGGGACTCGAGGGTGTCGAGGGTCTGTCCGTATTGCGTTCCTTTTCGAT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  tgctgcgtgttattcaaactggcaagtcttggcccacacttaatttactcattcgatta    2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2761  TGCTGCGTGATTCAAACTGGCCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTA     2820

Db  2821  tgggacgcaccatggcgctttgggtaatcgacatttgtacttgtcattatcatcttca    2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821  TGGGACGCACCATGGCGCTTTGGGTAATCGACATTTGTACTTGTCATTATCATCTTCA     2880

Db  2881  tctttggctgtggaatgcaactgttcggaaagaattatcatgatcacaaggaccgct     2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881  TCTTTGCGGTGATGGAATGGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCT    2940

Db  2941  ttccgatgtcgtgacctgcgcgctggcccgctggaacttcaccgacttgcacgacttcatgatcg   3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941  TTCCGGATGGCGACCTGCCGCGCTGGAACTTCACCGACTTGCACGCAGCTTCATGATCG    3000

Db  3001  tgttccggtgctctgcggaatgatcagtcgtcatcgtcatcttgtgcatcttgtggtactta  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001  TGTTCCGGGTGCTCTGCGGAATGATCGGGAATGGATCAGTGGGCATCATGGGCATGGGGCCG  3060

Db  3061  atgtctcgtgcattccttcttgtgccaatttggctcatcagcttatcagcgccgactg     3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061  ATGTCTCGTGCAATTCCTGTCGTTTGTCTTTGTCCAATTTGGCTCATTCTAGCTTATCGTGTGTACTTA   3120

Db  3121  acctttcttagcctgctttgtccaatttggctcatcagcttatcagcgccgatttaaaagtt    3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121  ACCTTTCTTAGCCTTGCTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCCGATTAAAAGTT  3180

Db  3181  ccgataacgatacgaataaaatagccgaggccttcaagttaatacgtaacaaatgacaaatcaaa  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181  CCGATAAACGATACGAATAAAATAGCCGAGGCCTTCAATCAATGCAATTTCAATGTAACAAATGACAAAATCAAA  3240

Db  3241  ggttaagctgcaggtaatattgctgattgttcgtgattgtttcaagttaacgtaacaaatcaaa   3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241  GGGTTAAGCTGCAAGTAATATTGCTAATATTGCGTGATTGTTTCAAGTTAATACGTAACAAATGACAAAATTGACAAAAGTT 3300

Db  3301  taagtgatcaaccatcagttgagaggaccaaccagtcagttggatttggagcgaagagc   3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301  TAAGTGATCAACCATCAGTGGAGGACCAACCAGATCAGTTCGGGAAGTTCGGAATCAGTGGCAGGACCAACCAGATCAGTTCGGATTTGGAGCGAAGAGC  3360

Db  3361  atggtgacaacgaactgggagctggacgctggaggggtggccatcgaggtgccatcggggatg  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361  ATGGTGACAACGAACTGGGAGCTGGACGCTGGAGGGGTGGCCATCGAGGTGGCCATCGGGGATG  3420

Db  3421  agggatcaggagcagagcagaccaactggaggtggccatggggatcggggatcggatcggaattcacga  3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421  AGGGGATCAGGAGCAGAGCAGCAACTGGAGGGGTGGCCATCGGGGATCGGATCGGAATTCACGA  3480

Db  3481  tacacggcgacatgaagaacaagccgaagaaatccaaatatctaataacgcaacga    3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481  TACACGGCGACATGAAGAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA     3540

Db  3541  tgattggcaactcaattaaccaccaagaacaatagactggaacaccatataaaccataag  3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3541  TGATTGGCAACTCAATTAACCACCAAGAACAATAGACTGGAACACCATAAAAACCATAGAG    3600

Db  3601  gtttgtccttacgacgacgaggattcaggtcttcaggcattaactcatatggtagccataagaatc  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601  GTTTGTCCTTACGGACGACGAGGAGGATTTAGGTCTTCAGGCATTAACTCATATGGTAGCCATAAGAATC  3660

Db  3661  gaccattcaaggacgaggaggccaccatgccaccatgga                        3720
          |||||||||||||||||||||||||||||||||||||||
Qy  3661  GACCATTCAAGGACGCAGGGCCCAGAGGGCCCAGGAGGCCCATGA                 3720

Db  3721  gcgacgccagcaaggaggattaggtctcggacgagcagagggccgaggaggcggaatgcg   3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3721  GCGACGCCAGCAAGGAGGACGAGAGCGCCGAGGGAACTGGACGGACGGAAGGCGGAGGAGAAGC  3780

Db  3781  aggaggcgccgctgcacgcgatgatcattattcatgcacgacgagatactcgatg        3840
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Qy   3781 AGGAGGGCCCGCTCGACGGTGATAATCATTATTCATGCACACGACCAGGATATACTCGATG 3840

Db   3841 aatatccagctgattgctgcccgattcgtactataagaaatttcgatccttagccggtg   3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3841 AATATCCAGCTGATTGCTGCCCGATTCGTACTATAAGAAATTTCCGATCCTTAGCCGGGTG 3900

Db   3901 acgatgactcgcgttctggcaaggatggggcaatttacgactgaaaacttttcaattaa   3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3901 ACGATGACTCGCCGTTCGGCAAGGATGGGGCAATTTACGACTGAAAACTTTCAATTAA    3960

Db   3961 ttgaaaataaatatttgaaacagctgttatcactatgatttttattgagtagcttagctt 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3961 TTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTTACGATATCACTATT      4020

Db   4021 tggcattagaagatgtacatctgccacaaagacccatctgcaggatatttttatactata 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4021 TGGCCATTAGAAGATGTACATTCGCTGCCACAAAGACCCCATACTGCAGGATATTTATACTATA 4080

Db   4081 tggacagaatatttacggttatattcttcttggaaatgttaatcaagtggttggcgctcg 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4081 TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140

Db   4141 gcttcaaagtgtacttcaccaacgcgtggtgttggctcgatttcgtgattgtcatggtat 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4141 GCTTCAAAGTGTACTTCACCAACGCGTGGTGTTGGCTCGATTTCGTGATTGTCATGGTAT 4200

Db   4201 cgcttatcaacttcgttgcttcacttgttggagctcgtggtattcaagccttcaagacta 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTCGTGGTATTCAAGCCTTCAAGACTA 4260

Db   4261 tgcgaacgttaagagcactgagaccactacgtgccatgtcccgtatgccatgtgcgaggg 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4261 TGCGGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCCATGGGCATGAGGGG 4320

Db   4321 tcgtcgttaatgcgcgtggtacaagctataccgtccatcttcaagtgtcattggtcgtgtc 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4321 TCGTCGTTAATGCGCGTGGTACAAGCTATACCGTCCATCTTCAAGTGCTATTGGTGTGTC 4380

Db   4381 taatattttggctaatttttgccataatggtgtacagctttttgctggaaatatttta   4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4381 TAATATTTTGGCTAATTTTTGCCATAATGGTGTACAGCTTTTTGCTGGAAAATATTTTA   4440

Db   4441 agtgcgaggacataagtgaatggcacgagctcagcacgccgagatcatcaccaatcgcaatgcct 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4441 AGTGCGAGGACATGAATGGCACGAGGTGCACGAGCTCACGCAAAGGCTCAGCCAGTTGGAATAA 4500

Db   4501 gcgagagcggagaactacacgtgggtgaattcagcaatgacaatcatcgtgatcatgtaggtaacg 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4501 GCGAGAGCGGAGAACTACACGTGGGTGAATTCAGCAATGAATTTCAGCATCATGTAGGTAACG 4560

Db   4561 cgtatcctgtgcctttccaagtggccacctcaaaggctggatacaaatcatgaacgatg 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4561 CGTATCCTGTGCCTTTTCCAAGTGGCCACCTCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620

Db   4621 ctatcgattcacggaggttggacaagcaaccaattcgtgaaacgaacatctacatgtatt 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4621 CTATCGATTCACGGAGGTTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680

Db   4681 tatatttcgtattcttcatcatatttggatcctttttcacactcaatcgtcttcattggtg 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTTCACACTCAATCGTGTTCATTGGTG 4740

Db   4741 ttatcattgataattttaatgagcaaaagacaggtgagatcattagaaatgttca      4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4741 TTATCATTGATAATTTTAATGAGCAAAAGACAGGTGGATCATTAGAAATGTTCA      4800

Db   4801 tgacagagatcagaaagtactataatcgtctatgaaaagatggcctcaaaaaaccat   4860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4801 TGACAGAGATCAGAAAGTACTATAATCGTCTATGAAAGATGGCCTCAAAAAACCAT     4860

Db   4861 taaaagccattccaagaccaaggtggcgaccacaagcaatacaataagagttctttgaaatagtaaccg 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACAAGCAATACAATAGTCTTTGAAAATAGTAACCG 4920

Db   4921 ataagaaattcgatataatcattatgtttattcattggtcgtcgaacatgttcaccatgtaccc   4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4921 ATAAGAAATTCGATATAATCATTATGTTATTCATTGGTCGTCGAACATGTTCACCATGACCC     4980

Db   4981 tcgatcgttacgatgcgtcggacacgtataacgcgtcctagactatctcaatgcgatat 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4981 TCGATCGTTACGATGCGTCGGACACGTATAACGCGTCCTAGACTATCTCAATGCGATAT 5040

Db   5041 tcgtagttatttcagttccgaatgtctattaaaaatattcgcttacgatatcactactt 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5041 TCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATT 5100

Db   5101 ttattgagccatgcatgatttttgatgatgtagtagttgtcatttttatccatcttaggtcttg 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5101 TTATTGAGCCATGCCATGGAATTTTATTTATTTGATGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTG 5160

Db   5161 tacttagcgatattatcgagaagtacttcgtcgcgacccgtgctcccgagtggtgcgtg 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5161 TACTTAGCGATATTATCGAGAAGTACTTCGTCGCGCCGCCCTGTCCGCGGCCCTCCGGAGTGGTGCGTG 5220

Db   5221 tggcgaaagtgggccgtgtccttgcactggtgaagggaggccaagggcattcggacactgc 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5221 TGGCGAAAGTGGGCCCGTGTCCTTGCACTGGTGAAGGGAGGCCAAGGGCATTCGGACACTGC 5280

Db   5281 tcttcgcgttggccatgtcgtcgcggccctgttcaacactcgtcgctcgtctgtcctgg 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5281 TCTTCGCGGTTGGCCATGTCGTCGCGGCCCTGTTCAACATCTCGCCTGCTCGTCGTTCCTGG 5340

Db   5341 tcatgtcatctttgccatttcggcatgtgttcttcatgcacgtgttcttcatgcacctggc 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5341 TCATGTTCATCTTTGCCATTTCCATTTCGGCACGTCGTCGTTCATGCACGTGTCGTTCATGCAGA 5400

Db   5401 gcattaacgacgtcacaacttcaagacctttggccagagcacatgatcctgctctttcaga 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGGGCCAGAGCCATGCATGATGATCCTGCTCTTTCAGA 5460

Db   5461 tgtcgacgtcagcgcggtggatgtgtactggacgccattatcaatgagaagcatgcg  5520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5461 TGTCGACGTCAGCGCCGGTGGGATGTGTACTGGACGCCATTATCAATGAGGAAGCATGCG    5520

Db   5521 atccaccgacagcgacaaaggctatccgggcaattgtggttcagcgacccttggaataa  5580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5521 ATCCACCGACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCCGTTGGAATAA  5580

Db   5581 cgtttctcctcctcagttataagcttttgatagttattaatatgtacattgctg    5640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5581 CGTTTCTCCTCCTCAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTG      5640

Db   5641 tcattcctgagaactagtagtcagccaccgaggctgcaagagggtctaaccgacacg  5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5641 TCATTCCTGAGAACTAGTGTCCAGCCACCGAGGCGCAAGAGGGTCAAGGTCTAACCGACGACG  5700

Db   5701 actacgacatgtcatatgagatctggcagccaattcgtggatcgatccgcgagtacatac  5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5701 ACTACGACATGTCATATGAGATCTGGCAGCCAATTCGGATCGATCCGGAGGGCCACCCAGTACATAC 5760

Db   5761 gctatgatcagctgtccgaattcctggacgtactggagccccgctgcgagatccacaaac 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCGCTGCGAGATCCACAAAC 5820

Db   5821 cgaacaagtacaagatcatatcgaatcggacatacccatctgtcgcggtgacctcatgtact 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5821 CGAACAAGTACAAGATCATATCGAATGGACATACCCATCTGTCGCGGTGACCTGACCTCATGTACT 5880

Db   5881 gcgtcgacactcctcgacgcctccgaaaggacttctttcgcggtcgcggttcaatccgatg 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5881 GCGTCGACATCCTCGACGCGCCCGAAAGGACTTCTTTCGCGGTCGCGGTTCAATCCGATG 5940

Db   5941 aggagacgggtgagattggtgagataccgggcagagcggccgccgccgatacgcggagcccg 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5941 AGGAGACGGTGAGATTGGTGAGATACCGGGCAGAGCGGCCGCCGCCGATACGCGGAGGGGCTACGAGCCCG 6000

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Matches   1178; Conservative   0; Mismatches 646; Indels  30; Gaps  19;

Db  3927 ggacaagatgttcacctacgtcttgtgttggagatgctggtgctcaagtgggtggcctacgg 3986
         ||||||   ||- ||-|| ||-||||| ||| ||  ||-||||-|| ||||| |||  |||
Qy  4082 GGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCCGG 4141

Db  3987 cttcaagaagtacttcaccacgccctggtgctggctggacttcctgattgtggacgtctc 4046
         |||||| |-|| ||| || |||-|||  ||-|||||| ||- |||||  ||  |||  ||
Qy  4142 CTTCAAAGTGTACTTCACCAACGCCGTGGTGTGGCTCGATTCGTCGATTGTCATGGTATC 4201

Db  4047 gctggtcagcctcgtggcaaacacacttaggcttcgccgaaatgggtcccatcaagtcact 4106
         |||||| | | -||-||  ||-|| ||| || |||||-|| ||- ||| ||||| |-| ||
Qy  4202 GCTTATCAACTTCGTTGCTTCACTTGTGGTGGTATTCAAGCCTTCAAGACTAT 4261

Db  4107 gaggacactgcgtgcacttcgaccctgagggccttgtcgagattgagggcatgcgggt 4166
         | |||| ||-|| || ||-|| ||-|||-|| ||||| || ||| |||| |||||| |
Qy  4262 GCGAACGTTAAGGACACTGAGACCACTACGTGCCCATGTCCCGTATGCAGGGCATGAGGGT 4321

Db  4167 ggtggtcaatgcgctggtggggcgcatcccctcccatcatgaacgtcctcctcgtcgcct 4226
         |||  |||| ||-|| || -|||-|| || -||-|||- || |||||| |||| ||||-|
Qy  4322 CGTCGTTAATGCCCTGGTACAAGCTATACCGTCCCATCTTCAATGTCCTATTGGTGTGTCT 4381

Db  4227 catcttcgctcatctcagcatcatggcgtgaacctcttcgccggaagttcgtag 4286
         |||||- ||  ||  -|| | || |-|| ||  |-||- | ||  || |||| |
Qy  4382 AATATTTTGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTGCTGGAAAATATTTTAA 4441

Db  4287 gtgcatcaacagacagaagggaacctgccctgaactacacaccatcgtgaacaacaagag 4346
         |||||- | | -|| |   ||| || || -|  ||-|| ||-|||-|| ||   | ||||
Qy  4442 GTGCGAGGAC---AT-GAATGGCACGAAGCTCAGC-C-ACGAGATCATACCAAATCCCAA 4495

Db  4347 tgagtgcgagtcctcaacgtgaccggagagttgtactggacaaggtgaggtcaactt 4406
         ||-||| ||-|| -||-|| ||| ||  | |||-|||-|| | || ||| |||| ||
Qy  4496 TGCCTGCGAGCGAGAAC-T-ACACGTGGGT-GAATTC-AGCAA--TGAATTCGA--- 4546

Db  4407 tgacaacgtgggagccgggtacctgccctccctgcagtggcgacatttaaaggctggat 4466
         || |||||-||| ||-||-|| || ||- || -|-|| |||  | ||  ||||| ||||
Qy  4547 T--CAT-GTAGGTAACGCGTATCGTGTGCTTTTCCAAGTGGCCACCTTCAAAGGCTGGAT 4603

Db  4467 ggacatcatgtatgcggctgtggactccagaggggtatgaggacggcagccgcagtgggaaga 4526
         ||||  |   |  |||- || || |-||||| ||| ||-|||  ||   |-||-|||| ||| |
Qy  4604 ACAAATCATGAACGATGCTATCGATTCAGAGAGGTGGACAAGCAACCAATTCGTGAAAC 4663

Db  4527 caacctcacatgtacatctactttgtcgtctcatcatcttcggctgtccttcttcaccct 4586
         ||||  | |||-||-||||||   ||  |-| | ||-||   ||| || || || |||
Qy  4664 GAACATCTACATGTATATTATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACT 4723

Db  4587 caacctcttcatcggtgtcatcattgacaacttcaaccagcagagaaagaaaagtagggg 4646
         ||| || |||| || ||-|| |-||||  |||-||||  || || ||| ||| |||||-
Qy  4724 CAATCTGTTCATTGGTGTTATCATCATTGATAATTTTAATGAGCAAAGAAAAGCAGGTGG 4783

Db  4647 c-cag--gatatcttcatgacggaggagcagaagaagtactacaatgccatgaagaagct 4703
           ||-  || |-|||||| | || |||  || |  -||-|| || ||  ||||| ||| |
Qy  4784 ATCATTAGAAATGTTCATGACAGAAGATCAGAAGAAAGTACTATAATGCTATGAAAAAGAT 4843

Db  4704 gggctcccagaaacccagaagcccatccacagcagatacccgacaagtaccagggtttcat 4763
         ||||| ||| ||-|| || |||| |||-|-||  |||  ||| ||-|| |||  | |||
Qy  4844 GGGCTCTAAAAACCATTAAAAACCATTCAACAGACCAACCAAGGTGGCCACCAAGCAATAGT 4903

Db  4764 attcgacattgaccaagcaggccttgatgtcaccatcatgttcctcatctgtttgaa 4823
         |||||| |||| ||||| |||  || || ||-||-||  |-|||-|||-|  |||||
Qy  4904 CTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTATATGTTCATTGGTCTGAA 4963

Db  4824 catggtgaccatgatggtggagacagatgaccagagccctcgagaagtcaacatcttggc 4883
         ||||| || || ||-|| |||  | || |-|  || ||-||| ||  ||   ||-|| ||
Qy  4964 CATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGACACGTATAACCGCGGTCCTAGA 5023

Db  4884 caagatacaacctgctcttcgttgtccatcttcacaggcgagtgtattgtcaagatggctgc 4943
         ||| |-||||| |- |||| || |-|  ||| |||  |||  |-| |||||  ||| || |
Qy  5024 CTATCTCAATGCGATATTCGTAGTTATTTCAGTTCGTCCGAATGTCATTAAAATATTCGC 5083

Db  4944 cctgcgccactattacttcaccaacagcagctgaacatcttcgactttgtggtcatcct 5003
         |||| || |||-|| |||-|| ||| |||  |-|| |||-||-|||  |-|||| |||-||
Qy  5084 TTTACGATCACTATTTATTGAGCCATGGAATTGATTAGTAGTGTCATTTT 5143
```

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Db  6001 tctcatcaacgctgtgggctgagcgtcagcgtgaggagtactgcgcccggctaatccagcacgcct 6060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6001 TCTCATCAACGCTGTGGGCTCAGCGTGAGGAGTACTGCGCCCGGCTAATCCAGCACGCCCT 6060

Db  6061 ggcgaaagcacaaggcgcgcggcgcggaggaggtggtccttgagccggatacggatcatg 6120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6061 GGCGAAAGCACAAGGCGCGCGGCGCGGAGGAGGTGGTCCTTGAGCCGGATACGGATCATG 6120

Db  6121 gcgatggcggtgatccggatgcgcccggccggcgcccgatgaagcaacggacggcgcgatg 6180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6121 GCGATGGCGGTGATCCGGATGCGCCCGGCACCCGGCGCCCGATGAAGCAACGGACGGCGATG 6180

Db  6181 cgcccgctggtggagatggtagtgttaacggtactgcagaaggagctgccgatgccgatg 6240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6181 CGCCCGCTGGTGGAGATGGTAGTGTTAACGGTACTGCAGAAGGAGCTGCCGATGCCGATG 6240

Db  6241 agagtaatgtaaatagtccgggtgaggatgcagcggcgcggcgcagcagcagcagccag 6300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6241 AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCGGCGCGGCGCAGCAGCAGCAGCCAG 6300

Db  6301 cgcggcggcggcggcgacgacgacgacgcggggaagtcccgggagcggtagcgcgggcgacaga 6360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6301 CGGCGGCGGCGGCGACGACGACGACGCGGGGAAGTCCCGGGAGTCCCGGAGCGGCGGCGGACAGA 6360

Db  6361 ccgcgttctcgtggagagcgacgggttcgtgacgaagaacggccacaaggtggtcatcc 6420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6361 CCGCCGGTTCTCGTGGAGAGCGACGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC 6420

Db  6421 actcgcgatccgcgagcatcacgtcgcgcacgcgcacggccgatctgagccaggcctcgcccc 6480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6421 ACTCGCGATCGCCGAGCATCACGTCGCGCACGCGCGGCCGATGTCTGAGCCAGGCCTCGCCCC 6480

Db  6481 ccctccaagatcacgcgagtattagctctaga 6513
         ||||||||||||||||||||||||||||||||
Qy  6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513
```

RESULT   3
ID   Q81328  standard; cDNA; 7555 BP.
AC   Q81328;
DT   05-AUG-1995  (first entry)
DE   Cardiac sodium channel protein coding sequence.
KW   Sodium channel protein; ds; therapeutic; diagnostic; prognostic;
KW   antiarrythmic; cardiant; cardioglycoside; pRH3-1; pRH4-23; pRH14-31.
OS   Rattus rattus.
FH   Key         Location/Qualifiers
FT   cds         196..6253
FT               /*tag=  a
PN   US5380836-A.
PD   10-JAN-1995.
PF   13-FEB-1989;  331330.
PR   13-FEB-1989;  US-331330.
PR   30-SEP-1991;  US-768107.
PA   (ARCH-) ARCH DEV CORP.
PI   Rogart RB;
DR   WPI; 95-060381/08.
DR   P-PSDB; R67913.
PT   Purified DNA's encoding rat and human cardiac sodium channel
PT   protein - useful for recombinant expression to produce sodium
PT   channel proteins.
PS   Claim 8; Fig 1a-1n; 39pp; English.
CC   The cDNA is derived from 3 overlapping cDNA clones, designated
CC   plasmid pRH3-1 (ATCC 67885), plasmid pRH4-23 (ATCC 67886) and
CC   plasmid pRH14-31 (ATCC 67887). A virus/circular DNA plasmid vector
CC   comprising the cDNA may be transformed or transfected into a
CC   prokaryote/eukaryote host cell, and the resulting recombinant sodium
CC   channel protein has various therapeutic, diagnostic and prognostic
CC   uses.  It may also be used to develop more effective antiarrythmic,
CC   cardiant and cardioglycoside drugs.
SQ   Sequence 7555 BP;  1577 A;    2309 C;    2103 G;    1566 T;

Query Match        5.4%;    Score 352;  DB 13;  Length 7555;
Best Local Similarity 63.5%;  Pred. No. 3.19e-221;
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CC   The sequence is derived from 3 overlapping clones, pRH3-1,pRH4-23,
CC   and pRH4-31. (Deposited as ATCC 67885, 67886, and 67887 resp.)
CC   The clones were isolated from a cDNA library in the lambda zap
CC   vector prepd. from mRNA obtd. from newborn rat hearts using rat
CC   brain II cDNA probe. The isolated DNA can be used to screen a
CC   similar human derived cardiac cDNA library for the corresponding
CC   human gene. Proteins produced by expression of the DNA have
CC   diagnostic therapeutic, and prognostic applications.
SQ   Sequence 7555 BP;   1576 A;   2314 C;   2101 G;   1564 T;

Query Match            5.3%;   Score 344;  DB 1;  Length 7555;
Best Local Similarity 63.3%;   Pred. No. 1.63e-215;
Matches 1174;  Conservative 0;  Mismatches 650;  Indels 30;  Gaps 19;
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Db  3927 ggacaagatgttcacctacgtctttgtgttggagatgctgctcaagtggtggtgcctacgg 3986
          |||| ||  |   |||| ||  | || | || | |||| ||| | |||||||| || || ||
Qy  4082 GGACAGAAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGG 4141

Db  3987 cttcaagaagtacttcaccaacgctgtggtgctggacttcctgggtgatggtggacgtctc 4046
          ||||||  | ||||||||||| | ||||||| |||| |  | | | |||| | |||| |||
Qy  4142 CTTCAAAGTGACTTCACCAACGGCGTGGTGTTGGCTCGATTTCGTGGATTGTCATGGTATC 4201

Db  4047 gctgtcagcctcgtcgtggcaaacacccttaggcttcgccgaaatggtcccatcaagtcact 4106
          ||| | | || ||  | || ||||  |  |  |||| | || || || || ||| | |||||
Qy  4202 GCTTATCAACTTCGTGCTTCACTTGTTGGAGCTGGTGGTATTCAAGCCTTCAAGACTAT 4261

Db  4107 gaggacactgcgtgcacttcgacttcgagaccctggtcgagatttgagggcatgcgggggt 4166
          | |||||| || | |  | | ||  | |||||| | ||| ||||| | ||||||| ||| |
Qy  4262 GCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCGTATGCAGGGCATGAGGGT 4321

Db  4167 ggtggtcaatgcgcttgtggggccgccatccccatcatgaacgtgtctcctcgtctgtcct 4226
          | | || || || |||| | |  || |||  | ||  |||| |||| |||  | ||| | |
Qy  4322 CGTCGTTAATGCCGTGGTACAAGCTATACCGTCCCATCTTCAATGTGCTATTGGTGTGTCT 4381

Db  4227 catcttctggctcatcttcagcatcatggggctgaacctcttcgccggagttcggtag 4286
          | | ||| |||| ||| ||| || | ||||  || ||| ||| |||  | | ||| |
Qy  4382 AATATTTTGGCTAATTTTGCCATAAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTAA 4441

Db  4287 gtgcatcaaccagcagagagggacctggcctgccatcgtgactacaccatcgtgaacaacaagag 4346
          ||||  |||| | |    | | | || || |||| | |    | ||| || ||| |||||
Qy  4442 GTGCGAGGAC---AT-GAATGCACCAAGCTCAGC-C-ACGAGATCATACCAAATCGCAA 4495

Db  4347 tgagtgcgagtccttcaacgtgaccggagagttgtactggacaagtgaagtcaactt 4406
          |   |||| ||  | | ||| | || | || |||||| | ||||| |||| |||  |
Qy  4496 TGCCTGCGGAGCGCGAGAAC-T-ACACGTGGGT-GAATTC-AGCAA--TGAATTCGA--- 4546

Db  4407 tgacaacgtgggagccgggtacctggcccctcctgcaggtggcgcgacatttaaaggctggat 4466
          |   | | | || | | | || || ||  | || |||| | |  |||||||||| |||||
Qy  4547 T--CAT-GTAGGTAACGCGGTATCTGTCCTTTCCAAGTGCCACCTTCAAAGGCTGGAT 4603

Db  4467 ggacatcatgtatgcggctggctgggactccaggaggtgtatgagaggagcagccgcagtgggaaga 4526
          | ||| |||| || |   |   || ||| |||| |||||| | ||| |||| |||||||| ||||| |
Qy  4604 ACAAATCATGAACAGCTATCGATTCACGAGAGGTGGACAAGCAAGCAACCAATTCGTGAAAC 4663
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Db  4527 caacctctacatgtacatctacttgtcgtcttcatcatctccggtctcctccttccacct 4586
          ||| ||||| ||||| ||| | ||||| |||||||| | || |||| ||  | || ||| |
Qy  4664 GAACATCTACACATGTATTATATTTCGTATTCTTCATCAATTTTGGATCCTTTTCACACT 4723

Db  4587 caacctcttcatcggtgtcatcattgtcgtcttcaaccagcagaagaaagtagggg 4646
          |||| || || || | || | || ||| ||||  |  ||  | |||||| || |||
Qy  4724 CAATCTGTTCATTGTGTTGTTATCATGATAATTTAATGAGCAAAGAAGAAAAGCAGGTGG 4783

Db  4647 c-cag--gatatcttcatgacgaggagaggagaagtactacaatgccatgaagaagagct 4703
          | ||   || ||||| | || | ||||  ||||| |||||| |  || || ||||| ||
Qy  4784 ATCATTAGAAATGTTCAGAGACAGAGATCAGAAAGAGTTACTATAATGTCTAGAAAAGAT 4843

Db  4704 gggctccaagaaacccagaagcccatcccacgccctgaacaagtaccaggttcat 4763
          ||||| |||| |||| | ||||  |||| | || ||||||| | |||||| |||
Qy  4844 GGGCTCTAAAAAACCATTAAAAGCCATTCCAAGACCAAGGTGCGACCAAGCAATAGT 4903

Db  4764 attcgacattgtgaccaagcagccttgactgatgtcaccatcatgtgtcctgtttgaa 4823
          |||||| || || ||  | ||    | |  || ||| |||| | | | |  | ||||||
Qy  4904 CTTTGAAATAGTAACCGATAAGAAAATTCGATAATAATCATTATTGTTATTCATTGGTCTGAA 4963
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Db  5004 ctccattgttggcactgtcctctccgacatcatccagaagtacttcttctcccgacact 5063
          || |||| | ||  | ||  | || ||| | ||| ||||| ||| |||| ||| ||| |
Qy  5144 ATCCACTTAGGTCTTGTACTTAGCGAATTATCCGAATTATCCGAAGAAGTACTTCGTCTCGCGCCACCCT 5203

Db  5064 cttccggtcatccgctgccaggatcggccgcatcctcaggctgatccggcgcggagccaa 5123
          ||||| ||| || | ||||   || | || | ||| || ||| | |||| ||| |||||
Qy  5204 GCTCCGAGTGGTGCGTGCGTGGCGAAAGTGGGCCGGTGTCCTTCGACTGGTGAAGGGAGCCAA 5263

Db  5124 ggggattccacgcagtgctcttcgccctcatgatgtcctgcgcgccctcttcaacatcgg 5183
          ||| ||| | || | |||||||||| | || |||||| || || || ||||| |||| |
Qy  5264 GGGCATTCGGACACTGCTCTTCGCCGGTTGGCCATGTCGCCGCGCCCTGTTCAACATCTG 5323

Db  5184 cctcctcctctgcatgttcatctactctcatctccatcttcggcatggccatgtcgttcttcatgca 5243
          ||| || || |||||||||| || |  | |||||||||| ||| |||| |||||||||| ||||||||
Qy  5324 CCTGCTGCTTGCTCCTGGTCATGTTCATCTTTCGGCACATGTCGTTCTTCATGCA 5383

Db  5244 cgtcaagtgggaggccggcatcgatgacatgttcaacttccagacgttcagcaacagcat 5303
          |||||| | ||| | | |||| |||| | | |  |||| ||| || || || |||| |||
Qy  5384 CGTGAAGGAGAAGAGCGGCATTAACGACGCTATTAACGCACCTTTGGCCAGAGCAT 5443

Db  5304 gctgtgctgttccagatacaccacacagccgcggctgggacggcctcctcagcccccatcct 5363
          | || |||| |||||||  | | |||| || || ||||| |||| |  |||| |||| || |
Qy  5444 GATCCTGCTCTTCAGATGTCGACGTCAGCCCGGTTGGGATGTGTACTGGACGGCCATTAT 5503

Db  5364 caacacgggggcctccctactgcgacccccaacctgcccaacagcaacggctccgggggaa 5423
          |||   ||| || |    || |   ||| | || | ||| || | |  |||| || |||||
Qy  5504 CAAT--GAGGAAGC---A-TGCGATCC--ACCCGAC-AGCGACAAAAGCTATCCGGCGCAA 5554

Db  5424 ctgtgggagcccgccggcggtggagccgccatctcttcttcaccacctacatctcctcct 5483
          ||||||  | || || ||  | | || |||||| | ||| | ||| |||| |  | |
Qy  5555 TTGTGGTTCAGCGACCCGGGAATAACGTTCTCCCTCATACCTAGTTATTATAAGCTTTTT 5614

Db  5484 catcggtggtcaacatgtacatagccatcagccgcgtggctggctggcaccggaggcacaccga 5543
          || | || | |||| ||| | | |||| || |||| | |  | ||| |||| ||| || | |||
Qy  5615 GATAGTTATTATTATACAATGCATTGCTGTCAATTCTCGAGAACTATAGTCAGGCCACCGAGGA 5674

Db  5544 gagcacagagcccctgaggcgaggacgacttcgagatcgtcatggagatctgggagaagtt 5603
          | ||| ||| || || | |||   | ||| ||||| ||||| ||||| ||||| | ||||
Qy  5675 CGTGCAAGAGGGTCTAACCGACGACGACTACGAGGATCTGGCAGCAATT 5734

Db  5604 cgaccagaccgcaccagtcattgagtatctggcccctgtcgagctttgcagatgccttt 5663
          ||| | | | |||| ||| || || || | ||| | || | || || |||| | || |
Qy  5735 CGATCCGGAGGCGAGGGCCACCCAGTACATACGCTATGATCAGCTGTCCGAATTCCTGGACGTACT 5794

Db  5664 gtctgagccgctccgacatcgcaaccaaccaacagataagcctcatcaacatcatgatcatctgcc 5723
          | | ||| | || ||| | |  ||| |  || |||||| | | |||  |  | |||| | |||||
Qy  5795 GGAGCCCCCGCGCAGAGATCCACAAACCGACAAGTACAACAGATCATATCGATGGACATACC 5854

Db  5724 catggtgagcgagacgatccactgtatgaacatcatgtgctttgtcgtctttcaccaa 5777
          ||| ||  | | || | || ||| | | | || | | |  | |  || | || ||| |
Qy  5855 CATCTGTCGGCGTGACCTGCATCGCGTCGACATCCTTCGACGCCCTTACGAA 5908
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RESULT 4
ID   Q05831 standard; cDNA; 7555 BP.
AC   Q05831;
DT   10-JAN-1991 (first entry)
DE   Cardiac sodium channel gene.
KW   Rat; arrhythmia; ss.
OS   Rattus rattus.
PN   WO9009391-A.
PD   23-AUG-1990.
PF   09-FEB-1990; U00768.
PR   13-FEB-1989; US-310330.
PA   (ARCH-) ARCH DEV CORP.
PI   Rogart RB;
DR   WPI; 90-275095/36.
DR   P-PSDB; R06584.
     New rat cardiac sodium channel proteins - and associated DNA
     ...quences, polypeptides and peptides associated with
     ...ns, useful as antiarrythmic and cardiotonic drugs.
     ...ig 1; 65pp; English.
```

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KW   hypotensive; antinflammatory; trauma; pain; neurological disorder;
KW   antisense; gene therapy; ss.
OS   Rattus rattus.
FH   Key                Location/Qualifiers
FT   conflict           1
FT                      /*tag= a
FT                      /note= "T30193 contains G at this position"
FT   misc_feature       697..1665
FT                      /*tag= b
FT                      /note= "Probe used in differential tissue
FT                      expression studies"
FT   primer_bind        complement (1132..1151)
FT                      /*tag= c
FT   primer_bind        1495..1518
FT                      /note= "Binds primer T30196"
FT                      /*tag= d
FT                      /note= "Binds primer T30197"
PN   WO9614077-A1.
PD   17-MAY-1996.
PF   02-NOV-1995; U14251
PR   02-NOV-1994; US-334029.
PR   07-JUN-1995; US-482401.
PA   (TROP-) TROPHIX PHARM INC.
PA   (UVNY ) UNIV NEW YORK STATE RES FOUND.
PI   Borden LA,  Halegoua S,  Mandel G;
DR   WPI; 96-251547/25.
DR   P-PSDB; R99638.
PT   Nucleic acid encoding peripheral nervous system specific sodium
PT   channel peptide - useful for sodium channel-associated disease or
PT   trauma.
PS   Claim 2; Fig 7; 80pp; English.
CC   The sequence encodes repeat domain-II of a rat peripheral nervous
CC   system sodium channel peptide-II alpha-subunit (PNI), with sodium
CC   channel activity, and has been isolated from a rat PC12 subclone
CC   PKI-4 cell culture, expressing high levels of cAMP-dependent
CC   protein-kinase-inhibitor. A cDNA library has been screened with
CC   primers T30196-97, and the product has been used as a probe to
CC   re-screen the library to isolate this sequence. The full-length
CC   gene is given in T30193. A probe derived from the sequence may be
CC   used in differential tissue expression studies. The peptide may be
CC   used to isolate sodium-agonists and sodium-antagonists for use as
CC   analgesics, hypotensives, antiinflammatories, and in therapy of
CC   sodium channel-associated pathology or trauma, e.g. neurological
CC   disorders. The DNA (in sense or antisense orientation) may be used
CC   in gene therapy.
SQ   Sequence  3033 BP;   860 A;   689 C;   687 G;   797 T;
```

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Query Match             4.8%;  Score 312;  DB 22;  Length 3033;
Best Local Similarity   62.3%;  Pred. No. 1.0e-192;
Matches 1210;  Conservative  0;  Mismatches 700;  Indels 33;  Gaps 21;
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```
Db     736 atgatcctgctcagcagtggagctctggcttttgaagatatctatattgaaagaaagag  795
           |||||  | |||||||  |||| ||| | ||||| | || || |||||||  ||| ||||
Qy    3996 ATGATTTAATGAGTAGCTTAGCTTGGCATTAGAAGATGTACATCTGCCACAAAGACCC   4055

Db     796 accattaagattatcctggatgtgctgacaagatattcacctcacatcattctgaa    855
           ||||  ||| | ||||| || ||| || | | || || || |||| || |||||||
Qy    4056 ATACTGCAGGATATTTTATACTATATGGACAGAATATTTACGGTTATATTCTTCTTGGAA  4115

Db     856 atgcttctaaaatgggtcgcatatgggtataaaacatattcactaatgcctgtgttgg   915
           |||||||   ||||| |||| || | ||||| || ||| |  ||||| || ||| | ||
Qy    4116 ATGTTAATCAAGTGGTTGGCGCTGCGCTCGGTTCCAAAGTGTACTTCACCAACGACACTG  4175

Db     916 ctggacttcttaattgttgatcgtgtctctagttatcgccttatcaacttcttggctac  975
           || | |||| |||| ||| || ||| | |||||| || ||||||||| || || ||| ||
Qy    4176 CTTCGATTTCGTCGATTGCATTGTCATGGTATCGCCTTATCAACTTCGTTGCTTGTTGGAGCT  4235

Db     976 tcagaccttggcccattaaatctctacggacactgagggccctaagaccccttaagagagcc  1035
           ||||| ||| |  |  |||| |  | || ||| ||||| |  ||||  |||||||  |||
Qy    4236 GGTGGTATTCAAGCCTTCAAGACTATGCGAACGTTAAGAGCACTGAGACCACTACGTGCC   4295

Db    1036 tgtctagattgaaggaatgaaggagggtagtgtgtcaacgcactcatagagagcaatccctcc  1095
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Db    4824 catggtgaccatgatggtggagacagatgaccagacccctgagaaggtcaacatcttggc  4883
           ||||| |||||| |||||||  |||| |||||||  |  ||||| || || |||||||  |
Qy    4964 CATGTTCACCATGACCATCGTTCGATCGTTACGACGTCCGACACGTATAACGCGGTCCTAGA  5023

Db    4884 caagatcaacctgctcttcgtgccatcttcacaggcgagtgtattgtcaagatggctgc   4943
           || | |||||||| ||||| || || | |||||| || || |||  | |||| || ||
Qy    5024 CTATCAATGGCGATATTCGTAGTTGTATTTTCAGTTCCGAATGTCATTAAAATATTCGC   5083

Db    4944 cctgccactattacttcaccaacagcgtggaacatcttgacttttgtggttcatcct   5003
           ||||||||||| | |||| | |||| ||| | |  | ||| | | ||| || || |
Qy    5084 TTTACGATATCACTATTTTATTGAGCCATGGAATTATTTGATGTAGTAGTTGTCATTTT   5143

Db    5004 ctccattgttggcactgtctcctccgacatcatccagaagtacttgctctcccgacact  5063
           ||  ||| ||| | | ||  | || ||  |  ||| || ||  ||| | || | | |
Qy    5144 ATCCATCTTAGGTCTTGTACTTACGCCGATATTATCGAGAACTACTTCGTGTCGCGACCCT  5203

Db    5064 cttccgggtcatccgtctggccaggatcggccgagatcctcaggctgatccgccggagccaa  5123
           || ||||| ||| |   ||| |  || | |||  | | ||| |||| ||  ||| || | |
Qy    5204 GCTCCCAGTGCGTGGCGTGGCGAAAGTGGGCCGTGTCCTTGACTGGTGAAGGGAGGCCAA   5263

Db    5124 gggattcgcaacgcgctcttcgtgtctctgatgtgcccctcttcaacatcgg  5183
           ||| ||||| | | || | |||||||| |||| | ||||| || |||| ||
Qy    5264 GGGCATTCGGACACTGCTCTTCGCGTGGCCATGTCGCTGCCGGCCGTGTTCAACATCTG   5323

Db    5184 cctcctcctcttcctcgtcatgtttcatctactccatcttcggcatggcaacttcgctta  5243
           || ||| ||| || ||  ||   ||||| |  | |||| ||  | |  | |  |||| ||
Qy    5324 CCTGCTGCTGTCCTGCATGTTCATTCATCTTCGGCATGTCCCATTTTCGGTTCTTCATGCA  5383

Db    5244 cgtcaagtggaggccggcatcgatgacacgcttcaacttccagacagcagcat   5303
           || ||||| |||||| || |||  ||| || ||||| || |  || || || |
Qy    5384 CGTGAAGGAGAGAGCGGCCATTAACGACGTCTACAACTTCAAGACCTTGCCCAGAGCAT   5443

Db    5304 gctgtgctgttccagatcaccacacagccgctggacgcgctgagacgccctccagcccatcct  5363
           ||||| ||||| || | |||| | |||  ||||| || | || | | | |||||||| ||
Qy    5444 GATCCTGCTCTTTCAGATGCGACGCGGTTGGGATGCGTGACTGACGGCCATTAT       5503

Db    5364 caacacgggcctccctactgacgtcccctactgccccaacagcaacgcgctcccgggggaa  5423
           ||  || ||| | ||  |   ||| | | ||  | | ||| | |||  || || ||||
Qy    5504 CAAT--GGAAGC---A-TGCCATCC--ACCCGAC-AGCGACAAAGGCTATCCGGGCAA   5554

Db    5424 ctgtgggagccggcggtgggcatcctcttcaccacctacatcatcctccttcct  5483
           ||||  | || || | | |||| ||| || | |||| | |||| || || |||
Qy    5555 TTGTGGTTCAGCGACCCGTTGGAATAACGTTCTCTCCTCATCATCCTAGTTATAAGCTTTTT   5614

Db    5484 catcgtggtcaacatgtacatcgccatcatcctcgagaacttcagcgtggccaccgagga  5543
           || ||| || ||| | ||| |  || | ||| ||  |   ||  || || ||||| ||
Qy    5615 GATAGTTATTAAATGTACATTGCTGTCATTCTCCGAGAACTATAGTCAGGCCACCGAGGA   5674

Db    5544 gagcacagagcccctgagcggggccaccgttcatgagatctgggagaagtt  5603
           || |||| || || || | ||| || |||  | |||| | ||| || ||
Qy    5675 CGTGCAAGAGGGTCTAACCGACGACGACCATGGTACATGGATCTCGGCAGCAATT   5734

Db    5604 cgacccgggaggccaccagttcattggagtatctggccctgtcgacatttgcgatgcctt  5663
           || |||||||| || ||||  |||| |  | || ||  ||| ||| | || |||
Qy    5735 CGATCCGGGAGGGCACCAGTACATAACGCTATGGCCCTGTCCGAATTCCTGGACGTACT   5794

Db    5664 gtctgagcggctccgcatcgccaacagccaaccagataagcctcatcaacatggatctgcc  5723
           || | ||| |   |||| | | || ||  | | || || || |   |  || || |  ||
Qy    5795 GGAGCCCGGAGGCGCGATCCACAAACCGGACATCCTCGACGTGTATATCAACGATGGACATACC   5854

Db    5724 aggtgagcggagagccgtatccactgtatggacatactgttcgctttcaccaa  5777
           |||| || |||| || |  || ||  | || |  ||| |||  || || ||
Qy    5855 CATCTGCGCGGTGACCCATGTACTGCGTCGACATCCTTCGACGTCCGACGCCCTTACGAA   5908
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RESULT  5
ID   T30192 standard; cDNA; 3033 BP.
AC   T30192;
DT   25-OCT-1996 (first entry)
DE   Peripheral nervous system sodium channel sodium channel peptide-1 alpha-subunit gene.
KW   Rat; peripheral nervous system; sodium channel; PN1; PC12; PKI-4;
KW   sodium-agonist; sodium-antagonist; drug screening; analgesic;
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Qy   4296  ATGTCCCGTATGCAGGCATGAGGGTCGTCCGTTAATGCGCTGGTACAAGCTATACCGTCC  4355
Db   1096  atcatgaacgtgctttcctgtgtgcctatatctggctaatatttagcatcatgggagtc  1155
Qy   4356  ACTTCAAGTGCTATTGGTGTCGTCTAATATTTTGCCTAATAATGGGTGTA            4415
Db   1156  aatctgtttggctggcaagttctatgagtgtgtcaacaccaccgatggtcacgattcct  1215
Qy   4416  CAGCTTTTGCTGGAAAAATATTTTAAGTGCCAGGACATGA---ATGG--CACGAAGCTCA  4470
Db   1216  acatctcagtgtgcaaacgtctgagtgtttgccctgatgaacgttagtggaaatgtg     1275
Qy   4471  GC--CACGAGATCATACCCAAATCGCAATGCCT-GC---GA-GAGCGAGAACT-ACACGTG  4522
Db   1276  cgatggaaaaacctgaaacgtaaacttcgacaacgtgggcttggttacctgtcgctgctt  1335
Qy   4523  GG-TG---AATTCAGCAA-TGAATTCCATCATGTAGGTAACGCGTATCGTGTGCCTTTTC   4577
Db   1336  caagtcgaacattcaagggctggatggatgatattatgtatgcagcagttgactctgttaat  1395
Qy   4578  CAAGTGGGCACCTTCAAAAGGCTGGATACCAACATCATGAACGATGCTATCCGATTCACGAGAG  4637
Db   1396  gtaaatgaacagccgaaatacgaatacagtacagtctctacacatgtacatttacttgtcatcttc  1455
Qy   4638  GTGGACAAGCAACCAATTCGTGAAACGAACATCTACACTGTATTATTATTCGTATTCTTC  4697
Db   1456  atcatcttggctcattctcacgttgaacctgttcattggtgtcatcatagataatttc   1515
Qy   4698  ATCATATTTGGATCCTTTTTCACACTCAGTCTGTTCATTGGTGTTATCATTGATAATTTT  4757
Db   1516  aaccaacaga-aaaaaagcttggaggtca--agtatcttatgacagagaagaacagaag  1572
Qy   4758  AATGAGCAAAGAAAAGAAAAAGCAGGTGGATCATTAGAAAATGTTCATGACAAGAGATCAGAAA  4817
Db   1573  aaatactataatgcaatgaagaagctgggtgtccaaaaaaccacaaaaaccaattccaagg  1632
Qy   4818  AGTACTATAAATGCTATGAAGAAGAGAAGAGTAGGGCTCTAAAAAACCATTAAAAGGCCATTCCAAGA  4877
Qy   1633  ccaggaacaaattccaaggatgtatattggtagtttgacttagttgacgaacaagcttttgatatc  1692
Qy   4878  CCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATA  4937
Qy   1693  accatcatggttcttttgttgtagtagtgctcaacatgtaaccatgatgtagaaagagagggcaa  1752
Db   4938  ATCATTATTGTTATTCATTGGTCTGAACATGTTCACCATGGCAATGCTTCACTAGTAGCG  4997
Db   1753  actgagtacatggtatgttttacactgatcaacatggtcttcattatcctgttcact  1812
Qy   4998  TCGGCACGTATAACGGCGGTCCGTCCTAGACTATCTCAATGCGATATTCCTAGTTATTTTCAGT  5057
Db   1813  ggggagtgtgtgctgaagctaatctccctcagacattaactacttcactgtggtgggac  1872
Qy   5058  TCCGAATGTCTATTAAAAAATATTCGCTTTACGATAATCACTATTTATTTTGAGCCATGGAAT  5117
Db   1873  atttgtatttgtggtagtgttcaatgctccatttgtaggaatgtttctcgctgagatgata  1932
Qy   5118  TTATTGATGTAGTAGTGTCATTTGTCATTTTTATCCATCTTAGGTCTTGTACTTAGCGATAATTATC  5177
Db   1933  gagaagtatttcgtcgtcccctaccctgttccggatcatccggctggccaggattggacga  1992
Qy   5178  GAGAAGTACTTCGTCGTCGTCCCACCCCGGTCCGTGGCGTGGGCGAAAGTGGGCCGT  5237
Db   1993  atcctacgcctgatcaaaggcgcaaggggatccaagggggatccgcactctgctcttgatgatg  2052
Qy   5238  GTCCTTCGCACTGGTGAAGGAGCCAAGGGCCATTCGGACACTGCCTTCGCCGGTTGGCCATG  5297
Db   2053  tccttcctgccgctgttcaacatcggcctttctcctgtttttctggtcatctcatacgcc  2112
Qy   5298  TCGCTGGGGATGCCGGCCCCTTCGTTCAACATCCGTCGTCCTGTCTGCTGCTGGTCATGTCATCTTTGCC  5357
Qy   2113  atctttgggatgtccaactttgctctacgttaaataatgacatgttc                5417
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Db   2173  aacttgagacttttggcaacagcacatgatctgcttgttccaaataccaccctgccggc   2232
Qy   5418  AACTTCAAGACCTTTGGCCAGAGCATGATCCTCTTTCAGATGTCGACGTCAGCCGGT     5477
Db   2233  tgggacggactgctgccccatcctcaacagcgcacctccgactgtgacccctaaaaaa   2292
Qy   5478  TGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGCGA-TCC-ACCGACAGC-  5534
Db   2293  gttcacccaggaagttcagtggaagggactgtgggaaccatccgtggggattttttac   2352
Qy   5535  GA-CAA--AGGCTATCCGG-GCAATG--TG-GTTCACGGA-CCGTTGGAATAACGTTT   5585
Db   2353  tttgtcagctacatcatcatcttccgtgtggtggtgaacatgtaacatgctgtcatc    2412
Qy   5586  CTCCTCTCATACCCAGTTATAAGCTTTTTGATAGTTATTAATATGTACAATTGCTGTCATT  5645
Db   2413  ctggagaactcagcgtcgccaacagagagcactgagcctcgagtgaggacgacttt     2472
Qy   5646  CTCGAGAACTATAGTCAGGCCACCAGACGTCTAACCGACGACGACTAC            5705
Db   2473  gagatgttctacgaggtctggagaagttcgacccctgacgccactcagttcatagagttc  2532
Qy   5706  GACATGTACTATGAGATCTGCAGCAATTCCATCCGAGGGCACCCAGTACATACGCTAT   5765
Db   2533  tgcaagctctctgactttgcagctcgcctgatcctgatcctcatcgcaaggcaaac    2592
Qy   5766  GATCAGCTGTCCGAATTCCTGGACGTACTGCGAGCCCCGCTGCAGATCCACAAACCGAAC  5825
Db   2593  aagtccagctcattgccatgaccctgcccatggtgagtggagaccgcatccactgcctg   2652
Qy   5826  AGTACAAGATCATATCGATGACATCCCATCGTCGCCGGTGCCGTGACCTCTCATGTACTGCGTC  5885
Db   2653  gacatcttgttgcttttacaaa                                       2675
Qy   5886  GACATCCCGACGCCCTTACGAA                                       5908
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RESULT 6
ID   T30193 standard; DNA; 6452 BP.
AC   T30193;
DT   25-OCT-1996 (first entry)
DE   Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
KW   Rat; peripheral nervous system; sodium channel; PN1; PC12; PKI-4;
KW   sodium-agonist; sodium-antagonist; drug screening; analgesic;
KW   hypotensive; antiinflammatory; trauma; pain; neurological disorder;
KW   antisense; gene therapy; ss.
OS   Rattus rattus.
FH   Key             Location/Qualifiers
FT   cds             326..6280
FT                   /*tag= a
FT                   /product= Full-length PN1 protein
FT   conflict        3185
FT                   /*tag= b
FT                   /note= "T30192 contains A at this position"
FT   misc_feature    3185..6217
FT                   /*tag= c
FT                   /note= "Fragment T30192 (claim 2)"
FT   misc_feature    3881..4847
FT                   /*tag= d
FT                   /note= "Probe used in differential tissue
FT                   expression studies"
FT   primer_bind     complement (4316..4335)
FT                   /*tag= e
FT                   /note= "Binds primer T30196"
FT   primer_bind     4679..4702
FT                   /*tag= f
FT                   /note= "Binds primer T30197"
PN   WO9614077-A1.
PD   17-MAY-1996.
PF   02-NOV-1995.
PR   02-NOV-1994; US-334029.
PR   07-JUN-1995; US-482401.
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PA (TROP-) TROPIX PHARM INC.
PA (UINY ) UNIV NEW YORK STATE RES FOUND.
PI Borden LA, Halegoua S, Mandel G;
DR WPI: 96-251547/25.
DR P-PSDB: R99639.
PT Nucleic acid encoding peripheral nervous system specific sodium
PT channel peptide - useful for sodium channel-associated disease or
PT trauma.
PS Example 1; Fig 9; 80pp; English.
CC The sequence encodes a rat peripheral nervous system sodium channel
CC peptide-1 alpha-subunit (PN1), with sodium channel activity, and
CC has been isolated from a rat PC12 subclone PKI-4 cell culture.
CC expressing high levels of cAMP-dependent protein-kinase-inhibitor.
CC A cDNA library has been screened with primers T30196-97, and the
CC product has been used as a probe to re-screen the library to
CC isolate the fragment given in T30192. This has been used to isolate
CC the full-length gene. A probe derived from the sequence may be
CC used in differential tissue expression studies. The peptide may be
CC used to isolate sodium-agonists and sodium-antagonists for use as
CC analgesics, hypotensives, antiinflammatories, and in therapy of
CC sodium channel-associated pathology or trauma, e.g. neurological
CC disorders. The DNA (in sense or antisense orientation) may be used
CC in gene therapy.
SQ Sequence 6452 BP; 1816 A; 1454 C; 1550 G; 1632 T;

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Query Match          4.8%;   Score 312;   DB 22;   Length 6452;
Best Local Similarity  62.3%;   Pred. No. 1.0e-192;
Matches  1210;  Conservative    0;  Mismatches 700;  Indels   33;  Gaps  21;

Db  3920 atgatcctgctcagcagtggagctctggcttttgaagatatctatattgaaagagaaaag 3979
          |||| ||||  ||||||||| ||| |||||||  ||||||| ||||| ||||||||||
Qy  3996 ATGAGTTTAATGAGTAGCTTAGCTTGGCATTAGAAGATGTACATCTGCCACAAAGACCC 4055

Db  3980 accattaagatatctcggagtatgctgacagagatattcacctacatcttcattctggaa 4039
          |  |||| |||| |||| |||| ||  ||||  ||||||| || |||||| |||||
Qy  4056 ATACTGCAGGATATTTATACTATARTGGACAAGAGAATATTTACGGTTATATTCTTCTTGGAA 4115

Db  4040 atgctctaaatggtcgcatatgggtataaaacatatttcactaatggctggtggttgg 4099
          | ||| ||||  |||  |  |||  ||||||  || |||  |||||| ||||| |||
Qy  4116 ATGTTAATCAAGTGGTTGGCCTCGGCCTCCGCTTCAAAGTGCTTTAGTGTACTTCACCAACGCGTGGTGTTGG 4175

Db  4100 ctggacttcttaattgttgatgtctctagtactcttagtagccaacactcttggctac 4159
          ||||| ||  ||||| ||||||  || ||  |||||  || |||||||| ||||
Qy  4176 CTCGATTTCGTGATTGTGTCATGGTATCATGCTTTATCAACTTCGTTGCTTGCTTGTTGGAGCT 4235

Db  4160 tcagaccttggcccattaaaatctctacggacactgagggccccctaagagacc 4219
          |||||||| || |||  |||  ||| |  |||| |  ||| |  || |||||
Qy  4236 GGTGGTATTCAAGACCTTCAAGACTACTATGCGAACGTTAAGACGACTGAGAGCCACTAGGTGCC 4295

Db  4220 tgtctagatttgaaggaatgagtagtggtcaacagcactcattagcatcccttcc 4279
          |||  || |||||| || |||  |||| ||||  |||||| |||| ||| |||
Qy  4296 ANGTCCCGTATGCAGGGGCATGAGGGTCGTCGTTAAGTGCTGGGTACAAGCTATACCGTCC 4355

Db  4280 atcatgaacgctgcttctgtgctcctgtatatttgctaatatttagcatcatgggagtc 4339
          |||||||  || ||||  | |||  ||  ||||||  |||  |||  |||||| |
Qy  4356 ATCTTCAATGTGCTATTGGTGTGTCTATTTGGCCTAATTTTTGCCATAAAATGGGTGTA 4415

Db  4340 aactgtttgctggcaagttctcatgatgtgtcaacaccaccgatggtcacgatttcct 4399
          ||| ||| |||||| || |  || | |||  || ||||||  |||| |||||  ||
Qy  4416 CAGCTTTTTTGCTGGAAAATATTTTAAGTGCGGAGGACATGA---ATGG--CACGAAGCTCA 4470

Db  4400 acatccaagttgcaaaccgttctgagtgtttgccctgatgaacgttagtggaaatgtg 4459
          ||||||||||| ||||  | |||||||  |||||| |||| |||| |||| |||||||
Qy  4471 GC--CACGAGATCATACCACCAAATCGCAAATGCCT-GC---GA-GAGCGAGAACT-ACACGTG 4522

Db  4460 cgatgaaaacctgaaatgaactcgacaacgtgggcttggttacctgtcgctgttt 4519
          | ||||| ||  ||||| | | ||| | |||||  ||||||  |||| | | |||
Qy  4523 GG-TG--AATTCAGCAA-TGAATTCGAATCCATCAATCATGTGGTAACGCGTATCTGTGCCTTTTC 4577

Db  4520 caagttgcaacatccaagggctgatggatatttatgtgatcagtagttgactctgttaat 4579
          |||||||  || ||||  |||| |||| ||||||||||||||| ||||||| ||| ||
Qy  4578 CAAGTGGCCCACCTTCCAAAGCCTGGATACAAATCATGAACGATGCTATCGATTCGAGTTCACGAGAG 4637

Db  4580 gtaaatgaacagccgaatacgaatacagtctctacatgtacattactttgtcatcttc 4639
          ||||| || ||  ||   || |||  || ||  |||||||||| || || |||||
Qy  4638 GTGGACAAGCAACCAATTCGTGAAACGAACATCTACACATGTATTATATTCGATTCTTC 4697

Db  4640 atcatcttcggctcattcttcacgttgaacctgttcattggtgtcatcatagatatttc 4699
          ||||| || |||| |||||||  || ||| |||||||||||||||||||||| |
Qy  4698 ATCATATTTGGATCCTTTTCACACTCAATCGTTCAATCTGGTGTTATCATTGATAATTTT 4757

Db  4700 aaccaacagaa-aaaaaagctggaggtca--agtatcttatgacagaagaacagaag 4756
          ||  |  ||| ||||  |||||||||     | |  || ||  || |||| |||||
Qy  4758 AATGACCAAAGAAAAAAAGCAGGTGGATCATTAGAAAGTTCATGACAGAAGATCAGAAA 4817

Db  4757 aaatactataatgcaatgaagaagctggtgtcaaaaaccacaaaaaccaattccaagg 4816
          || |||| |||| ||| ||| ||| |  ||| |||| |||| |||||  |||||||||
Qy  4818 AAGTACTATAATGCTATGAAAAAGATGGGTCTAAAAAACCATTAAAAGCCATTCCAAGA 4877

Db  4817 ccagggaacaaattccaaggatgtatatttgactagtgcaaaccaagctttgatatc 4876
          ||||| ||c|| |||  |||||||| ||| ||||||||| ||   ||| |||| |||
Qy  4878 CCAAGGTGGGACCACAAGCAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATA 4937

Db  4877 accatcagttcttatatgctcaacatgtaaccatgatggtaaccatgatggtagaaaaagagggggcaa 4936
          ||||| |||  |||| |||  ||||||| |  ||||||| |  ||  |||| | ||
Qy  4938 ATCATTAGTTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATGTTACGATGCG 4997

Db  4937 actgatacatggatatgtttacactggtcaacactggtcttcattacctgttcact 4996
          |||||||  |||| |||||| |||| ||||||| |||  || |||||||||||||
Qy  4998 TCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGT 5057

Db  4997 ggggagtgtgtgctgaagctaatctccctcagacattactacttcactggtggttggaac 5056
          |||||||||||| |||| ||||| |||| |||| |||||||||| |||| |||||||||
Qy  5058 TCCGAATGTCATTAAAAATATTCGGCTTACGATATCACTATTTATTGAGCCATGGAAT 5117

Db  5058 atttgtatttgtgtagtgactgtcattttgatgtctcgtgtacgtacttctgctgagtgata 5116
          | ||| ||  ||||| |||   || ||  |||||| |||| || ||| |||| |||||
Qy  5118 TRATTTGATGTAGTAGTAGTGTCATTTTTATCCATCTAGGTCTTCGTAGCGGATATTATC 5177

Db  5117 gagaagtatttcgtgtcccctacccgttccagtcatccgcctggccaggattggacga 5176
          |||||| ||  |||| || ||  ||||||| |  |||  || ||||||| |||| ||
Qy  5178 GAGAAGTACTTCGTCGTGTCCGACCCGTGCCGAGTGGTGCGTGGCGAAGTGGGCCGT 5237

Db  5177 atcctaccctgatcaaaggcgccaagggga tccgcactctgctctttgcttgtatg 5236
          |||| | |||| |  || |||  || |||  |  || ||  ||||| ||| | | |
Qy  5238 GTCCTTCGACTGGTGAAGGAGCCAAGGCATTCGGACACTGCTCTTCGCGTCATCTACGCC 5297

Db  5237 tccttcctgcgtgttcaacatcggcctcctgcttttctggtcatgttcatctacgcc 5296
          ||||||| || ||| ||  ||||| |||| || |||| || ||| |||| ||  ||
Qy  5298 TCGGCTGCCGGCCCCGTTCAACATCTGCGTCCTGTCCTGTGCTGTTCATGTTCATCTTTGCC 5357

Db  5297 atctttgggatgtccaacttgcctacgttaaaaaggaggcggcaatcccttcc 5356
          | |||||| ||| ||||||| || | ||||||  |||| || || |||| |||
Qy  5358 ATTTTCGGCATGTCGTTCTTCATGCAGCTAGCACCGTGAAGGAGAGAGCGGCATTAACGACGTCTAC 5417

Db  5357 aacttgagactttggcaacagcatgatgctgcttgttccaaatcaccacctctgccggc 5416
          |||||||  |||||||||  ||| |||| |||||  |||||||| |||  |||||||||
Qy  5418 AACCTCAAGACCTTTGGCTGGGCCGCCATCCTCAACATGCTTCGTTCCCATTTTCAGATGTCGACGTCAGCCGGT 5477

Db  5417 tggacggactgctgccccatcctcaacagcgcacctcccgactgtgacctgaaaa 5476
          || |||||||||||  || ||| ||  ||||  ||||||||||||||  ||||||
Qy  5478 TGGGATGGTGTACTGGACGTCGGCCATTACTGCCGA-TCC-ACCCGACAGC- 5534

Db  5477 gttcaccaggaagttcagtggaaatgtgttggaacccatccgtggggattttttac 5536
          ||||||||||  || |||||  |||||| |||  |  ||||||||| ||||||||
Qy  5535 GA-CAA--AGGCTATCCGG-GCAATG---TG-GTTCAGCGA--CCGTTGGAATAACGTTT 5585

Db  5537 tttgtcagctacatcatcatatcctctggtggtgttgaacatgtacatgtcgtcatc 5596
          ||| |||||||| |||| | |  |||| |||||  ||   | ||| ||  | |||
Qy  5586 CTCCTTCTCATACCTAGTTATAAGCTTTTTGTAGCTTTTGTATAATGTCATTCTCGTCATT 5645

Db  5597 ctggagaacttcagcgtcgcaccgaagaagactggctctcgagtggaggaggacgctt 5656
          ||||| |||  || || | ||  ||  |  ||  || | ||||  || |||||| |||
Qy  5646 CTCGAGAACATAGTCAGGCCACGAGGGTCAAGAGGGTCTAACCGACGAGACTACAC 5705

Db  5657 gagatgttctacgaggtctggagagttcgaccctgacgccacttcatagagttc 5716
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              ||||| ||||   ||||  ||||| |||||||| |||||| ||  ||| |||||| |||| || ||||
Qy   5706 GACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATACGGCTAT 5765
              |||||||  ||  ||| | ||||||  || |||||| ||| ||||  |  || |||  |||
Db   5717 tgcaagctctcgacttgcagctgccctggatcctcccctcctcatgcgcaagccaaac 5776
              |||||| |||  |||   ||||| || ||| |||| ||| ||  ||||||
Qy   5766 GATCAGCTCGTCCGGAATTCCTGGACGTACTGGAGCGCCCGCTGACGTCCACAAAACGGAAC 5825
              |||| | ||| ||||  |||||| |||| |||||  |||||||| |  |||
Db   5777 aaagtccagctcattgccatggactgccatggtgagtggagaccgcatccactgcctg 5836
              ||||| |||| ||||  |   ||||||||||||||||  |||  |||| ||
Qy   5826 AAGTACAAGATCATATCGATGACAATCCCATCCCATCTGTCGCGGTGATTCAAGCCTTCAAGACTA 5885

              ||||| ||  ||| |||||| ||
Db   5837 gacatccttgtttgctttacaaa 5859
              ||||| |||  |||  |
Qy   5886 GACATCCCTCTCCGACGCGCCCTACGAA 5908

RESULT  7
ID   T30194 standard; cDNA; 6371 BP.
AC   T30194;
DT   25-OCT-1996  (first entry)
DE   Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
KW   Human; peripheral nervous system; sodium channel; PN1A;
KW   dorsal root ganglion; sodium-agonist; sodium-antagonist;
KW   drug screening; analgesic; hypotensive; antiinflammatory; trauma;
KW   pain; neurological disorder; antisense; gene therapy; ss.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   cds            49..5982
FT                  /*tag= a
FT                  /product= PN1A protein
PN   WO9614077-A1.
PD   17-MAY-1996.
PF   02-NOV-1995; U14251.
PR   02-NOV-1994; US-334029.
PR   07-JUN-1995; US-482401.
PA   (TROP-) TROPHIX PHARM INC.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
PI   Borden LA, Halegoua S, Mandel G;
DR   WPI; 96-251547/25.
DR   P-PSDB; R99640.
PT   Nucleic acid encoding peripheral nervous system specific sodium
PT   channel peptide - useful for sodium channel-associated disease or
PT   trauma.
PS   Example 4; Fig 13; 80pp; English.
CC   The sequence encodes a human peripheral nervous system sodium channel
CC   peptide-1 alpha-subunit (PN1A), with sodium channel activity. A
CC   probe has been isolated by PCR from a human peripheral nervous
CC   system cDNA library, using probes derived from the rat PN1 protein
CC   sequence (R99638-39), and has been used to screen a human dorsal
CC   root ganglion cDNA library, to give the full-length sequence, using
CC   PCR primers T30198-99 and T18167.  A related sequence (T30195) has
CC   also been isolated.  The sodium channel peptide may be used to
CC   isolate sodium-agonists and sodium-antagonists for use as
CC   analgesics, hypotensives, antiinflammatories, and in therapy of
CC   sodium channel-associated pathology or trauma, e.g. neurological
CC   disorders.  The DNA (in sense or antisense orientation) may be used
CC   in gene therapy.
SQ   Sequence  6371 BP;   1948 A;   1231 C;   1374 G;   1818 T;

Query Match      4.7%;  Score 308;  DB 22;  Length 6371;
Best Local Similarity  62.2%;  Pred. No. 7.08e-190;
Matches 1231;  Conservative   0;  Mismatches 713;  Indels  35;  Gaps  25;

Db   3581 ttgaacacagttggtttgaaagcttcattgtcctcatgatcctgctcagcagtggtgccc 3640
              |||||| ||   |||  ||  |||||||  ||  |||||||||  || |
Qy   3961 TTGAAATAAATAATTTTGAAACAGCTGTTATCACTAGTATTTCAGTTCCGAATGCTATAAAATATTC 4020
              |||||| ||   |||||||||| ||||||  ||||||||||
Db   3641 tggctttgaagatattatatggaaggaaaaagaccattgaagttatcctggagtatg 3700
              || ||| ||| |||  ||||| |||  || |||||  |||||| |||||
Qy   4021 TGCCATTAGAAGATGTACATCGCCCACAAGACCCATACTGCAGGATATTTTATACTATA 4080
              ||||| |||| |||||  ||||||  |||  ||| ||||||  |||
```

                                                              4140

    4081 TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG

                                                              3820

    3761 gttataaaacatattgccaatgcctggtcggattcctaattgttgatgtttt

                                                              4200

    4141 GCTTCAAAGTGTACTTCACCAACGCGTGGTGTTGGCTTCGATTTCGTGATTGTTCATGGTAT

                                                              3880

    3821 ctttggttacttagtggcaaacacttggctactcagatcttggcccattaaatccc

                                                              4260

    4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTGTATTCAAGCCTTCAAGACTA

                                                              3940

    3881 ttcggacactgagagcttaagaccctgagatttgaaggaatgaggg

                                                              4320

    4261 TGGGAACGTTAAGAGCACTGAGACACTACGTGCCATGCGCGTCCCGTATGCAGGGCATGAGGG

                                                              4000

    3941 tcgtgtgaatgcactccatcaggagcaattccttccatcatgaatgtgctactgtgtgtc

                                                              4380

    4321 TCGTCGTTAATGCGCGTGGTGTACAAGCTATACCGTCCATCTTCAATGTGTCATTGGTGTGTC

                                                              4060

    4001 ttatattcggctgcgtatattcagcatcatggaggagtaaatttgtttgctggcaagttcatg

                                                              4440

    4381 TAAATATTTTGGCTAATTTTGGCTATATTTTGGGTATACAGCCTTTTTTTGCTGGAAAATATTTTA

                                                              4120

    4061 agtgtattaacacacagatggtcacggtttcctgcagtcaagttccaaatcgttccg

                                                              4493

    4441 AGTGCGGAGGACATGAATGGCACGA-A-GCTCAGCCACCAGAGATCA-TACCAAATCG---C-

                                                              4180

    4121 aatgtttttgccccttatgaatgttagtcaaaatgtgcgatggaaaaacctgaaagtgaact

                                                              4542

    4494 AATGCCT-GCG---A-GAGCGAGAA-CTACACGTGGG-TG---AATTCAGCAA-TGAATT

                                                              4240

    4181 ttgataatgtcgacttggttacctactctctgtcgcttcaagttgcaactttaagggatgga

                                                              4602

    4543 TCGATCATGTAGGTAACGCGTATCGTGTGCCTTTTCCAAGTGGCCACCTTCAAAGGCTGGA

                                                              4300

    4241 cgattattatgtgcagcagtggattctgttaatgtagacagcagcccaaatatgaat

                                                              4662

    4603 TACAAATCATGAACGATGCTATCGAATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAA

                                                              4360

    4301 atagcctacatgtgtatattatttgtcgtcttatcatccttgggtcattcttcactt

                                                              4722

    4663 CGAACATCTACACGTATTATTCGTATTCTTCATCATATTTGGATCCTTTTTCACAC

                                                              4419

    4361 tgaacttgttcattggtgtcatcatagataatttcaaccaacagaa-aagaagcttgga

                                                              4782

    4723 TCAATCGTTCATTGGTGTTATCATTGATAATTTTAATGAGCAAAAGAAAAAGCAGGTG

                                                              4477

    4420 ggtca--agacatctttatgcagagaagaacagagaaaatactataatgcatgaaaagc

                                                              4842

    4783 GATCATTAGAAGTGTCATGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGA

                                                              4537

    4478 tggggtccagaagccacaaaagccaattcctgacgacatccaggggaacaaaatccaaggatgta

                                                              4902

    4843 TGGGCTCTAAAAAACCATTAAAAGCCATTCCAAGACCAAGGTGGCGACCAAGCAATAG

                                                              4597

    4538 tatttgacctagtgacaaatcaagccttgatatagtagtatcatggtcttatcgtctca

                                                              4962

    4903 TCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTATTATGTTATTCATTGGTCTGA

                                                              4656

    4598 acatgtgaccatggatggtagaaaaggaggt-caagtcaacatatgactgaagttta

                                                              5021

    4963 ACATGTTCACCATGAACCTCGATCGTTACGATGCGTCGGACACGTATAAC-GCGGTCCTA

                                                              4716

    4657 tattggataaatgtgttttatatatccttttcactggtggaatgtgtgctaaaactgatc

                                                              5081

    5022 GACTATCTCAATGCGATATTCGTAGTATTTCGTAGTAGCTTAGCTT

                                                              4776

    4717 tccctcagacactacttcacttgtaggatggaatattttgatttgttgggtttgtgatt

                                                              5141

    5082 GCTTTACGGATATCACTATTTTATTGAGCCATGGCCATGCGAATTTATTTGATGATGAATGTTCATT

                                                              4836

    4777 atctccattgtaggtatgttctagctgattgaaacgtatttgtgtccctacc

                                                              5201

    5142 TTATCCATCTTAGGTCTTTGACTTAGGCGATATTAATCGGCATATTAATGGATAGCATATG

```
PR   02-NOV-1994; US-334029.
PR   07-JUN-1995; US-482401.
PA   (TROP-) TROPHIX PHARM INC.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
PI   Borden LA, Halegoua S, Mandel G;
DR   WPI; 96-251547/25.
DR   P-PSDB; R99641.
PT   Nucleic acid encoding peripheral nervous system specific sodium
PT   channel peptide - useful for sodium channel-associated disease or
PT   trauma.
PS   Example 4; Fig 14; 80pp; English.
CC   The sequence encodes a human peripheral nervous system sodium channel
CC   peptide-1 alpha-subunit (PN1B), with sodium channel activity. A
CC   probe has been isolated by PCR from a human peripheral nervous
CC   system cDNA library, using probes derived from the rat PN1 protein
CC   sequence (R99638-39), and has been used to screen a human dorsal
CC   root ganglion cDNA library, to give the full-length sequence, using
CC   PCR primers T30198-99 and T18167. A related sequence (T30194) has
CC   also been isolated. The sodium channel peptide may be used to
CC   isolate sodium-agonists and sodium-antagonists for use as
CC   analgesics, hypotensives, antiinflammatories, and in therapy of
CC   sodium channel-associated pathology or trauma, e.g. neurological
CC   disorders. The DNA (in sense or antisense orientation) may be used
CC   in gene therapy.
SQ   Sequence 6404 BP;   1961 A;   1236 C;   1381 G;   1826 T;

Query Match             4.7%;  Score 308; DB 22; Length 6404;
Best Local Similarity   62.2%;  Pred. No. 7.08e-190;
Matches 1231;  Conservative    0;  Mismatches 713;  Indels 35;  Gaps 25;

Db   3614  ttgaacacagttggttgaaagcttcattgtcctcatgatcctgctcagcagtggtgccc  3673
             ||||| ||   ||||||||| |   | |||||  ||||  | |  |||| ||||  ||||
Qy   3961  TTGAAATAAATAATATTTGAAACAGCTGTATCACTATGATTTAAATGAGTAGCTTAGCTT  4020

Db   3674  tggctttgaagatattatattgaaaggaaaagacccatacgcaggatatttTATACTATA  3733
             |||| || |||| || |  | ||||| |  | ||||   || ||| ||||||||||||||
Qy   4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCCAGGATATTTTATACTATA  4080

Db   3734  cagacaagatcttcacttacatctcattctgaaatgtcttcttaaatggatagcacatg  3793
             ||   |  | ||| || ||| || ||| |||| |||  | |  | ||||| ||  ||||
Qy   4081  TGGACAGAATAATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG  4140

Db   3794  gttataaaacatattccaccaatgcctggtgttggctggctggattcctaattgttgatgttt  3853
             ||| |  |||  | | |||  ||||  | | ||| | ||| |  | |||||||||
Qy   4141  GCTTCAAAGTGACTTCACCAACGCGTGGTGTTGGCTCGCATTTCGTGATTGTCATGGTAT  4200

Db   3854  ctttggttacttagtggcaaacactcttggctactcagatcttggcccattaaatccc  3913
             |    |  |||  ||  | ||  | |||  | ||||  || | |||||  |||||||||
Qy   4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTCGTTGGTATTCAAGACTA  4260

Db   3914  ttcggacactgagagctttaagacctctaagagctcagagaggccttatctagatttgaaggaatgaggg  3973
             |  ||| |||||| || | ||||||| |  |||||||||| || || |  ||  | |||||||
Qy   4261  TGCGAACGTTAAGAGCACTGAGACCCACACGTGCCATGTCCGTATGCAGGGGCATGAGGG  4320

Db   3974  tcgttgaatgcactcataggagcaattccttccatcatgaatgtgtcatgtcgatgtgtc  4033
             |  ||||  | | ||  | |||| ||| || | |||  || ||| |    | ||| |
Qy   4321  TCGTCGTTAATGCGTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC  4380

Db   4034  tatattctggctgatattcagcatcatgggagtaaatttgttgctgctgcaagttctatg  4093
             |  |  | ||  | ||  || | | |    |  |    |||| ||| || ||||  | ||
Qy   4381  TAATATTTGGCTAATTTTGCCATAATGGGTGTACAGCTTTTGCTGGAAAAATATTTTA  4440

Db   4094  agtgtattaacaccacagatggtcacggttcctgcaagtcaaatcgttccg  4153
             ||| | ||||  |  || ||||| | ||   | |  ||| ||  ||||| ||
Qy   4441  AGTGCGAGGACATGAATGGCACGA-A-GCTCAGCCACGAGATCA-TACCAAATCG---C-  4493

Db   4154  aatgttttgccctttagtgtagttagtcaaatgtgcgatgaaaaacctgaaagtgaact  4213
             || || ||| ||| ||    ||| |||| |  |||  ||||  ||  |||| |||  |  |
Qy   4494  AATGCCT-GCG---A-GAGCGAGAA-CTACACGTGGG-TG---AATTCAGCAA-TGAATT  4542

Db   4214  ttgataatgtcgacttggttacctatctctgcttcaagttgcaactttaagggatgga  4273
             | |||| ||| |||| |||||| || |||   |  |||||||   |||| | |||||||
Qy   4543  TCGATCATGTAGGTAACGTGATCGTGTCCTTTTGCCTTTTCCAAAGTGGCCACCTTCAAAGGCTGGA  4602
```

RESULT 8
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ID   T30195 standard; cDNA; 6404 BP.
AC   T30195;
DT   25-OCT-1996  (first entry)
DE   Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
KW   Human; peripheral nervous system; sodium channel; PN1B;
KW   dorsal root ganglion; sodium-agonist; sodium-antagonist;
KW   drug screening; analgesic; hypotensive; antiinflammatory; trauma;
KW   pain; neurological disorder; antisense; gene therapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             49..6015
FT                   /*tag= a
FT                   /product= PN1B protein
FT   misc_difference 334..336
FT                   /*tag= b
FT                   /codon= seq:ACA, aa:Ala
FT   misc_difference 1738..1740
FT                   /*tag= c
FT                   /codon= seq:ATA, aa:Leu
PN   WO9614077-A1.
PD   17-MAY-1996.
PF   02-NOV-1995; U14251.
```

```
Db  5350  gaagaaagtactgaacctctgagtgaggatgactttgaagtgttctatgaggttgggag  5409
          ||-|| |||| | |||||||||||| ||  || |||| || | ||||||| - ||||||| |||
Qy  5670  GAGGACGTGCAAGAGAGGTCTAACCAGCCAGTTGACGACGACGACATGTACTAGAGATCTGGCAG  5729

Db  5410  aagtttgatcccgatgcgacccagtttagagtctctaaactcctgatttgtcagct  5469
          - ||  ||||| || |||||||||||||||||||||||||| || |||||| ||||||
Qy  5730  CAATTCGATCCCGGAGGCACCCAGTACATACGTATGATCAGCGTCCGAATTCCTGGAC  5789

Db  5470  gccctggatcctcctccatcagcaaaccaacagaa-aaagaagcttgga  5529
          ||||| | ||||| || |||||| |||||||| || |||| ||||||||||
Qy  5790  GTACTGGAGCCCCCGCTCGAGATCCACAAACCAACAAGTACAAGACATAATCGATGGAC  5849

Db  5530  ctgccatggttagtgtgaccggatccattgtcttgacatcttattgtcttttacaaa  5588
          - ||||| ||||||||||||||| ||||| | ||||||||||||| |||||||||||
Qy  5850  ATACCCATCTGTCGCGGTGACCTCATGTACTGGCTGCGACATCCTCGACGCCCTACGAA  5908
```

RESULT  9
```
ID   T77803 standard; cDNA; 6524 BP.
AC   T77803;
DT   09-OCT-1997 (first entry)
DE   cDNA encoding wild type rat DRG (SNS-B).
KW   Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
KW   neuropathic pain; impulse; sensory neuron; acute pain; chronic pain;
KW   enteric nervous system; glia; muscle; parasympathetic nervous system;
KW   cranial ganglia; central nervous system; dorsal root ganglia;
OS   Rattus rattus.
FH   Key             Location/Qualifiers
FT   cds             204..6077
FT                   /*tag= a
FT                   /product= Rat_DRG(SNS-B)
PN   WO9701577-A1.
PD   16-JAN-1997.
PF   25-JUN-1996; G01523.
PR   28-JUN-1995; GB-013180.
PA   (UNLO ) UNIV COLLEGE LONDON.
PI   Akopian AN, Wood JN;
DR   WPI: 97-100165/09.
DR   P-PSDB; W21737.
PT   New isolated mammalian sensory neuron sodium channel protein - used
PT   to identify modulators of the sodium channel, partic. for the
PT   treatment of pain
PS   Claim 9; Page 50-58; 128pp; English.
CC   The sequences given in T77803-06 encode the wild type and three
CC   variant forms of a rat sensory neuron sodium channel protein which
CC   is insensitive to tetrodotoxin. The proteins can be used for
CC   identifying modulators of the sodium channel. Blockers of the
CC   sodium channel will block or prevent the transmission of impulses
CC   along sensory neurons and thereby be useful in the treatment of acute,
CC   chronic or neuropathic pain. The novel protein is found only in sensory
CC   neurons and not in glia, muscle or the neurons of the (para)sympathetic,
CC   enteric or central nervous system. The protein is found preferably in
CC   the neurons of the dorsal root ganglia or cranial ganglia.
SQ   Sequence  6524 BP;  1540 A;  1866 C;  1662 G;  1456 T;
```

Query Match             4.5%;     Score 296;  DB 32;  Length 6524;
Best Local Similarity  63.8%;     Pred. No. 2.37e-181;
Matches  890;  Conservative  0;  Mismatches 486;  Indels 18;  Gaps 11;

```
Db  4254  aacttcgacaacgtcgctatggctacccgcacctcttcaggtgcaaccttcaaagc  4313
          | ||||| || ||| | ||||| | || ||  | |||| ||||||| |||| || |||
Qy  4539  AATTCGATCATGTAGGTAACGCGGTATCTGTGCCTTTTCCAAGTGGCCACCTCAAAGGC  4598

Db  4314  tggatggacataatgtatgcagctgttgattccggagagatcaacagtcagcctaactgg  4373
          || |  | || | | ||| |||||||| || | ||||| |||||||||||||| || |||
Qy  4599  TGGATACAAATCATGAACGATGCTATCAGCGTTCTCCTCTCATCACCTAGTTATAAGC  4658

Db  4374  gagaacaacttgtacatgtacctgtacctcgtacttcgtgttttcatcatttcggtggcttcttc  4433
          |||| || ||||| || ||||||| |||| | ||||||| |||| ||| ||| || ||| |||||
Qy  4659  GAACGAACATCACTACATGTTCATTCTCGAGAACTACATATTTCATCATATTTGGATCCTTTTTC  4718

Db  4434  acggtgaatctcttttgtggggtcataatcgacaactcaaccacagaaaagaaagcta  4493
```

```
Qy    5784 CTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAACCGAACAAGTACAAGATCATATCG 5843
           ||||| ||||   || |  |||||||  ||    ||        ||   ||   |||||
Db    5571 atggacctgccgttggtccccgggataagatccactgtctggacatccttttgccttc 5630
           ||||| | || || | ||    |||  ||   |  |||  |||||| |||||||||||
Qy    5844 ATGGACATACCCATCTGCTGCGGTGACCTCATGTACTGCGTCGACATCCTCGACGCGCCCTT 5903

Db    5631 acaaagaacgtctt 5644
           ||| || || ||||
Qy    5904 ACGAAAGACTTCTT 5917
```

```
RESULT  10
ID      T77806 standard; cDNA; 6527 BP.
AC      T77806;
DT      09-OCT-1997 (first entry)
DE      cDNA encoding variant rat DRG (SNS-B) #3.
KW      Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
KW      modulator; impulse; sensory neuron; acute pain; chronic pain;
KW      neuropathic pain; glia; muscle; parasympathetic nervous system;
KW      enteric nervous system; central nervous system; dorsal root ganglia;
KW      cranial ganglia; ss.
OS      Rattus rattus.
FH      Key              Location/Qualifiers
FT      cds              204..6602
FT                       /*tag= a
FT                       /product= Variant_Rat_DRG(SNS-B)
FT                       299
FT      mutation
FT                       /*tag= b
FT                       /label= C>G
FT                       1092
FT      mutation
FT                       /*tag= c
FT                       /label= G>A
FT                       1096
FT                       /note= "Causes Val > Ile substitution"
FT      mutation
FT                       /*tag= d
FT                       /label= C>T
FT                       1964
FT                       /note= "Causes Ser > Phe substitution"
FT      mutation
FT                       /*tag= e
FT                       /label= G>C
FT                       1965
FT      mutation
FT                       /*tag= f
FT                       /label= C>G
FT                       2472
FT                       /note= "Causes His > Asp substitution"
FT      mutation
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FT                       /label= A>T
FT                       2986
FT                       /note= "Causes Thr > Ser substitution"
FT      mutation
FT                       /*tag= h
FT                       /label= G>T
FT                       3019
FT                       /note= "Causes Ser > Ile substitution"
FT      mutation
FT                       /*tag= i
FT                       /label= A>G
FT                       3158
FT                       /note= "Causes His > Arg substitution"
FT      mutation
FT                       /*tag= j
FT                       /label= C>T
FT                       3525
FT      mutation
FT                       /*tag= k
FT                       /label= C>G
FT                       3556
FT                       /note= "Causes His > Asp substitution"
FT      mutation
FT                       /*tag= l
FT                       /label= G>C
FT                       5893
FT                       /note= "Causes Arg > Thr substitution"
FT      mutation
FT                       /*tag= m
FT                       /label= T>G
FT                       6525..6527
FT                       /note= "Causes Ile > Ser substitution"
FT                       /*tag= n
```

```
Qy    4719 ACACTCAATCTGTTCATTGGTGTTATCATTGATAATTTAATCAGCAAAGAAAAAAGCA 4778
           ||  ||||||    ||||  ||    ||  || || | ||||||||||
Db    4494 ggaggc-cag--gacatcttcatgacagaagagaagtactacaatgccatgaag 4550
           |||||| ||   ||||||| || ||| || |||| |||||| |||| |||  |
Qy    4779 GGTGGATCATTAGAAAATGTTCATTGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAA 4838

Db    4551 aagctgggctccaagaaacccagagagcccatcccacggcccctgaataagtaccaaggc 4610
           |||  ||||||||||  | |||||| |||||||| |||||   | |||||| |||||||
Qy    4839 AAGATGGGCTCTAAAAAACCATTAAAGAAGACCATTCCAAGACAAGGTGGCGACCACAAGCA 4898

Db    4611 ttcgtgttgacatcgtgaccaggcaagcctttgacatcatcatgcatggttctcatctgc 4670
           ||||||  |  ||||||||   ||||||||| |||||||| |||| || ||||  || ||
Qy    4899 ATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTCATTATGTTATTCATTGGT 4958

Db    4671 ctcaacatgatcaccatgatggtggtaacgcgacgagcaggcgcaggcagagagacgaaggtt 4730
           || ||||||||||||| ||||||     | |    || || ||| |||
Qy    4959 CTGAACATGTTCACCATGACCCTCGATCGTTACGATGCCGGACACGTATAACGCGGTC 5018

Db    4731 ctgggcagaatcaaccagttcttgttggccgtcttcacgggcgagtgtgtgatgaagatg 4790
           || || ||||| |   |  |||| ||  | |||   |||  | |  |||| || |||
Qy    5019 CTAGACTATCCAATGCGATATTCGTAGTATTTTCAGTTCCGAATGTCTATTAAAAATA 5078

Db    4791 ttcgccctgcgacagtactacttccaccaacggctggaacgtgttcgactcatagtggtg 4850
           ||| | |||   || || |  || || ||||   |  |  || |||| ||| ||| |||
Qy    5079 TTCGCTTTACGATATCACTATTTATTGAGCCATGGAATTTATTGATCGTAGTAGTTGTC 5138

Db    4851 atcctgtccattgggagtctgctgtttttctgcaatcctcaagtcactggaaaactactc 4910
           ||  |   |||||| ||| |  |||| ||   |||  || |   | |    || | | |
Qy    5139 ATTTTATCCATCATCTTAGGTCT--TGTACTTAGCCGATA-TTA--TCGA-GAAGTACTTCGTG 5192

Db    4911 tccccgacgctcttccgggtcatccgtctggccaggatcggccgcatcctcaggctgatc 4970
           | |||  |||  |||   ||| |     |||  | |  | ||  |||| ||   ||||||
Qy    5193 TCGCCGACCCTGCTCCGAGTGGTGCGTGTGCGGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTG 5252

Db    4971 cgagcagccaagggattcgcacgcgctgtctcctggccctcatgatgtccctgccccgcctc 5030
           | | | |  ||   | || ||  | || |  | |    || ||  ||| || |   | |
Qy    5253 AAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCTGCCGGCCCTG 5312

Db    5031 ttcaacatggccctccctcctctctccctgtcatgttcatctactcctcggcatggcc 5090
           ||||| | |  || |  |  | || | || | || ||| |  |  | || ||  ||
Qy    5313 TTCAACATCTGCCTGCTGCTCCTGGTCCTGGGCCATTTTCGCCATTTCGGCATGTCG 5372

Db    5091 agcttcgctaacgtcgtcggacgaggccggcacgacagcatgttcaacttcaagaccttt 5150
           |||||||  ||   ||  | || |||  |  | |  | ||| | ||| ||  |||  |||
Qy    5373 TTCTTCATCACGTCACAGTGAAGGACAGAGAGCGGCCATTAACGACGTCTACAACTTCAAGACCTTT 5432

Db    5151 ggcaacagcatgctgtgctgttccagatcaccacacctggccggccggcctggacgggcctcctc 5210
           || ||| | ||  |||||  |||||| || | | | ||| |||  |||  ||| ||  || |
Qy    5433 GGCCAGAGCATGACATCCTGCTCTTCAGATGTCGACGTCAGCCGGTTGGGATGGTGTACTG 5492

Db    5211 agcccatcctcaacacgggggcctccactgcgaccccaactgccaacagcaacggc 5270
           ||||| ||   ||| ||| | | ||||  ||  |||| | | ||  ||| |||  |
Qy    5493 GACGCCCATTATCAAT--GAGGAAGC---A-TGCGATCC--ACCCGAC-AGGACAAAGGC 5543

Db    5271 tcccgggggggaactgcgggagcccggcggtggccatcatccttcttcaccacctacatcatc 5330
           || ||| |||  |  |  |  | ||| |  |||| || || |||| |  |||| ||||| |||
Qy    5544 TATCCGGGGCAATGTGGTTCAGCGACCGGTTGGAATAACGTTTCCTCCTCATTACCTAGTT 5603

Db    5331 atctcctcctcatcgtggtcaacatgtacatcgcagttatctcggagaacttcaacgta 5390
           || | | | |  |||||  | || |  || ||| | || |  |||| | ||| ||
Qy    5604 ATAAGCTTTTTTGATATGATATAATAATATGTACATCGTCATTCCGCGAGAACTATAGTCAG 5663

Db    5391 gccaccgaggagagacggagcccctgacgcgaggacgactcagcacatgttctatgagacc 5450
           |||||||||| |  ||
Qy    5664 GCCACCGGAGGACGTGCAAGAGGGTCTAACCGACGACTACGACGACTACTATGAGATC 5723

Db    5451 tgggagagttcgacacggacccgaggcacccagttcattgcctttctgccctctcagacttc 5510
           |||| || ||  |||| |  |||| |||  |||  | |  ||  | |  | | |  ||
Qy    5724 TGGCAGCAATTCGATCCGGAGGCACCCAGAGTACCAGTAGTCGTATGATCAGCGTGTCCGAATTC 5783

Db    5511 gcggacacgctcctccggcgccctcttagaatcccaaacccaaccaagaatattaatccag 5570
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FT                  /note= "Addition of AAA"
PN   WO9701577-A1.
PD   16-JAN-1997.
PF   25-JUN-1996; G01523.
PR   28-JUN-1995; GB-013180.
PA   (UNLO ) UNIV COLLEGE LONDON.
PI   Akopian AN, Wood JN;
DR   WPI; 97-100165/09.
DR   P-PSDB; W21740.
PT   New isolated mammalian sensory neuron sodium channel protein - used
PT   to identify modulators of the sodium channel, partic. for the
PT   treatment of pain
PS   Claim 9; Page 85-93; 128pp; English.
CC   The sequences given in T77803-06 encode the wild type and three
CC   variant forms of a rat sensory neuron sodium channel protein which
CC   is insensitive to tetrodotoxin.  The proteins can be used for
CC   identifying modulators of the sodium channel.  Blockers of the
CC   sodium channel will block or prevent the transmission of impulses
CC   along sensory neurons and thereby be useful in the treatment of acute,
CC   chronic or neuropathic pain.  The novel protein is found only in sensory
CC   neurons and not in glia, muscle or the neurons of the (para)sympathetic,
CC   enteric or central nervous system.  The protein is found preferably in
CC   the neurons of the dorsal root ganglia or cranial ganglia.  This
CC   sequence contains 12 nucleotide differences to the wildtype rat
CC   DRG(SNS-B) (see also T77803) causing nine amino acid changes.
SQ   Sequence 6527 BP;    1542 A;   1663 C;   1663 G;   1459 T;

Query Match       4.5%;   Score 296;   DB 32;   Length 6527;
Best Local Similarity   63.88%;   Pred. No. 2.37e-181;
Matches  890;   Conservative   0;   Mismatches  486;   Indels  18;   Gaps  11;

Db    4254 aacttcgacaacgtcgctatgggctaccccgcacttcttcaggtggcaaccttcaaaggc 4313
            ||||||| || ||| ||  |||| ||||||||||||  ||
Qy    4539 AATTCGATCATGTAGGTAACGCGTATCGTGCCTTTCCAAGTGGCCACCTTCAAAGGC 4598

Db    4314 tggatggacataatgtatgcagctgttgattccggagagatcaacagtcagcctaactg 4373
            ||||||  ||| ||  |||||| |
Qy    4599 TGGATACAAATCATGAACGATGCTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGT 4658

Db    4374 gagaacaactgtacagtgtacctgtacttcgtcgtttcatcatttcggtggcttcttc 4433
            |  |||  ||| ||||  ||| |||
Qy    4659 GAAACGAACAACATCTACACATGTATTATATTTCGTATGTCTTCATCATATTTGGATCCTTTTC 4718

Db    4434 acgctgaatcctcttgttgggtgcataatgcaacttcaaccacagaaaaaagcta 4493
            ||||| |||||| | ||||||  || ||  |||| ||
Qy    4719 ACACTCAATCTGTCATTGGTGTTATCATTGATGTTTATCATTGATAATTTAATGAGCAAAAGAAAAAAGCA 4778

Db    4494 ggaggc-cag--gacatcttcatgacagaagagaagaagaagtaccataacaatgccatgaag 4550
            |||| | |||||||| ||||||  |||
Qy    4779 GGTGGATCATTAGAAAATGTTCATGACAGAAGAATCAGAAAAAGTACTATAATGCTATGAAA 4838

Db    4551 aagctgggctccaagaaaacccccagaagccatcccacggcccctgaataagtaccaaggc 4610
            ||| || ||| |||||| || ||||||  | ||
Qy    4839 AAGATGGGCTCTAAAAACCATTAAAAACCATTAAAAGCCATTCCAAGACCAAGGTGGCGACCACAAGCA 4898

Db    4611 ttcgtgttgacatcgtgaccaggcaagcctttgacatcatcatggttctcatcctgc 4670
            |||||||| || || ||  ||||  || ||||||| || |||
Qy    4899 ATAGTCTTTGAAATAGTAACCGATAAGAAATTCATTATGTTATTCATTGGT 4958

Db    4671 ctcaacatgatcaccatgatggtgaccaggcggcggaggtcggaggagacgaaggtt 4730
            ||||||  |||||  ||| || |||| || |  |
Qy    4959 CTGAACAATGTTCACCATGACCATGATCGTTACGATGCCTCGGACACGTATAACGCCGGTC 5018

Db    4731 ctgggcagaatcaaccagttcttgtggcgctcttcacgggcagtgtgatgaagatg 4790
            |||| || ||| |||| ||  || ||  |
Qy    5019 CTAGACTATCTCAATGCGGATAATTCCGGATATCTTCCGAATGTCTATTAAAATA 5078

Db    4791 ttgcccctgcgacagtactacttcaccaacggctgaacgtgttcgacttcatcagtggtg 4850
            |||||  |||| ||  ||  ||||||
Qy    5079 TTCGCTTTACGATATCACTATTTTTATTGGCCATGGAATTATTTGATGTAGTAGTTGTC 5138

Db    4851 atcctgtccattgggagtccgtctgtttttctgcaatcctaagtcactgaaaactactc 4910


Qy    5139 ATTTTATTCCATCTTAGGTCT--TGTACTTAGCGATA-TTA--TCGA-GAAGTACTTCGTG 5192
            ||   | |||| || |  |    || |  |||  ||  |      ||  |||||| |||||
Db    4911 tcccgacgctcttccgggtcatcgtctgcaggatcggccgatcctcaggcgtgatc 4970

Qy    5193 TCGCCGACCCTGCTCCGAGTGGTGCGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTG 5252
            |  | ||| | ||| || |||||| |||||  |||| |||  ||||| ||
Db    4971 cgagcagcaaggggattcgcacgtgctcttcgccctcatgatgtccctcgccccctc 5030

Qy    5253 AAGGGAGCCAAGGGCATTCGACCACTGCTCTCTTGGCCATGTCGCTCGGCGCCCTG 5312
            |||||||||||||| ||| ||  || ||||||| ||||||||||||||||| |||
Db    5031 ttcaacatcggcctcctcccttcctcgtcatgttcatctactccatctcggcatggcc 5090

Qy    5313 TTCAACATCGGCCTGCTGCTGTCTTCCGTGTCATGTTCATCTTTGCCATTTTCGGCATGTCG 5372
            |||||||||||||| || || || |  |||||||||||||||  |  ||||||  | ||
Db    5091 agcttgctaacgtcgtggacgaggcggcatcagacgacatgttcaacttcaagacctttt 5150

Qy    5373 TTCTTCATGCACGTGAAGGAAGGAGAAGAGACGGCGGCATTAACGACGTCTACAACTTCAAGACCTTT 5432
            ||  |  |||  ||  ||  |||  |   |  |||    |||   ||  ||  ||||| |||||| ||||
Db    5151 ggcaacagcatgctgtgcctgttccagatcaccaactccggcgtggacggcgcctcctc 5210

Qy    5433 GGCCAGAGCATGATCCTGTCTTTCAGATGTCGACGTCAGCCGGTTGGGATGGTGTACTG 5492
            |||| ||||||| |||||| || |||||  |  ||||| || |||| | ||| ||  ||
Db    5211 agcccatctcaacacgggcgctcctcctgctgaccccaacgccgccaacagcaacggc 5270

Qy    5493 GACGCGCCATTATCAAT--GAGGAAGC---A-TGCGATCC--ACCCGAC-AGGCACAAAGGC 5543
            |||||||||||  || |  ||  |||     | ||| | |    |||  |     |||  ||
Db    5271 tcccggggggaactgcgggagccgcgcgtgggcatcatctcttcaccaccactacatcatc 5330

Qy    5544 TATCCGGGCCAATTGTGGTTCAGCGAGCCGTTGGAATAACGTTTCTCCCTCATACCTAGTT 5603
            |||||||||||||||||||||||  ||||||||||||||||| | || ||  ||||  |||
Db    5331 atctcctcctcatcgtggtcaacatgtacatgcagtgattcgcagtgattctggaaacctcaacgta 5390

Qy    5604 ATAAGCTTTTTGATAGTTATTATATATGTACATTGCTGTCATTCTCGAGAACTATAGTCAG 5663
            |||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||||
Db    5664 GCCACCGAGGACGTGCAAGAGAGGTCTAACCGACGACGAGCACAGACATGTACTATGAGATC 5723

Qy    5391 gccacggaggagagcacgaggccctgagcgaggagacgactgcagatgttcatgagacc 5450
            ||||| |||||  |||||| |  |||||||||||||||||  || |||  |  || | |
Db    5664 GCCACCGAGGACGTGCAAGAGAGGTCTAACCGACGACGAGCACAGACATGTACTATGAGATC 5723

Qy    5724 TGGCAGCAATTCGATCCGAGGCCACCCAGTACATACCGTATGCATCAGCGTCCAAATTC 5783
            ||| || |||||| || |||||||||||||  ||| |  |  |  || | || || |||
Db    5451 tgggagaagttcgacccgaggccacccagttcattgcctttcctcttctgccctctcagacttc 5510

Qy    5784 CTGGACGTACTGGAGCCCCGCTGCAGATCCAGAGATTCACAAACCGAACAAGTACAAGATCATATCG 5843
            |||||| | ||  | |||||  |   |||  || || || |  |||  || | || ||||| | ||
Db    5511 gcggacacgctctccggccctcttagaatcccaacccaaccagaatatattatccag 5570

Qy    5844 ATGGACATACCCATCTGTCGCGGTGACCTTCATGTACTGCGCTGCACATCCTCGACGCCCCTT 5903
            ||||||   |||||||| || ||| ||||| |||| |||||||| | ||||||  |  |||||
Db    5571 atggacgctgccgttggtcccggggataagatccactgtgctggacatcctttttgcctcc 5630

Db    5631 acaaagaacgctt 5644
            || ||| |||||
Qy    5904 ACGAAAGACTTCTT 5917


RESULT  11
ID   T77805 standard; cDNA; 7052 BP.
AC   T77805;
DT   09-OCT-1997 (first entry)
DE   cDNA encoding variant rat DRG (SNS-B) #2.
KW   Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
KW   modulator; impulse; sensory neuron; acute pain; chronic pain;
KW   neuropathic pain; glia; muscle; parasympathetic nervous system;
KW   enteric nervous system; central nervous system; dorsal root ganglia;
KW   cranial ganglia; ss.
OS   Rattus rattus.
FH   Key             Location/Qualifiers
FT   cds             204..6602
FT                   /tag= a
FT                   /product= Variant_Rat_DRG(SNS-B)
PN   WO9701577-A1.
PD   16-JAN-1997.
PF   25-JUN-1996; G01523.
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PR   28-JUN-1995; GB-013180.
PA   (UNLO ) UNIV COLLEGE LONDON.
PI   Akopian AN, Wood JN;
DR   WPI; 97-100165/09.
DR   P-PSDB: W21739.
PT   New isolated mammalian sensory neuron sodium channel protein - used
PT   to identify modulators of the sodium channel, partic. for the
PT   treatment of pain
PS   Claim 9; Page 69-78; 128pp; English.
CC   The sequences given in T77803-06 encode the wild type and three
CC   variant forms of a rat sensory neuron sodium channel protein which
CC   is insensitive to tetrodotoxin.  The proteins can be used for
CC   identifying modulators of the sodium channel.  Blockers of the
CC   sodium channel will block or prevent the transmission of impulses
CC   along sensory neurons and thereby be useful in the treatment of acute,
CC   chronic or neuropathic pain. The novel protein is found only in sensory
CC   neurons and not in glia, muscle or the neurons of the (para)sympathetic,
CC   enteric or central nervous system.  The protein is found preferably in
CC   the neurons of the dorsal root ganglia or cranial ganglia.  This
CC   sequence encodes a 2132 amino acid protein that contains a 176 amino
CC   acid repeat inserted after amino acid 585 of wildtype rat DRG(SNS-B)
CC   (see also W21737).
SQ   Sequence 7052 BP;      1655 A;      2009 C;      1795 G;      1593 T;

Query Match             4.5%;   Score 296;  DB 32;  Length 7052;
Best Local Similarity  63.8%;   Pred. NO. 2.37e-181;
Matches   890;  Conservative    0;  Mismatches 486;    Indels  18;  Gaps  11;
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Db   4779 aacttcgacaacgtcgctatggctacctgcacttcttcaggtggcaacttcaaaggc 4838
           |||| | | |||  ||||| ||| | ||| | | ||| | |||||||||||||||||
Qy   4539 AATTTCGATCATGTAGGTAACGCGTATCTGTGCCTTTTCCAAGTGGCCACCTTCAAAGGC 4598

Db   4839 tggatggacataatgtatgcagctgttgattccggagagatcaacagtcagcctaactgg 4898
           | ||| | | ||| ||| |  || |||||  |||| ||| |||| | || |||| ||
Qy   4599 TGGATACAAATCATGAACGATGCTATCGATTCACGAGGAGGTGGACAACCAACCAATTCGT 4658

Db   4899 gagaacaacttgtacatgtacctgtacttgtgtttcatcatttcggtggctcttc 4958
           || | | | |||| || |  ||  || |  ||  |||  || |||| ||| ||
Qy   4659 GAAACGAACATCTACACATGTATTATTATTTCGTATTCTTCATCATATTTGGATCCTTTTC 4718

Db   4959 acgctgaatctctttgttgggtcataatgcaacacttcaccacagaaaaaagcta 5018
           ||| || ||||| | ||||| | ||| | | | | |||||| |||| |||||| |
Qy   4719 ACACTCAATCTGTTCATTGGTGTTATCATTGAACAATTTAATGAGCAAAAGAAAAAAGCA 4778

Db   5019 ggaggc-cag--gacatcttcatgacagaagagcagaagaagtactacataatgccatgaag 5075
           | | |  |   |  | |||||||||||| | |||||| |||  ||||||| || |||||
Qy   4779 GGTGGATCATTAGAAAATGTTCATGACAGAAGAATCAGAAAAAGTACTATAATGCTATGAAA 4838

Db   5076 aagctggctccaagaaaacccagaagcccatcccacggcccctgaataagtaccaaggc 5135
           ||||| || | ||   |  | |||||||| ||| | ||||| ||| | | | ||||||
Qy   4839 AAGATGGGCTCTAAAAAACCATTAAAAGCCATTCCAAGAACCAAGGTGGCGACCAACAAGCA 4898

Db   5136 tccgtgtttgacatcgtgacaggcaagcctttgacatcatcatggttctcatctgc 5195
           ||||| |||||||  |||| | |||| |   || |   | |||||  ||| |||||
Qy   4899 ATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTATTGTTATTCATTGGT 4958

Db   5196 ctcaacatgatcaccagtcagttcttgtggcgctcacggacggcagtggagaagacgaaggtt 5255
           || ||||| |||| || || || | |||| ||||| | || | |||| |
Qy   4959 CTGAACAATGTTCACCATGACCTTCGATCGTTACGATGCGTCGGACACGTATAACGGCGGTC 5018

Db   5256 ctggcagaatcaaccagttcttgtggccgtctcacgggccgagtcgtgtgatgaagatg 5315
           || | || |  || || |||  | | || |||||| || || | | | | | |
Qy   5019 CTAGACTATCTCAATGCGATATTCGTAGTTATTTCAGTTCCGAAATGCTATTAAAAAATA 5078

Db   5316 ttcgccctgcgacagtactacttcaccaacgctggaacgtgttcgacttcatagtggtg 5375
           ||||| | |  ||   |  | ||||| ||| | |||| ||||| |  |  |   ||||||
Qy   5079 TTCGCTTTACGATATCACTATTTTTATTGAGCCATGGAATTTATTTGATGTAGTAGTTGTC 5138

Db   5376 atcctgtccattgggagtccgtcgtctgttttctgaatccttagtcactggaaactacttc 5435
           ||| | ||    | || | ||| | |||  ||| || || |  |
Qy   5139 ATTTATCCATCTTAGGTCT--TGTACTTAGCCGATA-TTA--TCGA-GAAGTACTTCGTG 5192

Db   5436 tccccgacgctcttccgggtcatccggtctggccagatcgcggccgcatcctcaggcgtatc 5495
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Qy   5193 TCGCCGACCCTGCTCCGAGTGGTGGTCCGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTG 5252
           || |||| ||||| ||| | ||||||||| | | |||| |||| ||| | ||||| |||
Db   5496 cgagcagccaagggattcacacgtgctcttcggccctcagctccctgatgtccctgcccgccctc 5555

Qy   5253 AAGGGAGCCAAGGCATTCGGACACTGCTCTGCTCCGCGTTGGCCATGTCGCCGGCGCCTG 5312
           |||||||||||||||||| || | ||||| |||||| |  | | | ||||| |
Db   5556 ttcaacatcggctcctcctcctcgtcatgttcatctactcatccttcggcatggcc 5615

Qy   5313 TTCAACATCTGCCTGCTGCTGTCCTCGTGTCCTGGTCATGTTCATTTGCCATTTCGGCCATGTCG 5372
           |||||||| || | |||||||||  ||  ||||||| |||| | ||| ||||||||||||
Db   5616 agcttgctaacgtcgtggacaggccggcatcgcgacgacgagttcaacttcaagacctt 5675

Qy   5373 TTCTTCATGCACGTGAAGAGACGAGGCGGCATTAACGACGGCTACAACTTCAAGACCTTT 5432
           ||| ||||  |   |   |   | | ||  | |||||| | |||| |||||||||||||
Db   5676 gcaacgacatgtcgtgctgttccagatcaccaccctcggccgggctgggacggccctcctc 5735

Qy   5433 GGCCAGAGCATGATCCTGCTCTTTCAGATGTCGACGTCAGCCGGTTGGGATGGTGTACTG 5492
           || | | | | || | | |  |  |  |  | ||| | | | ||| | |
Db   5736 agcccatccaacacgggctcctcctactgcgaccccaacctgcccaacagcaacggc 5795

Qy   5493 GACGCCATTATCAAT--GAGGAAGC---A-TGCGATCC--ACCCGAC-AGGGACAAAGGC 5543
           | ||||  |||| |        | |     | || || |
Db   5796 tcccgggggaactgcgggagcccggcgggtgggcatcatcttcaccaccactacatcatc 5855

Qy   5544 TATCCGGGCAATTGTGGTTCAGGGCCGTTGGGATGGTTCGACGTTTCTCCCTCATACCTAGTT 5603
           ||| | |  |  || | || | | || || | ||| || | ||||  | |  | |   |
Db   5856 atctccttcctcatcgtggtcaacatgtacatcgcagtgattctggagaacttcaacgta 5915

Qy   5604 ATAAGCTTTTGATAGTTATTAATAATGTACATTGCNGTCATTCTCGAGAACTATAGTCAG 5663
           | |  |  |||| | ||   |  |  || ||| || | ||| | |||||  |
Db   5916 gccaccgagagagcacggagcccctgagcgaggagcgacttcgatgagacc 5975

Qy   5664 GCCACCGAGCGACGTGCAAGAGGTCTAACCGACGACGACGACGATCATGAGATC 5723
           || || | | | | |||||||||  | |  |||| | || | || |||| |||
Db   5976 tgggagaagttcgacccagagccgaggccaccagttcattgcctctgccctccagacttc 6035

Qy   5724 TGGCAGCAATTCGATCCGGAGGCCACCCAGTACATACGCTATGATCACGTGTCGGAATTC 5783
           ||| || ||||||| ||| | |||| ||| |  |  | || |  | ||| |  |||||
Db   6036 gcggacacgctctccggccctcttagaatcccaaaccaaccagaatattaatccag 6095

Qy   5784 CTGACGCTACTGGAGCCCCCGCTGCAGATCCACAAACCGAACAAGTACAAGATCATATCG 5843
           || |||  || |||| | | | || |  ||| |  |  | || ||  ||| | |
Db   6096 atggacatgaccatcgtgctggtccccggggataagatccactgctctgacatccttgcctc 6155

Qy   5844 ATGGACATACCATCGTGCTGGTGCCCGGTGGGTGACCTCATGTATGCTCTGCGTCGACATCCTCGACGCGCCCTT 5903
           ||||| |  ||| || |||  |  | |  |  |||  |  | | | | ||||| |||
Db   6156 acaaagaacgtctt 6169

Qy   5904 ACGAAAGACTTCTT 5917
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RESULT   12
ID   T77804 standard; cDNA; 2573 BP.
AC   T77804;
DT   09-OCT-1997 (first entry)
DE   cDNA encoding variant rat DRG (SNS-B) #1.
KW   Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
KW   modulator; impulse; sensory neuron; acute pain; chronic pain;
KW   neuropathic pain; glia; muscle: parasympathetic nervous system;
KW   enteric nervous system; central nervous system; dorsal root ganglia;
KW   cranial ganglia; ss.
OS   Rattus rattus.
FH   Key            Location/Qualifiers
FT   cds            561..2126
FT                  /*tag= a
FT                  /product= variant_Rat_DRG(SNS-B)
PN   WO9701577-A1.
PD   16-JAN-1997.
PF   25-JUN-1996; G01523.
PR   28-JUN-1995; GB-013180.
PA   (UNLO ) UNIV COLLEGE LONDON.
PI   Akopian AN, Wood JN;
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DR    WPI; 97-100165/09.
DR    P-PSDB; W21738.
PT    New isolated mammalian sensory neuron sodium channel protein - used
PT    to identify modulators of the sodium channel, partic. for the
PT    treatment of pain
PS    Claim 9; Page 64-67; 128pp; English.
CC    The sequences given in T77803-06 encode the wild type and three
CC    variant forms of a rat sensory neuron sodium channel protein which
CC    is insensitive to tetrodotoxin.  The proteins can be used for
CC    identifying modulators of the sodium channel.  Blockers of the
CC    sodium channel will block or prevent the transmission of impulses
CC    along sensory neurons and thereby be useful in the treatment of acute,
CC    chronic or neuropathic pain. The novel protein is found only in sensory
CC    neurons and not in glia, muscle or the neurons of the (para)sympathetic,
CC    enteric or central nervous system.  The protein is found preferably in
CC    the neurons of the dorsal root ganglia or cranial ganglia. This
CC    sequence represents bases 4512-6524 of wildtype rat DRG(SNS-B) (see
CC    also T77803), and encodes residues 1437-1957 of the mature protein.
SQ    Sequence  2573 BP;    635 A;    741 C;    610 G;    587 T;

Query Match        3.5%;       Score 231;   DB 32;  Length 2573;
Best Local Similarity  63.4%;   Pred. No. 2.04e-135;
Matches   724;   Conservative     0;   Mismatches 403;   Indels  15;   Gaps   9;

Db    552  gacatcttcatgacgaagacgagaagaagtactacaatgccatgaagaagctgggctcc  611
           || ||||||||||||| | |||||||| |||||| ||| ||||| ||||| ||||||||
Qy   4791  GAAATGTTCATGACGACAGAAGATCAGAAAAAGTACTATAAGTGCTATGAAAAAGATGGGCTCT 4850

Db    612  aagaaacccagaagccatcccacggccccctgaataagtaccaaggcttcgtgtttgac  671
           ||| || ||||||| || |||| |||  || ||||||| || |||||| || || ||||
Qy   4851  AAAAAACCATTAAAAGCCATTCCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAA 4910

Db    672  atcgtgaccaggcaagcctttgacatcatcatgttctcatctgcctcaacatgatc  731
           || |||||| ||| || ||||||| || |||||||| || || ||||| ||||||
Qy   4911  ATAGTAACCGATAAGAAATTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTC 4970

Db    732  accatgatggtggagaccgacgagcaggcgaggagaggcagaggttctggcagaatc  791
           |||||| || ||| ||| |||  ||| ||||||| ||| ||||  |  || ||  |
Qy   4971  ACCATGACCCTGCGATCGTTACGATCGTCGGACACGTATCGGTCCTAGACTATCTC 5030

Db    792  aaccagttctttgtggccgtcctcacgggacgagtgtgtgtgaagatgttcggccctgcga  851
           |||||| |  |  || |||   |||||||  ||| || |||||| || || ||||||| |
Qy   5031  AATGCCGATATTCGTAGTATTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTACGA 5090

Db    852  cagtactacttcaccaacggctggaacgtgttcgacttcatagtggtgatcctgtccatt  911
           ||| || || ||||||||| ||| ||| |  ||| || ||  | |||  || ||||||
Qy   5091  TATCACTATTTTATTGAGCCATGGAATTATTATTGATGTAGTGTCATTTTATCCATC 5150

Db    912  gggagtctgctgtttctgcaatccttaagtcactggaaaactacttctccccgacgtc  971
           |||| |||| ||| || || ||| ||  | |||  || ||||||| ||| || |||||
Qy   5151  TTAGGTCT--TGTACTTAGCCATA-TTA--TCGA-GAAGTACTTCGTGTCGCCGACCCTG 5204

Db    972  ttccgggtcatcgtgctggccgatgtggccaggatggccgcatcctcaggctgatccagg  1031
           || |||||||| |||  ||| ||| || |||||  ||||| || || ||| ||  |||||
Qy   5205  CTCCGAGTGGTCGTGCGTGGCGAAAGTGGGCCCGTGTCCTTCGACTGGTGAAGGGAGCCCAAG 5264

Db   1032  gggattgcacgtgctcttcgcctcttcgcaatcatgatgctcccatcttcaaacatcggc  1091
           ||||||||| || || |||||| || || ||| |||| || ||| || || ||||||||
Qy   5265  GGCATTCGGACACTGCTCTTCGCTCTGCCCATGTCCATGGCCCTGTTCTTCAACAACTGC 5324

Db   1092  ctcctcctcctccgtcatgttcatctactactccatcttcggcatggccagcttcgctaac  1151
           || || || ||||  ||||||| || || ||||||| |||||| ||||||||  || ||
Qy   5325  CTGCTGCGTGTTCCCTGGCGCCATGTCATCTTTGCCCATTTTCGGCATGTCGTTCTTCATGCAC 5384

Db   1152  gtcgtgacgaggccggcatcgacgacatgtcaacttcaagacctttggcaacagcatg  1211
           || || |||||||| ||| || |||| || ||||| ||||||||| ||| ||  || |||
Qy   5385  GTCAAGGAGAAGAGAGGCGGCATTAACGACGTCTACAACTTCAAGAACCTTTGGCCAGAGCATG 5444

Db   1212  ctgtgcctgttccagatcaccaccacctcggccggctggacggcctcctcagcccatcctc  1271
           |||| ||||| |||||||| | ||| ||| || ||||| ||  ||  ||| || || ||
Qy   5445  ATCCTGCTCTTTCAGATGTCGACGCTCAGCGTTGGGATGGCGTGTACTGGACCGCCATTATC 5504

Db   1272  aacacggggcctccctactgcgaccccaacctgccaacagcaacggctcccggggggaac  1331
```

```
Qy   5505  AAT--GAGGAAGC---A-TCGGATCC--ACCCGAC-AGGGACAAAGGCTATCCGGGCAAT  5555
                || |||    ||||| || |   | |  || |  |  |||| ||| ||||||||||||
Db   1332  tcgggagccgccggcgggtggcatcatctttcaccacctacatcatcatcctcctttcctc  1391
           |  |||||||| || | || ||||| || | |||| || || || | |||||  |||
Qy   5556  TGTGGTTCAGCGACCGTTGGAATAAACGTTCTCCCTCATACCCTAGTTATAAGCTTTTTG  5615
           || | | |||   ||| ||||| |  | | |||  || || || ||||||||||||||
Db   1392  atcgtggtcaacatgtacatcgcagtgattctgggagaacttcaacgtagccaccgaggag  1451
           || | |||||| ||| ||| | ||| || || |||||| || ||||| || || ||||
Qy   5616  ATAGTTATTAATATGTACATTGCTCATTCTGCATTCTCGGAACATTCCGAAACTATAGTCAGGCCACCGAGGAC  5675
           |||  || |||||| |  || |||| || ||||| | |||| || ||||  ||| || |||
Db   1452  agcacgaggccctgagcgaggacgactcgcatgttcatgagacctgggagaagttc  1511
           || |  || ||| |||| |||||| || || ||| ||||||  ||||||| || ||
Qy   5676  GTGCAAGAGGGTCTAACCGACGACGACTACGACGACTACTAGGATCTGGCAGCAATTC  5735
           || | ||| | | ||| |||||||||||| || ||  ||| | ||  ||| ||||
Db   1512  gaccggaggccaccagttcattgcctttctgccctctcagacttcgccggaccgctc  1571
           || |||||||| ||||  ||  ||| || |||| |||| |  |||||| ||||| | |
Qy   5736  GATCCGGAGGGCCACCCAGTACATACACGCTATGATCAGCTGTCCGAATTCCTGGACGTACTG  5795
           ||| || |||||||| |||| ||  |||| |||  ||||| |  ||  || |||||| |||
Db   1572  tccggcctcttagaatcccaaccagaataatccagatgaccatggaccg  1631
           || || || ||| |||| | || | ||  ||||||||||||||||||||
Qy   5796  GAGCCCCGCTGCAGATCCACAAAACCGAACAAGTACAAGATCATATCGATGGACATACCC  5855
           ||  |||| ||||| ||  ||| | |||| |||| |||| ||  || ||||||||||||
Db   1632  ttggtcccgggataagatccactgtcgacatcctttgcttcacaaagaacgtc  1691
           || || |||| || ||  |||  ||| | ||||||| || |||| | ||| | |
Qy   5856  ATCTGTCGCGGTGACCTCACTGCGTCCGCGACATCCTGCGACATCCTTACGAAAGACTTC  5915

Db   1692  tt  1693
           ||
Qy   5916  TT  5917
```

```
RESULT   13
ID   Q71202    standard; DNA; 2308 BP.
AC   Q71202;
DT   11-MAY-1995  (first entry)
DE   scd131, a subclone of hscp1, encodes a non-dipteran sodium channel.
KW   non-dipteran sodium channel; lepidoptera; insecticide; sensitivity;
KW   target site; pyrethroids; marker; resistance; probes; detection;
KW   PCR; polymerase chain reaction; Heliothis; degenerate;
KW   Drosophila melanogaster; homologue; hspc1; para locus; scd13; ss.
OS   Heliothis virescens.
FH   Key           Location/Qualifiers
FT   intron        169
FT                 /*tag=   a
FT                 /note=  "end of putative intron"
FT   exon          170..292
FT                 /*tag=   b
FT                 /note=  "putative exon"
FT   intron        293..388
FT                 /*tag=   c
FT                 /note=  "putative intron"
FT   exon          389..583
FT                 /*tag=   d
FT                 /note=  "putative exon"
FT   intron        584..679
FT                 /*tag=   e
FT                 /note=  "putative intron"
FT   exon          680..923
FT                 /*tag=   f
FT                 /note=  "putative exon"
FT   intron        924..1252
FT                 /*tag=   g
FT                 /note=  "putative intron"
FT   exon          1253..1523
FT                 /*tag=   h
FT                 /note=  "putative exon"
FT   intron        1524..1607
FT                 /*tag=   i
FT                 /note=  "putative intron"
FT   exon          1608..1912
FT                 /*tag=   j
FT                 /note=  "putative exon"
```

```
FT   intron        1913..2095
FT                 /*tag= k
FT                 /note= "putative intron"
FT   exon          2096..2308
FT                 /*tag= l
FT                 /note= "putative exon"
FT   cds           170..2308
FT                 /*tag= m
FT   misc_feature  2107
FT                 /*tag= n
FT                 /note= "any of T,C,G or A"
FT   misc_feature  2158
FT                 /*tag= o
FT                 /note= "either T or C"
FT   misc_feature  2203
FT                 /*tag= p
FT                 /note= "any of A, T, G, or C"
PN   CA2112445-A.
PD   01-JUL-1994.
PF   24-DEC-1993; 112445.
PR   30-DEC-1992; US-998289.
PA   (AMCY ) AMERICAN CYANAMID CO.
PI   Black BC, Kreitman M, Taylor M;
DR   WPI; 94-272316/34.
DR   P-PSDB; R60497.
PT   Gene fragment encoding a non-dipteran sodium channelm channel - for
PT   detecting insecticide sensitivity or resistance in insects, pref.
PT   Lepidopterans
PS   Example 2; Fig 1; 32pp; English.
CC   Q71200-202 are the DNA sequences of the subclones, scd61, scd72, and
CC   scd131 respectively, from the genomic clone "hscp1".The hscp1 clone is
CC   approximately 8000 bp and encodes a sodium channel protein. The
CC   clone was isolated from a pyrethroid resistant PEG-87 library. The
CC   non-dipteran sodium channel is thought to be the target site for
CC   sensitivity to a variety of different insecticides and is useful as a
CC   marker for target insensitive insecticide resistance. Q71198-99 are
CC   degenerate primers used to isolate hscp1. The primers are based on an
CC   homologous sequence of the Drosophila para locus, in particular a
CC   portion of an exon in the fourth transmembrane domain of the a-subunit.
SQ   Sequence 2308 BP;      623 A;    511 C;    482 G;    689 T;
```

```
Query Match        2.7%;   Score 177;  DB 12;  Length 2308;
Best Local Similarity  78.5%;  Pred. No. 1.07e-97;
Matches  244;  Conservative  0;  Mismatches  67;  Indels  0;  Gaps  0;

Db  1602 tctcagtttggtattgagtgatattatagaaaaatatttgtgtcaccacgttactga 1661
         |||-||||| |||| ||| ||||||| | || ||||| |||-|| |||| | | |||
Qy  5149 TCTTAGGTCTTGTACTTAGCGGATATTATCGAGAAGACACTGCGTGTCGGCGACCCTGCTCC 5208

Db  1662 gggtggtgagagtagcgaaggtcggtcgtctcgtgttcgttctcgtcgtgaaggtgcgaagggta 1721
         || |||||| || | | || | ||| | ||| | |-|||||| || ||||
Qy  5209 GAGTGGTGGCGTGTGGCGAAAGTGGGCCGTGGTCCATGCCACCATCTGCCTGC 5268

Db  1722 tccggacgttattgttcgggctggccatgtcactgcagccttattcaacatctgtctgc 1781
         | ||||| || | ||||||| ||||||||| || |||||||
Qy  5269 TTCGGACACTGCTCTTCGCGTTGGCCATGCGTGGCCCGTGCGCCCTGTTCAACATCTGCCTGC 5328

Db  1782 tgctgttccttgtgatgttcatcttcgccatcttcggcatgtcgttcttatgcacgtca 1841
         ||| ||||| |-|||| |||||||||| |||| |||||||||
Qy  5329 TGCTGTTCCTGGTCATGTTCATCTTTCGGCATGTCGTTCTTCATGCACGTGA 5388

Db  1842 aagacaaaggtggtctcgacgacgtgtacaacttcaagacccttcgtgcagagtatgatcc 1901
         ||| ||||| ||||||||||| | ||||||||||||||||| | | |||||
Qy  5389 AGGAGAAGAAGGTGGTCTCGACGACGTCTACAACTTCAAGACCCTTGGCCAGAGCATGATCC 5448

Db  1902 tgctatttcag 1912
         |||| ||||||
Qy  5449 TGCTCTTTCAG 5459
```

```
RESULT 14
ID   Q71200 standard; DNA; 2416 BP.
AC   Q71200;
```

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```
DT   12-MAY-1995 (first entry)
DE   scd61, a subclone of hscp1, encodes a non-dipteran sodium channel.
KW   non-dipteran sodium channel; lepidoptera; insecticide; sensitivity;
KW   target site; pyrethroids; marker; resistance; probes; detection;
KW   sense primer; PCR; polymerase chain reaction; Heliothis; degenerate;
KW   Drosophila melanogaster; homologue; hspc1; para locus; scd61; ss.
OS   Heliothis virescens.
FH   Key          Location/Qualifiers
FT   intron        297
FT                 /*tag= a
FT                 /note= "end of intron"
FT   exon          298..441
FT                 /*tag= b
FT   primer_bind   complement (319..338)
FT                 /*tag= c
FT                 /note= "HSC 3455+ ("abelard") (numbering based on
FT                 the Drosophila homologue 'para')"
FT   intron        440..522
FT                 /*tag= d
FT   exon          523..795
FT                 /*tag= e
FT   intron        796..882
FT                 /*tag= f
FT   exon          883..1055
FT                 /*tag= g
FT   intron        1056
FT                 /*tag= h
FT                 /note= "start of intron"
PN   CA2112445-A.
PD   01-JUL-1994.
PF   24-DEC-1993; 112445.
PR   30-DEC-1992; US-998289.
PA   (AMCY ) AMERICAN CYANAMID CO.
PI   Black BC, Kreitman M, Taylor M;
DR   WPI; 94-272316/34.
DR   P-PSDB; R60495.
PT   Gene fragment encoding a non-dipteran sodium channel - for
PT   detecting insecticide sensitivity or resistance in insects, pref.
PT   Lepidopterans
PS   Example 2; Fig 1; 32pp; English.
CC   Q71200-202 are the DNA sequences of the subclones, scd61, scd72, and
CC   scd131 respectively, from the genomic clone "hscp1". The hscp1 clone is
CC   approximately 8000 bp and encodes a sodium channel protein. The
CC   clone was isolated from a pyrethroid resistant PEG-87 library. The
CC   non-dipteran sodium channel is thought to be the target site for
CC   sensitivity to a variety of different insecticides and is useful as a
CC   marker for target insensitive insecticide resistance. Q71198-99 are
CC   degenerate primers used to isolate hscp1. The primers are based on an
CC   homologous sequence of the Drosophila para locus, in particular a
CC   portion of an exon in the fourth transmembrane domain of the a-subunit.
SQ   Sequence 2416 BP;      709 A;    436 C;    487 G;    756 T;
```

```
Query Match        1.5%;   Score 96;  DB 12;  Length 2416;
Best Local Similarity  77.0%;  Pred. No. 1.14e-42;
Matches  137;  Conservative  0;  Mismatches  41;  Indels  0;  Gaps  0;

Db   882 ggctttagaagatgtaaattaccacatcgaccgattcctcaagatatccttgattat 941
         ||||| ||| ||||  |  || |||| || || |||||||||||| ||||
Qy  4022 GGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTATACTATAT 4081

Db   942 ggatcggatcttcaccgtcatttcttcatcgagatgttgatcaaatgcttgccctgg 1001
         ||| |||||| | |||| || |||||||| | |-|||| |  |||||||||
Qy  4082 GGACAAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGG 4141

Db  1002 cttccagaaatacttcacaaatgcgtggtgctgcggactcactgtcatggta 1059
         ||||  |   |||||||||||  ||||||||||||||||| || |||||||||||
Qy  4142 CTTCAAAGTGTACTTCACCAACGCGGTGGTGCTGCGGATTCGTGATTGTCATGGTA 4199
```

```
RESULT 15
ID   N81164 standard; DNA; 204 BP.
AC   N81164;
DT   08-NOV-1990 (first entry)
```

```
DE   Base substituted E.coli beta-galactosidase alpha-fragment.
KW   E.coli beta galactosidase alpha-fragment; base substitutions; ss.
OS   Escherichia coli.
FH   Key             Location/Qualifiers
FT   misc_feature    19..69
FT                   /*tag= a
FT                   /function=multiple cloning site
FT   primer_bind     187..204
FT                   /*tag= b
PN   EP-285123-A.
PD   05-MAY-1988.
PF   30-MAR-1988; 105163.
PR   03-APR-1987; US-034819.
PA   (SUSO) SUOMEN SOKERI OY.
PI   Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
DR   WPI; 88-279927/40.
PT   Introducing random point mutations into nucleic acods -
PT   by prepn of single stranded template, annealing a primer, elongation,
PT   misincorporation, completion of molecules and screening.
PS   Disclosure; P; English.
CC   Random point mutations were introduced into the alpha fragment of
CC   E.coli beta-galactosidase. The wild type sequence was obtained as a
CC   single stranded template and an oligonucleotide was hybridised to
CC   it to generate a popn of DNA molecules which terminate at all
CC   possible nucleotide positions within a specified region. The
CC   variable 3' ends generated in this way are used as primers for
CC   reverse transcriptase. Nucleotides are misincorporated by the
CC   transcriptase and the molecules are completed to forms that can be
CC   amplified and then expressed in a suitable host-vector system.
CC   The sequence covers all 176 difft base substitutions, most of which
CC   occurred singularly in any given mutant.
CC   See also P80575.
SQ   Sequence    204 BP;     21 A;     47 C;     17 G;     11 T;     108 Others;

Query Match             0.8%;  Score 50;  DB 1;  Length 204;
Best Local Similarity   17.2%;         Pred. No. 1.25e-13;
Matches    21;  Conservative   63;  Mismatches 36;  Indels   2;  Gaps   2;

Db        78 dchvgccqymrtt-hhyrrmrbnvyrdynrsdaaawyc-cyrrsvkydccynachhddh 135
              :!::::!! |:::::!|   :::.: .: .:::!|!:.::!:::::|! |: ::::
Qy      5722 TCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATACGCTATGATCAGCTGTCCGAAT 5781

Db       136 yvybbbvynvhnhnncnccccbnnhvchnvhbnnhrnwayvrhdarrddvhccvhccgat 195
              :!:::::!: : ||!: .: : .::! : .:|:::::.: : :|! |
Qy      5782 TCCTGGACGTACTGGAGCCCCGCCGTGCGAGATCCACAAACCGAACAAGTACAAGATCATAT 5841

Db       196 cg 197
              ||
Qy      5842 CG 5843

Search completed: Wed Jul  8 01:38:48 1998
Job time : 1620 secs.
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MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:       Tue Jul  7 22:17:15 1998;  MasPar time 7009.21 seconds
                                 1241.170 Million cell updates/sec
Tabular output not generated.

Title:         >US-08-554-424-7
Description:   (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence: 6513    1 TCTAGACGTTGGCCGATAG.........ACGCGGAGTATTAGCTCTAGA 6513
Comp:                    AGATCTGCAACCGGCGTATC.........TGCGCCTCATAATCGAGATCT

Scoring table: TABLE default
               Gap 6

Nmatch  STD :  Dbase 0; Query 0

Searched:      1759237 seqs, 667866413 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:     embl-est54
              1:em_est1 2:em_est3
Database:     genbank-est106
              3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13
              8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17
              12:gb_est18 13:gb_est19 14:gb_est20 15:gb_est2
              16:gb_est21 17:gb_est22 18:gb_est3 19:gb_est4 20:gb_est5
              21:gb_est6 22:gb_est7 23:gb_est8 24:gb_est9 25:gb_gss
              26:gb_sts

statistics:   Mean 12.783;  Variance 2.249;  scale 5.685

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
```

| Result No. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 124 | 1.9 | 343 | 20 | HSC2HD061 | H. sapiens partial cDN | 2.56e-199 |
| 2 | 121 | 1.9 | 529 | 23 | AA183990 | ms53e02.r1 Life Tech m | 1.13e-192 |
| 3 | 99 | 1.5 | 594 | 24 | AA272867 | vb09f10.r1 Soares mous | 1.36e-144 |
| 4 | 91 | 1.4 | 619 | 25 | FR0002753 | F.rubripes GSS sequenc | 1.85e-127 |
| 5 | 77 | 1.2 | 413 | 10 | AA427267 | ve83f11.r1 Soares mous | 4.40e-98 |
| c 6 | 70 | 1.1 | 252 | 13 | AA754459 | 97SN1787 Rice Immature | 9.27e-84 |
| c 7 | 62 | 1.0 | 214 | 4 | AA360938 | EST70140 T-cell lympho | 8.97e-68 |
| 8 | 64 | 1.0 | 252 | 13 | AA754459 | 97SN1787 Rice Immature | 1.00e-71 |
| 9 | 65 | 1.0 | 573 | 13 | AA699257 | HL08049.5prime HL Dros | 1.03e-73 |
| 10 | 59 | 0.9 | 247 | 13 | AA754458 | 97SN1784 Rice Immature | 6.62e-62 |
| 11 | 60 | 0.9 | 247 | 13 | AA754458 | 97SN1784 Rice Immature | 7.47e-64 |
| c 12 | 49 | 0.8 | 435 | 16 | AA885211 | am34c11.s1 Soares NFL | 5.67e-43 |
| 13 | 50 | 0.8 | 437 | 25 | FR0002729 | F.rubripes GSS sequenc | 8.14e-45 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 14 | 43 | 0.7 | 225 | 16 | AA214661 | zq89e09.r1 Stratagene | 3.33e-32 |
| 15 | 45 | 0.7 | 386 | 25 | FR0002750 | F.rubripes GSS sequenc | 9.81e-36 |
| 16 | 45 | 0.7 | 407 | 25 | FR0002732 | F.rubripes GSS sequenc | 9.81e-36 |
| 17 | 45 | 0.7 | 604 | 25 | FR0002761 | F.rubripes GSS sequenc | 9.81e-36 |
| 18 | 45 | 0.7 | 619 | 25 | FR0002759 | F.rubripes GSS sequenc | 9.81e-36 |
| 19 | 40 | 0.6 | 267 | 10 | AA620400 | ae57d03.s1 Stratagene | 4.91e-27 |
| c 20 | 42 | 0.6 | 407 | 25 | FR0002725 | F.rubripes GSS sequenc | 1.83e-30 |
| c 21 | 40 | 0.6 | 499 | 7 | AA446878 | zw90c04.s1 Soares tota | 4.91e-27 |
| c 22 | 36 | 0.6 | 546 | 7 | AA446997 | zw90c04.r1 Soares tota | 2.04e-20 |
| 23 | 42 | 0.6 | 619 | 25 | FR0002754 | F.rubripes GSS sequenc | 1.83e-30 |
| 24 | 36 | 0.5 | 2275 | 12 | AF034173 | Homo sapiens ntcon2 co | 2.04e-20 |
| c 25 | 35 | 0.5 | 163 | 13 | AA798309 | ub61c07.r1 Soares mous | 8.09e-19 |
| 26 | 34 | 0.5 | 267 | 5 | AA383040 | EST96341 Testis I Homo | 3.03e-17 |
| c 27 | 34 | 0.5 | 269 | 16 | AA867902 | TENS0009 T.cruzi epim | 3.03e-17 |
| c 28 | 34 | 0.5 | 271 | 26 | G16013 | human STS CHLC.GCT13C0 | 3.03e-17 |
| c 29 | 33 | 0.5 | 355 | 21 | HS278350 | H.sapiens mRNA, expres | 1.07e-15 |
| 30 | 34 | 0.5 | 374 | 23 | AA144007 | mr75b01.r1 Stratagene | 3.03e-17 |
| 31 | 35 | 0.5 | 384 | 12 | AA112441 | zm27g02.r1 Stratagene | 8.09e-19 |
| 32 | 33 | 0.5 | 405 | 24 | AA065344 | b02501t Testis 5 Homo | 1.07e-15 |
| 33 | 34 | 0.5 | 409 | 23 | AA153254 | mr77c01.r1 Stratagene | 3.03e-17 |
| c 34 | 35 | 0.5 | 413 | 4 | AA306559 | EST177527 Jurkat T-cel | 8.09e-19 |
| 35 | 34 | 0.5 | 419 | 20 | HSDHEC059 | H.sapiens partial cDN | 3.03e-17 |
| 36 | 33 | 0.5 | 437 | 25 | FR0002733 | F.rubripes GSS sequenc | 1.07e-15 |
| c 37 | 34 | 0.5 | 443 | 21 | HS278389 | H.sapiens mRNA, expres | 3.03e-17 |
| c 38 | 33 | 0.5 | 467 | 12 | AA705382 | zj89h09.s1 Soares feta | 1.07e-15 |
| c 39 | 34 | 0.5 | 532 | 7 | AA445889 | SWAMCA1728SK Brugia ma | 3.03e-17 |
| c 40 | 33 | 0.5 | 559 | 26 | G16023 | human STS CHLC.GCT14F0 | 1.07e-15 |
| c 41 | 35 | 0.5 | 599 | 26 | G16014 | human STS CHLC.GCT14A0 | 8.09e-19 |
| 42 | 34 | 0.5 | 650 | 20 | W27487 | 31g4 Human retina cDNA | 3.03e-17 |
| 43 | 34 | 0.5 | 736 | 11 | AA567426 | HL01171.5prime HL Dros | 3.03e-17 |
| c 44 | 33 | 0.5 | 770 | 26 | AF021116 | Homo sapiens trinucleo | 1.07e-15 |
| 45 | 33 | 0.5 | 2275 | 12 | AF034173 | Homo sapiens ntcon2 co | 1.07e-15 |

```
                            ALIGNMENTS

RESULT       1
LOCUS        HSC2HD061      343 bp  RNA           EST       21-SEP-1995
DEFINITION   H. sapiens partial cDNA sequence; clone c-2hd06, mRNA sequence.
ACCESSION    F07776
NID          g677276
KEYWORDS     EST; partial cDNA sequence; transcribed sequence fragment.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 343)
AUTHORS      Genexpress.
TITLE        Direct Submission
JOURNAL      Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France
             and Genetique Moleculaire et Biologie du developpement, CNRS UPR420
             B.P. 8, 94801 Villejuif Cedex France E-mail: genexpress@genethon.fr
REFERENCE    2  (bases 1 to 343)
AUTHORS      Genexpress.
TITLE        The Genexpress cDNA program
JOURNAL      Unpublished
REFERENCE    3  (bases 1 to 343)
AUTHORS      Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
             Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
             Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
             Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE        IMAGE: molecular integration of the analysis of the human genome
             and its expression
JOURNAL      C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE      95277534
COMMENT      Cloning_method: total mRNA was oligo-(dT) primed and directionally
             cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
             vector;
             Sequencing_method: single read, full automatic;
             Primer: M13_reverse
             cDNA sequence colinear to mRNA
             stretch_removed: nothing
             Normalization_method: Bento Soares, P.N.A.S. 91:9228-9232(1994);
```

```
                 Fax: 314 286 1810
                 Email: mouseest@watson.wustl.edu
                 This clone is available royalty-free through LLNL; contact the
                 IMAGE Consortium (info@image.llnl.gov) for further information.
                 MGI:376114
                 Seq primer: -28M13 rev1 from Amersham
                 High quality sequence stop: 263.
FEATURES         Location/Qualifiers
     source      1..529
                 /organism="Mus musculus"
                 /strain="C57BL/6J"
                 /note="vector: pCMV-SPORT2; Site_1: SalI; Site_2: NotI;
                 Cloned unidirectionally.  Primer: Oligo dT. 13.5dpc
                 embryos. pCMV-SPORT2 vector."
                 /db_xref="taxon:10090"
                 /clone="615290"
                 /clone_lib="Life Tech mouse embryo 13 5dpc 10666014"
                 /dev_stage="13.5dpc embryos"
                 /lab_host="DH10B"
     mRNA
BASE COUNT       96 a       169 c      121 g      143 t
ORIGIN

Query Match             1.9%;  Score 121;  DB 23;  Length 529;
Best Local Similarity 70.1%;  Pred. No. 1.13e-192;
Matches 220;  Conservative  0;  Mismatches 93;  Indels  1;  Gaps  1;

Db    190  TCCCCACGCTCTTACGGCTGCATCCGTCTGGCCAGGATCGGCCGCATCCTCAGGCTGATT  249
           ||||  ||  ||||||  ||| ||||| |||||  ||||  |||| |||||||||| ||||
Qy   5193  TCGCCGACCCTGCTCCGAGTGGCGTGTGCGGGCGGAAAGTGGGCCCGTCCTTCGACTGGTG 5252

Db    250  CGAGCAGCCAAGGGAGGATTCGCACCGTGCCTTCGGCCGCTCTTCGCGTTGGCCATGATGT 309
           | |||||||||| || |||| |||||| ||| ||||||||||  |||  |||||||||||
Qy   5253  AAGGGAGCCAAGGGCCATTGGACACTGCTTCTCCGTGGCCATGTCCTTGGCCATGGCA    5312

Db    310  TTCAACATCGGCCTCCTCTTCGTCATGTTCATCTACTCCATCTTCGGCCATGGCA      369
           ||||||||| ||||| ||| ||||||||||||| ||||||||| ||||||||||
Qy   5313  TTCAACATCTGCCTGCTGCGTTCCTGGTCATCTTTCATCTTTCGGCCATGTCG       5372

Db    370  G-CTTCGCTAATGTCATAGATGAGGCTGGCATCGACGACATGTTCAACTTCAAGACCTTT  428
           | |||||| ||||||  ||||||  || |||||||| |||| |||||||||||||||||
Qy   5373  TTCTTCATGCACGTGAAGGAGAGAGCGGCCATTAACGACGTCACAACTTCAAGACCTTT   5432

Db    429  GGCAACAGCATGCTGTGCCCTTTCCAGATCACCACGTCCGCTCGGCTGGCATGGCCTCCTC 488
           |||  ||||  |  ||| ||||||||||  ||  | |||| ||||||| |||| |||
Qy   5433  GGCCAGAGCATGATCCTGCTCTTTCAGATGTCGCAGGTTCAGCCGGTTGGGATGGTGTACTG 5492

Db    489  AGCCCCATCCTCAA  502
           |||| ||||| |||
Qy   5493  GACGCCATTATCAA  5506

RESULT 3
LOCUS       AA272867     594 bp    mRNA       EST        26-MAR-1997
DEFINITION  vb09f10.r1 Soares mouse NML Mus musculus cDNA clone 748459 5'
            similar to gb:M81758 SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE
            ALPHA-SUBUNIT (HUMAN); gb:U26707 Mus musculus voltage-gated sodium
            channel alpha subunit SCN8A (MOUSE);, mRNA sequence.
ACCESSION   AA272867
NID         g1907742
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Mus.
REFERENCE   1  (bases 1 to 594)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HHMI Mouse EST Project
```

```
                 Genexpress_library_idt: C;
                 Genexpress_sequence_idt: ylc-2hd06.
FEATURES         Location/Qualifiers
     source      1..343
                 /organism="Homo sapiens"
                 /isolate="muscular atrophy patient"
                 /db_xref="taxon:9606"
                 /clone_lib="normalized infant brain cDNA from B.Soares,
                 Psychiatry Dept. Columbia University USA"
                 /sex="female"
                 /tissue_type="total brain"
                 /dev_stage="3 months old"
BASE COUNT       68 a       78 c      80 g      112 t      5 others
ORIGIN

Query Match             1.9%;  Score 124;  DB 20;  Length 343;
Best Local Similarity 67.3%;  Pred. No. 2.56e-199;
Matches 231;  Conservative  0;  Mismatches 112;  Indels  0;  Gaps  0;

Db      1  TTCTCCCATTGTAGAAATGTTCTGGCTGAACTGATAGAAAAGTATTTTGTGTCCCTA    60
           || |||||| |||| ||||
Qy   5140  TTTATCCATCTTAGGTCTTGTACTTAGCGATATTATCGAGAAGTACTTCGTGTCGGCCGA 5199

Db     61  CCCTGTTNCGAGTGATCCGTCTTGCCAGGATTGGCCAGAATCCTACCTCTGATCAAAGGAG 120
           || || || || |||||| ||||| ||  |||  ||||||
Qy   5200  CCCTGCTCCGAGTGGTGCGTGGTGCGTGTGCGGGCCGTGTCCTTCGACTGTGAAGGGAG  5259

Db    121  CAAAGGGGATCCGCACGCTGCTCTTTGCTGTCTTTGATGATGTCCCTTCCGCGTTGTTTAACA 180
           | ||||| ||||||  |||||| ||||||| || |||  |||| || ||| ||  ||||
Qy   5260  CCAAGGGCCATTGGACACTGCTCTTCGCCGTGCCATGTCGCCGTTGGCCATGTCCAACA   5319

Db    181  TCGGNCTTCCTCTTTTTCTCGGTCATGTTCATCTACGNCATCTTTGGGATGTCCAATTTG  240
           |||| ||||||||| |||||||||||||||| ||||  ||||||| |||||| || |||
Qy   5320  TCTGCCTGCTGCGTTCCTGGTCATCTTTCATCTTTCGGCCATGTCGTTCTTCA      5379

Db    241  CCTATGTTAAGAGGGAAGTTGGGATGCGATGACATGTTNANCTTTGGACCTTGGCAACA    300
           | ||  ||| || ||||| |||||||| |  |||||  || | |||| ||||
Qy   5380  TGCACGTGAAGGAGAGAGCGGCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGA  5439

Db    301  GCATGATCTGCCTGTTCCAAATTACACACCTCTGCTGGCTGGGA  343
           ||||||  || || || |||| || ||  |||| || |||||
Qy   5440  GCATGATCCTGCTCTTTCAGATGTCGACGTGACGCCGGTTGGGA  5482

RESULT 2
LOCUS       AA183990     529 bp    mRNA       EST        07-JAN-1997
DEFINITION  ms53e02.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus
            cDNA clone 615290 5' similar to gb:M81758 SODIUM CHANNEL PROTEIN,
            SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN); gb:U26707 Mus musculus
            voltage-gated sodium channel alpha subunit SCN8A (MOUSE);, mRNA
            sequence.
ACCESSION   AA183990
NID         g1767357
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Mus.
REFERENCE   1  (bases 1 to 529)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HHMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
```

COMMENT     Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
            Vector: m13mp18
            V_type: phage
            PRIMER: M13
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1..619
                     /organism="Fugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 010M03"
                     /clone="010M03aE5"
BASE COUNT    156 a    164 c    177 g    120 t    2 others
ORIGIN

Query Match               1.4%;         Score 91;    DB 25;  Length 619;
Best Local Similarity   65.0%;         Pred. No. 1.85e-127;
Matches     195; Conservative     0; Mismatches 105;    Indels   0;    Gaps   0;

Db    17  CTTTCTTATCGTGGTCAACATNTACATCGCCATCATCCTGGAGAACTTCAGTGTGGCCAC  76
          |||| || | || | ||| ||   ||| | ||| | ||||||| ||||||| ||| |||||
Qy  5609  CTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTCCGAGAACTATAGTCAGGCCAC  5668

Db    77  GGAGGAGCAGCACGGAGCCCCTGAGCGAGGATGACTTTGAAATGTTCTATGAGGTTTGGGA  136
          ||| ||| |||| || |||| || || || || ||| || || ||| | ||| | ||||
Qy  5669  CGAGGACGTGCAAGAGGGTCTAACCGACGACGACGCACGATGTACTATGAGATCTGGCA  5728

Db   137  GAAGTTGACCCAGAAGCCACCACAGTTCATCGAGTAGCGCCAAGTTGTCGGACTTTGCAGA  196
          | |||||| ||| || || || | ||  ||||| | || | ||| ||| | ||| |||||||
Qy  5729  GCAATTCGATCCGAGGGCCACCCAGTATGATCACGTATGATCAGCGTGTCCGAATTCCTGGA  5788

Db   197  CTCTCTGTCAGAACCACTGCGGATCGCCAAACCTAACAAGATACAAGCTGATCTCCATGGA  256
          || |||  || |||| |||| ||| || ||||| | | ||  ||  || || || | ||||
Qy  5789  CGTACTGGGACCCCGCTGCAGATCCACAAAATCCACTGCCTCGATATCCTCTTTGCCTTCACAAA  5848

Db   257  TCTGCCGATGGTCAGCGGGGACAAAATCCACTGCCTCGATATCCTCTTTGCCTTCACAAA  316
          | ||  |  || ||||| | || || ||  || || || ||  ||  ||  ||  || |||
Qy  5849  CATACCCATCTGTCGCGGTGACCTCAGTGCCTCGCGACCATCCTCGACGCCCCTTACGAA  5908

RESULT   5
LOCUS       AA427267                413 bp    mRNA          EST          16-OCT-1997
DEFINITION  ve83f11.r1 Soares mouse NbMH Mus musculus cDNA clone 832845 5'
            similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT
            (HUMAN); gb:U26707 Mus musculus voltage-gated sodium channel alpha
            subunit SCN8A (MOUSE);, mRNA sequence.
ACCESSION   AA427267
NID         g2110055
KEYWORDS    EST.
SOURCE      house mouse.
            Mus musculus
  ORGANISM  Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 413)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
  COMMENT   Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:493061

JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:457443
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 456.
FEATURES             Location/Qualifiers
     source          1..594
                     /organism="Mus musculus"
                     /note="vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I, Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATCTTTTTTTTTTTTTTTT 3'];
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia) digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
                     /db_xref="taxon:10090"
                     /clone="748459"
                     /clone_lib="Soares mouse NML"
                     /tissue_type="Liver"
                     /lab_host="DH10B"
     mRNA            <1..>594
BASE COUNT    140 a    150 c    169 g    135 t
ORIGIN

Query Match               1.5%;         Score 99;    DB 24;  Length 594;
Best Local Similarity   73.0%;         Pred. No. 1.36e-144;
Matches     157; Conservative     0; Mismatches  58;    Indels   0;    Gaps   0;

Db   165  AATCCCAACTACGGCTACACCAGCTTCGACACCTTCAGCTGGGCCTTCCTGGCACGGTTC  224
          ||| || || || ||| ||| || ||||||| |||| ||||||||  || |||| ||||||
Qy  1110  AATCCGAATTATGGCTACACCAGCTTCGATTCGTTCGGATGGGCTTTCCTGGTCTGGCCCTTC  1169

Db   225  CGCCTCCATGACTCAGGACTCAGGAGGAGAACTTATACCAGCTGACCGACGGGCTGGG  284
          || ||| || || ||| ||||| |||||| | ||||| || ||| || ||| ||||||
Qy  1170  CGGCTGATGACACAGGACTTCTGGGAGGATCGTACCAGCTGTACCAGCTGGTGTTCGCGGCCGCCGGA  1229

Db   285  AAAACGTACATGACGATCTTCTTTGTCTTGGTGATCTTCGTCTGGGTTCTTTCTATTGGTGAAC  344
          | ||| | ||| || || || |||| | ||| || ||  | | |||| |||||| |||||| |||
Qy  1230  CCATGGCACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTGTGAAT  1289

Db   345  TTGATCTTGGCTGTGGTGGTGGCCATGGCTTACGAAGA  379
          |||||||  ||  | |||| |  ||||| || || ||||
Qy  1290  TTGATTTTGGCCATTGTTGCCCATGTGTCCATGATGACGA  1324

RESULT   4
LOCUS       FR0002753               619 bp    DNA           GSS          27-FEB-1997
DEFINITION  F.rubripes GSS sequence, clone 010M03aE5, genomic survey sequence.
ACCESSION   Z86536
NID         g1883448
KEYWORDS    GSS; genome survey sequence.
SOURCE      Fugu rubripes.
  ORGANISM  Fugu rubripes
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei;
            Tetraodontidae; Fugu.
REFERENCE   1 (bases 1 to 619)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource

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Putative full length read
vector to vector length is
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 354.
FEATURES
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                    /strain="C57BL/6J"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                    was primed with a Not I - oligo(dT) primer [5'
                    TGTAACAATCTGAAGTGGAGCGGCCGCCGGAAGTTTTTTTTTTTTTTTTTTTTTTT
                    3']; double-stranded cDNA was ligated to Eco RI adaptors
                    (Pharmacia), digested with Not I and cloned into the Not
                    I and Eco RI sites of the modified pT7T3 vector. RNA
                    provided by Dr. Minoru Ko, Wayne State Univ. Library
                    constructed and normalized by Bento Soares and M.Fatima
                    Bonaldo."
                    /db_xref="taxon:10090"
                    /clone="832845"
                    /clone_lib="Soares mouse NbMH"
                    /sex="male"
                    /tissue_type="heart"
                    /dev_stage="4 weeks"
                    /lab_host="DH10B"
BASE COUNT      117 a      92 c     110 g      94 t
ORIGIN
Query Match              1.2%;   Score 77;   DB 10;  Length 413;
Best Local Similarity  69.2%;   Pred. No. 4.40e-98;
Matches  139;  Conservative   0;  Mismatches  62;  Indels  0;  Gaps  0;

Db      1 TACACAAGCTTGACACGTTCGGCTGGGCCTTCTTGGCCTTGTTCGGCTAATGACTCAG   60
          |||||||||  || ||||||||| || ||||||| |||| ||| |||||||||| ||||||
Qy   1125 TACACCAGCTTCGATTCGTTCGGATGGGCCTTCCGTCCCCCTTCCGCTAATGACACACAG 1184

Db     61 GACTACTGGGAGAACCTTTATCAACAGACACTGCGTGCTGCTGGCAAAACCTACATGATT  120
          ||| ||||||||||||||  ||||  ||||||||||||||||||||||| |||||||||
Qy   1185 GACTTCTGGGAGGAGATCTGTACCAGCTGGTGTTGCCGCCCCCGGACCATGGCACATGCTG 1244

Db    121 TTCTTCGTCGTGGTGATATTTCTGGGATCCTTTTACCTGATAAACTTGATCCTGGCTGTG  180
          |||||||  | ||| |||| |||||||  ||| |||||  ||  ||| ||  |||| | ||||
Qy   1245 TTCTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTGAATTTGATTTGGCCATT 1304

Db    181 GTAGGCCATGGCGTACGAGGAA  201
          ||  ||||| ||||  ||  ||
Qy   1305 GTTGCCATGTCGTATGACGAA 1325
```

```
RESULT 6
LOCUS       AA754459      252 bp    mRNA          EST       20-JAN-1998
DEFINITION  97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
            cDNA Clone 97SN1787, mRNA sequence.
ACCESSION   AA754459
NID         g2801165
KEYWORDS    EST.
SOURCE      rice.
ORGANISM    Oryza sativa
            Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
            Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
            Poales; Poaceae; Oryza.
REFERENCE   1 (bases 1 to 252)
AUTHORS     Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
            Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
            Lee,M.C. and Eun,M.Y.
TITLE       Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL     Unpublished (1998)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr
            Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
            University, Yongin, Korea. 449-728 bnahm@bioserver.myongji.ac.kr
            Seq primer: M13 Reverse Primer.
FEATURES
    source          Location/Qualifiers
                    1..252
                    /organism="Oryza sativa"
                    /cultivar="Milyang23"
                    /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                    XhoI; Directional cDNA library inserted into lambda ZAPII
                    vector  at 5'end with EcoRI and 3' end with Xho I site."
                    /db_xref="taxon:4530"
                    /clone="97SN1787"
                    /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
                    /tissue_type="Immature Seed"
                    /dev_stage="5 days after pollination"
                    /lab_host="E. coli SOLR"
BASE COUNT        5 a      21 c      12 g      35 t      179 others
ORIGIN
Query Match              1.1%;   Score 70;   DB 13;  Length 252;
Best Local Similarity  13.2%;   Pred. No. 9.27e-84;
Matches  31;  Conservative  120;  Mismatches  80;  Indels  3;  Gaps  3;

Db     15 CBAWMTTSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSIMTWGTVNWBNVS  74
          |:|:   .|:   :|:: :::::   :|:::   |: :  |: :: :  ::|  :  ::  ||  |
Cp   6390 CGAACCCGTCGCTCTCCACGAGAACGGCGGTCTGTCGCCCGGCCTACCCGTCCGGGAC 6331

Db     75 GDWHYWBVBNTK-VDVGNHTRCSRWRBVTRMAHYHYDTNCBBYNNNDYHMWHBBMYBBTG 133
          |: :::  .::  ::::: :|::  .::  : ||::||::|:  |:|:  :  ::||:|
Cp   6330 TTCCCGCCGTCGTGCCCGCCCGCTGCTGCTGGCCGCGTCGTGCCGCCCGCCGCCGCTG 6271

Db    134 CMTCTMWCWBHYNKCTASGWHTSTN-YDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHT 192
          ::|||  :|::: .::  ::| |:| ::::: :  :::||:: :::  :
Cp   6270 CATC-CTCACCCGGACTATTTACATTACTTCATCATCGGCATCGGCAGCTCCTTCTGCAGTA 6212

Db    193 KVSTRATRSYTCVRKYCVMWMTKKVKKYHVVBBGCHBTDSKCKTMWMTNKHV 246
          :||:|:  :::  :|:  |:||::  ::||::: ::::::|  :  |:|
Cp   6211 CCGTTAAACTACCATCTCCACCAGCGGCGCCATCGCCCGTCCGTTGCTTCATCG 6158
```

```
RESULT 7
LOCUS       AA360938                214 bp    mRNA          EST       21-APR-1997
DEFINITION  EST70140 T-cell lymphoma Homo sapiens cDNA 5' end similar to
            similar to sodium channel 1, mRNA sequence.
ACCESSION   AA360938
NID         g2013258
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1 (bases 1 to 214)
AUTHORS     Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He.W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
TITLE       Initial assessment of human gene diversity and expression patterns
```

JOURNAL       based upon 83 million nucleotides of cDNA sequence
MEDLINE       Nature 377 (6547 Suppl), 3-174 (1995)
COMMENT       96026280
              Contact: Kerlavage, AR
              Bioinformatics
              The Institute for Genomic Research
              9712 Medical Center Drive, Rockville, MD 20850 USA
              Tel: 3018699056
              Fax: 3018699423
              Email: arkerlav@tigr.org
              For clone availability, additional sequence and expression
              information related to this EST, please check the TIGR Human Gene
              Index (http://www.tigr.org/tdb/hgi/hgi.html)
              Seq primer: M13 Reverse.
FEATURES      Location/Qualifiers
   source     1..214
              /organism="Homo sapiens"
              /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
              XhoI"
              /db_xref="ATCC (inhost):165061"
              /db_xref="taxon:9606"
              /clone_lib="T-cell lymphoma"
              /cell_type="T-lymphocyte"
   mRNA       <1. .>214
BASE COUNT    57 a    50 c    57 g    47 t    3 others
ORIGIN
Query Match   1.0%;    Score 62;    DB 4; Length 214;
Best Local Similarity  75.4%;    Pred. No. 8.97e-68;
Matches  95;  Conservative  0;  Mismatches  30;  Indels  1;  Gaps  1;

Db     89   AAGTTNGACATCCCAAAGATGGCATAGATAAACATGNCCAGGAGAGAGCAGGAGGCCGATG  148
            || |||||| || |||||| |||| ||||| |||||| |||||| ||||| ||||| ||||
Cp   5377   AAGAACGACATGCCGAAAATGGCAAAATGGCAAAGATGAACATGACCAGGAACAGCAGCAGCAGATG  5318

Db    149   TTAAACAACGCAGGAAGGGACATCATCANAGCAAAGAGCAAAGAGCAGCGTTGCGGATCCCCTTTGC  208
            || |||| || |||| |||||||||||| ||||| ||| |-||||||| ||-|||||||
Cp   5317   TTGAACAGGGCCGGCAGCGACCATGGCCAACGCGCAAGAGCAGCAGTGTC-CGAATGCCCTTGGC  5259

Db    209   TCCTTT  214
            ||| ||
Cp   5258   TCCCTT  5253

RESULT    8
LOCUS       AA754459       252 bp    mRNA       EST       20-JAN-1998
DEFINITION  97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
            cDNA clone 97SN1787, mRNA sequence.
ACCESSION   AA754459
NID         g2801165
KEYWORDS    EST.
SOURCE      rice.
ORGANISM    Oryza sativa
            Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
            Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
            Poales; Poaceae; Oryza.
REFERENCE   1  (bases 1 to 252)
AUTHORS     Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
            Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
            Lee,M.C. and Eun,M.Y.
TITLE       Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL     Unpublished (1998)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr
            Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
            University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr

FEATURES      Seq primer: M13 Reverse Primer.
   source     Location/Qualifiers
              1..252
              /organism="Oryza sativa"
              /cultivar="Milyang23"
              /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
              XhoI; Directional cDNA library inserted into lambda ZAPII
              vector  at 5'end with EcoRI and 3' end with Xho I site."
              /db_xref="taxon:4530"
              /clone="97SN1787"
              /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
              /tissue_type="Immature Seed"
              /dev_stage="5 days after pollination"
              /lab_host="E. coli SOLR"
BASE COUNT    5 a    21 c    12 g    35 t    179 others
ORIGIN
Query Match   1.0%;    Score 64;    DB 13; Length 252;
Best Local Similarity  11.6%;    Pred. No. 1.00e-71;
Matches  26;  Conservative  115;  Mismatches  82;  Indels  2;  Gaps  2;

Db     22   SYBCHGNBWVVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWB  81
            :::|:|| : :: .|:  : :||: : :  | :|  :
Qy    303   CGCCGGAATTGGCCTCCACTCCTCTCGGAGGATATCGATCCCTACTACAGCAATGTACTG  362

Db     82   VBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBTGCMTCTMWC  141
            :: |:|:  |  :.|||  ::|::: :: ::::::
Qy    363   ACATTCGTAGTTGTAAGCAAGGAAAGATATTTTCGCTTTTCTGCATCAAAAGCAATG  422

Db    142   WBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATR  201
            |: |||| :  :|| | : :|:::| :|::: ::|:::|: :::|||: ::| ||
Qy    423   TGG-ATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTCT-AGTGCATC  480

Db    202   SYTCVRKYCVMWMKKVVVKKYHVVBBGCHBTDSRCKTMWMTNKHV  246
            :-|: :::::::::::::::::| ::::::-|:|::|:::| :::
Qy    481   CATTATTTTTCCCTATTCATCATCACCACAATTCTGTCAACTGCA  525

RESULT    9
LOCUS       AA699257                            EST       18-DEC-1997
DEFINITION  HL08049.5prime HL Drosophila melanogaster head pOT2 Drosophila
            melanogaster cDNA clone HL08049 5prime similar to X14398:
            Drosophila put. sodium channel gene part 5 (AA 1320-1680), mRNA
            sequence.
ACCESSION   AA699257
NID         g2702186
KEYWORDS    EST.
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
            Eukaryotae; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
            Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 573)
AUTHORS     Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
            Brokstein,P., Lewis,S. and Rubin,G.M.
TITLE       BDGP/HHMI Drosophila EST Project
JOURNAL     Unpublished (1997)
COMMENT     Contact: Harvey, D.
            G. M. Rubin-Molecular and Cell Biology
            University of California Berkeley
            539 LSA, Berkeley, CA 94720-3200, USA
            Fax: 510 643 9947
            Email: httpd://fruitfly.berkeley.edu/EST, est@fruitfly.berkeley.edu
            Plate: 80  row: E  column: 1
            High quality sequence stop: 426.
FEATURES      Location/Qualifiers
   source     1..573
              /organism="Drosophila melanogaster"
              /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
              XhoI: sized fractionated cDNAs were directly ligated into
              pOT2."
              /db_xref="taxon:7227"

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                    /dev_stage="5 days after pollination"
                    /lab_host="E. coli SOLR"
BASE COUNT      7 a     16 c     21 g     34 t     169 others
ORIGIN

Query Match    0.9%;    Score 59;  DB 13;  Length 247;
Best Local Similarity 16.1%;  Pred. No. 6.62e-62;
Matches   40;  Conservative  119;  Mismatches 83;  Indels 6;  Gaps 6;

Db     1 HWDCTMNTVWRGCCCBAWMNKHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNA 60
         ::::|:| |:: | ||::::::: |:|:
Qy  2605 TTGGCCATCGAGGCCACCATGCAAGCTAATGCCATGAGCCCAAGTACTATTCCA-GG-A 2662

Db    61 HCRYTVBWTYARSKYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBT 120
         :::|::: :| |:: ::: | ::|:: : |  : |:|::::
Qy  2663 GGGCTGGAACATCTT-CGACTTCATTATCGTGGCCCTATTCGCTATTGGAACTGGGACTCG 2721

Db   121 AYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDK-TDSDCGGGCWRK 179
         :| ::::: :: :|:: ::  ::  :|:|::||::|:::||::::|:
Qy  2722 AGGGTGTCCAGGGTCGTCGTGTTCCTTTCGATTCGCTGCGTGATTCAAACTGG 2781

Db   180 VTYGSSBYBRCGVNVMVRTTSMWTDKSTKMBS-MDMSRR-SRVHYGRWMBNKKRGMSRNW 237
         :|:::|:: :|: :::|:::|: :::|::|  ::|:|::
Qy  2782 CCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTATGGGACGCACCATGGGCGCTT 2841

Db   238 TDTKTWRT 245
         |::|:||:|
Qy  2842 TGGGTAAT 2849
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RESULT  11
LOCUS       AA754458      247 bp    mRNA           EST        20-JAN-1998
DEFINITION  97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
            cDNA clone 97SN1784, mRNA sequence.
ACCESSION   AA754458
NID         g2801164
KEYWORDS    EST.
SOURCE      rice.
ORGANISM    Oryza sativa
            Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
            Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
            Poales; Poaceae; Oryza.
REFERENCE   1 (bases 1 to 247)
  AUTHORS   Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
            Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
            Lee,M.C. and Eun,M.Y.
  TITLE     Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr
            Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
            University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
            Seq primer: M13 Reverse Primer.
FEATURES             Location/Qualifiers
     source          1..247
                     /organism="Oryza sativa"
                     /cultivar="Milyang23"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Directional cDNA library inserted into lambda ZAPII
                     vector at 5'end with EcoRI and 3' end with Xho I site."
                     /db_xref="taxon:4530"
                     /clone="97SN1784"
                     /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
                     /tissue_type="Immature Seed"
                     /dev_stage="5 days after pollination"
                     /lab_host="E. coli SOLR"
BASE COUNT      7 a     16 c     21 g     34 t     169 others
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                    /clone="HL08049"
                    /clone_lib="HL Drosophila melanogaster head pOT2"
                    /sex="male and female"
                    /dev_stage="head--brain & sensory organ"
                    /lab_host="Xl1 Blue"
BASE COUNT    129 a    147 c    145 g    152 t
ORIGIN

Query Match    1.0%;    Score 65;  DB 11;  Length 573;
Best Local Similarity 62.9%;  Pred. No. 1.03e-73;
Matches  171;  Conservative  0;  Mismatches 100;  Indels 1;  Gaps 1;

Db    23 GGGCTATATTGCGGTTGATCAAGGCCGCCAAGGGGATCAGAAAGTTGCTATTCGCTCTC 82
         |||| || | || |  || ||||||| |||||| | | || |||| ||| ||| ||||
Qy  5232 GGGCTGTCCTTCGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGCGTTG 5291

Db    83 GTAGTGTCCCTGCGCCCCCTATTTAACATCGGAGCTCTGCTAGGACTGATCACCTTTATC 142
         ||| | |  ||| ||| |  || ||| || |||| | | || |||| | ||||||  |||
Qy  5292 GCCATGTCGCTGCCGCGCCGCCGCCTGTTCAACATCTGCCTGCTGCTGTTCCTGGTCATC 5351

Db   143 TACCGAATTCTGGGCATGTCGCGTCTGTGCGGAAATGTCAAGCTCCCAGGTGCTCTCGATGAC 202
         | ||| ||| ||||| | |   || ||||  ||||  |  ||  ||  |||  || ||  |||
Qy  5352 TTTGCCATTTCGGACGTCGTTCTTCATCGACGTGAAGGAGAGAGAGCGGCATTAAACGAC 5411

Db   203 ATGGTGAACTTCCAGACCTTCGGGCGCA-CATGCGAGTTACTGTTCCGGTTGATGACCTCA 261
         |||||  || |||| || |||| |||  | |  |  | || |||||||||||||| | |||
Qy  5412 GTCTACACTTCAAGACCTTTGGCCAGAGCCATGCATGGATCCTCGCTCTTTCAGATGTCGACGTCA 5471

Db   262 GCCGGTGGAATGACGTACTTGAGTCCCTGAT 293
         ||||| ||| ||||| ||| |||| ||| ||
Qy  5472 GCCGGTTGGGATGGTGTACTGGACGCGCCATTAT 5503
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RESULT  10
LOCUS       AA754458      247 bp    mRNA           EST        20-JAN-1998
DEFINITION  97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
            cDNA clone 97SN1784, mRNA sequence.
ACCESSION   AA754458
NID         g2801164
KEYWORDS    EST.
SOURCE      rice.
ORGANISM    Oryza sativa
            Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
            Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
            Poales; Poaceae; Oryza.
REFERENCE   1 (bases 1 to 247)
  AUTHORS   Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
            Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
            Lee,M.C. and Eun,M.Y.
  TITLE     Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr
            Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
            University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
            Seq primer: M13 Reverse Primer.
FEATURES             Location/Qualifiers
     source          1..247
                     /organism="Oryza sativa"
                     /cultivar="Milyang23"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Directional cDNA library inserted into lambda ZAPII
                     vector at 5'end with EcoRI and 3' end with Xho I site."
                     /db_xref="taxon:4530"
                     /clone="97SN1784"
                     /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
                     /tissue_type="Immature Seed"
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ORIGIN

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Query Match             0.9%;    Score 60;   DB 13;   Length 247;
Best Local Similarity  15.8%;    Pred. No. 7.47e-64;
Matches       34;    Conservative  102;   Mismatches  76;    Indels  3;   Gaps  3;

Db      5 TMNTVWRGCCCCBAWMNKH-THMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCR   63
          |: |:::||  |::||::: :::: ||||: :: :| :|
Cp   3657 TCTTATGGCTACCCATATGAGTTAATGCTGGCAGTGTCGTCGTCCTGTAAGGACAAACCTC  3598

Db     64 Y-TVBWYYARSXYGYGTBYYSWNVDTNTGGTGVGKTVNVHSGWNNRCSNSVYVYVWBTAY  122
          : | ::::::|||| :::: || ::: ::|
Cp   3597 TATGGTTAGCTCGTGTTCCAGTCTATTGTCTTGGTGTTAATGAGTTGCCA-ATCATC     3539

Db    123 CDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTY  182
          :::: |: ::|| :::: :|  : :|: ||:: :||:
Cp   3538 GTTGCGTTATTTAGATATTGGATTTCGGATTGTTGTCGGTTGTGTTCCTCATGTCGCCGTGTATC  3479

Db    183 GSSBYBRCGVNVMVRTTSMWTDKSTKMBSMDMSRR  217
          | : || ::|: | :: | |||: ||
Cp   3478 GTGAATTCCATCCGACCCCGATGGGCCACCTCCAG  3444
```

RESULT   12
LOCUS       AA885211      435 bp    mRNA            EST        27-MAR-1998
DEFINITION  am34c11.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone
            IMAGE:1468724 3' similar to TR:P70276 P70276 SODIUM CHANNEL, TYPE
            X, ALPHA POLYPEPTIDE ;, mRNA sequence.
ACCESSION   AA885211
NID         g2994288
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 435)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 390.
FEATURES             Location/Qualifiers
     source          1..435
                     /organism="Homo sapiens"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCb1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1468724"
                     /clone_lib="Soares NFL T GBC S1"
                     /lab_host="DH10B"
BASE COUNT      132 a     89 c     78 g    136 t
ORIGIN

Query Match             0.8%;    Score 49;   DB 16;   Length 435;
Best Local Similarity  59.5%;    Pred. No. 5.67e-43;
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Matches      153;    Conservative  0;    Mismatches  104;    Indels  0;   Gaps  0;

Db     16 CAAGGTCCGTGTTCGACATAGTCACAAGCCAGATCTTTGACATCATCATCAGTCTC      75
          ||||  | ||| || ||||| || || || |||||| || ||| ||
Qy   4893 CAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAAATTCGATATAAATCATTATGTTATTC  4952

Db     76 ATTATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAACCCAAAGCCATGAAA  135
          ||| | ||||||| ||| || || : || :| ||
Qy   4953 ATTGGTCTGAACATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGACACGTATAAC   5012

Db    136 TCCATCCTGACCATCTCAACTGGGTCTTGTGTCATCTTACGTTAGAAGTGTCTCATC     195
          | ||| ||| ||||| ||| || |
Qy   5013 GCGGTCGTTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAATGTCTATTA  5072

Db    196 AAAATCTTTGCTTGAGGCAATACTACTTCACCAATGGCTGGAATTTATTTGACTGTGTG   255
          |||||| |||| || || || || |||||||| |
Qy   5073 AAAATATTCGCTTTACGATATCACTATTTTATTGAGCCATGAGGAATTTATTTGATGTAGTA  5132

Db    256 GTCGTGCTTCTTTCCAT  272
          || || | |||||
Qy   5133 GTTGTCATTTATCCAT   5149
```

RESULT   13
LOCUS       FR0002729      437 bp    DNA             GSS        27-FEB-1997
DEFINITION  F.rubripes GSS sequence, clone 010M03aC8, genomic survey sequence.
ACCESSION   Z86512
NID         g1883424
KEYWORDS    GSS; genome survey sequence.
SOURCE      Fugu rubripes
  ORGANISM  Fugu rubripes
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei;
            Tetraodontidae; Fugu.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: m13mp18
            V_type: phage
            PRIMER: M13
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1..437
                     /organism="Fugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 010M03"
                     /clone="010M03aC8"
BASE COUNT       80 a    169 c     61 g    122 t      5 others
ORIGIN

Query Match             0.8%;    Score 50;   DB 25;   Length 437;
Best Local Similarity  69.6%;    Pred. No. 8.14e-45;
Matches       94;    Conservative  0;    Mismatches  40;    Indels  1;   Gaps  1;

Db    301 AGGGATCGTCCTCGCCGACCATAATTGAGAAAATACTTTGTCCCCGAGCGTTGTTCCGGGT  360
          ||| || |||||| | ||| | ||| |||||||||| |||||
Qy   5153 AGGTCTTGTACTTAGCGATATTATCGAGAGTACTTCGTTGTCGCGACCCTGCTCGCCGAGT   5212

Db    361 GATTCGATTGGCCCGGATCGGACGTATCCTTCGCCTCATCANGGGTGNCAAGGTAT-CG   419
          ||   |  ||| | ||| ||  | |||| || ||| |
Qy   5213 GGTGCGTGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGGTGAAGGGAGCCAAGGGCATTCG  5272

Db    420 GAACCTGCTGTTCGC  434
          || ||||| |||||
Qy   5273 GACACTGCTCTTCCC  5287
```

RESULT  14
LOCUS       AA214661       225 bp      mRNA          EST       12-MAR-1998
DEFINITION  zq89e09.r1 Stratagene hNT neuron (#9372333) Homo sapiens cDNA clone
            649192 5' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II
            ALPHA SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AA214661
NID         g1813315
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 225)
AUTHORS     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE       WashU-NCI human EST Project
JOURNAL     Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
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ACCESSION   Z85533
NID         g1883445
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REFERENCE   1 (bases 1 to 386)
AUTHORS     Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
TITLE       Direct Submission
JOURNAL     Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
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Job time : 10452 secs.

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    |_|  |_|_|   |____/|_| \_\\____|_| |_|  (TM)
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MPsrch_nn  n.a. - n.a. database search, using Smith-Waterman algorithm

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Nmatch STD :    Dbase 0;  Query 0

Searched:       104157 seqs, 26825796 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:       n-issued
                1:5_COMB 2:PCT9_COMB 3:backfiles

Statistics:     Mean 10.170;  Variance 5.407;  scale 1.881

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                            SUMMARIES
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CC      APPLICANT: Warmke, Jeffrey W.
CC      APPLICANT: Hall, Linda
CC      APPLICANT: Feng, Gouping
CC      APPLICANT: Van Der Ploeg, Leonardus
CC      TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC      TITLE OF INVENTION: PARA SODIUM CHANNEL
CC      NUMBER OF SEQUENCES: 7
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Roy D. Meredith
CC      STREET:  P.O. Box 2000, 126 E. Lincoln Avenue
CC      CITY:    Rahway
CC      STATE:   New Jersey
CC      COUNTRY: USA
CC      ZIP: 07065-0907
CC      COMPUTER READABLE FORM:
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CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US95/14378
CC      FILING DATE:
CC      CLASSIFICATION:
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Meredith, Roy D.
CC      REGISTRATION NUMBER: 30,777
CC      REFERENCE/DOCKET NUMBER: 19332 PCT
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (908) 594-4678
CC      TELEFAX: (908) 594-4720
CC      INFORMATION FOR SEQ ID NO: 7:
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1921 GCAATCTAGGCTCCCGGGTTCCTGGGGCA  1980

Db   1981 CACATGGGCTGCTCACCGAGATCTCGGCGGATCTCGGCGGATCTCAGCGAGTCGGCACTACCTGCGTCAGCGGTCCTGGGCA  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1981 CACATGGGCTGCTCACCGAGATCTCGGCGGATCTCGGCGGATCTCAGCGAGTCGGCACTACCTGCGTCAGCGGTCCTGGGCA  1980

Db   2041 GCAAATTGCGCAACCGCAACACGCAACAATCAGTCGGCGGCACCA  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2041 GCAAATTGCGCAACCGCAACACGCAACAATCAGTCGGCGGCACCA  2100
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Db   2101  CCTGTCTGACACCAATCACAAGCTCGATCATCGGCGACTACGAAATTGGCCTGGAGTGCA  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2101  CCTGTCTGACACCAATCACAAGCTCGATCATCGGCGACTACGAAATTGGCCTGGAGTGCA  2160

Db   2161  CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCTGAGCCCGTCCAGACAC  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2161  CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCTGAGCCCGTCCAGACAC  2220

Db   2221  AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2221  AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTG  2280

Db   2281  GTCGGCACAGTCGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGGAGGACG  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2281  GTCGGCACAGTCGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGGAGGACG  2340

Db   2341  ATGACGAGGATGGGCGACGTTCAAAGACAAGCACTGAAGTCATCCAAAGGCATCG  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2341  ATGACGAGGATGGGCGACGTTCAAAGACAAGCACTGAAGTCATCCAAAGGCATCG  2400

Db   2401  ATGTGTTTTGTGTGGGACTGTGCTGGGTTTGGTTGTTGAAATTTCAGGAGTGGGTATCGC  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2401  ATGTGTTTTGTGTGGGACTGTGCTGGGTTTGGTTGTTGAAATTTCAGGAGTGGGTATCGC  2460

Db   2461  TCATCGTCTTCGATCCCTTCGTCGGACGCTCTTCATCACGCTGTGCATTGTGGTCAACACGA  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2461  TCATCGTCTTCGATCCCTTCGTCGGACGCTCTTCATCACGCTGTGCATTGTGGTCAACACGA  2520

Db   2521  TGTTCATGGCAATGATCACCACCAGATGAACAAGGACCGTGCTGCTCAAGAGTG  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2521  TGTTCATGGCAATGATCACCACCAGATGAACAAGGACCGTGCTGCTCAAGAGTG  2580

Db   2581  GCAACTATTTCTTCACCGGCCACCTTTGCCATGCGAGGCCACCATGAAGCTAATGGCCATGA  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2581  GCAACTATTTCTTCACCGGCCACCTTTGCCATGCGAGGCCACCATGAAGCTAATGGCCATGA  2640

Db   2641  GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2641  GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT  2700

Db   2701  CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTCGTCCGTATTGCGTTCCTTCGAT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2701  CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTCGTCCGTATTGCGTTCCTTCGAT  2760

Db   2761  TGCTGCGTGTATTCAAACTGCCCAAGTCTCTGGCCCACACTTAATTTACTCATTTCGATTA  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2761  TGCTGCGTGTATTCAAACTGCCCAAGTCTCTGGCCCACACTTAATTTACTCATTTCGATTA  2820

Db   2821  TGGGACGCACCATGGCGCTTGCGGGAGAATGGATCGAGTCCATGTGGACTGCATGTACGTGGGCG  2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2821  TGGGACGCACCATGGCGCTTGCGGGAGAATGGATCGAGTCCATGTGGACTGCATGTACGTGGGCG  2880

Db   2881  TCTTTGCGGTGGATGGGAATGCAACTGTTCTCGGAAAGAATTATCATGATCACCAAGGACCGGCT  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2881  TCTTTGCGGTGGATGGGAATGCAACTGTTCTCGGAAAGAATTATCATGATCACCAAGGACCGGCT  2940

Db   2941  TTCCGGATGCGCGACCTGCCGCGCTGCGAACTTCACCGACTTCATGATCG  3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2941  TTCCGGATGCGCGACCTGCCGCGCTGCGAACTTCACCGACTTCATGATCG  3000

Db   3001  TGTTCCGGGTGCTCTGCGGAGAATGGATCGAGTCCATGTGGACTGCATGTACGTGGGGCG  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3001  TGTTCCGGGTGCTCTGCGGAGAATGGATCGAGTCCATGTGGACTGCATGTACGTGGGGCG  3060

Db   3061  ATGTCTCGTCGATTCCGTGCTGCTTTCTTCTTCTCTGGCCAATCTTGTCATCGGTGTACTTA  3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3061  ATGTCTCGTCGATTCCGTGCTGCTTTCTTCTTCTCTGGCCAATCTTGTCATCGGTGTACTTA  3120

Db   3121  ACCTTTTCTTAGCCTTGTCTTTGTCTCATCTGGCTCATCAGCTTATCAGCGCCGCGACTG  3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3121  ACCTTTTCTTAGCCTTGTCTTTGTCTCATCTGGCTCATCAGCTTATCAGCGCCGCGACTG  3180

Db   3181  CCGATAACGATACGAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTAAAAGTT  3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3181  CCGATAACGATACGAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTAAAAGTT  3240

Db   3241  GGGTTAAGGCTAATATTGCTGATTGTTTCAAGTTAATACGTAACAAATTGACAAATCAAA  3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3241  GGGTTAAGGCTAATATTGCTGATTGTTTCAAGTTAATACGTAACAAATTGACAAATCAAA  3300

Db   3301  TAAGTGATCAACCATCAGTGAGAGGACCAACCAGATCAGTCAGTTGGATTTGGAGCGAAGAGC  3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3301  TAAGTGATCAACCATCAGTGAGAGGACCAACCAGATCAGTCAGTTGGATTTGGAGCGAAGAGC  3360

Db   3361  ATGGTGACAACGAACTGGAGCTGGCCACGACGAGTCCTCGCCGACGAGCTCATCAAGA  3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3361  ATGGTGACAACGAACTGGAGCTGGCCACGACGAGTCCTCGCCGACGAGCTCATCAAGA  3420

Db   3421  AGGGGATCAAGGAGCGAGCGCAACTGGAGGTGGCCATCGGGGATCGGAATCGGAATTCACGA  3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3421  AGGGGATCAAGGAGCGAGCGCAACTGGAGGTGGCCATCGGGGATCGGAATCGGAATTCACGA  3480

Db   3481  TACACGGCGACAATGCATGAGAATCCGAAGAATCCAAATATCTAAATAACGCAACGA  3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3481  TACACGGCGACAATGCATGAGAATCCGAAGAATCCAAATATCTAAATAACGCAACGA  3540

Db   3541  TGATTGGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAG  3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3541  TGATTGGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAG  3600

Db   3601  GTTTGTCCTTACAGGACGACGACACTGCCAGCCATTCATGGTAGCCATAAGAATC  3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3601  GTTTGTCCTTACAGGACGACGACACTGCCAGCCATTCATGGTAGCCATAAGAATC  3660

Db   3661  GACCATTCAAGGACCAGAGCCACAAGGGCGCAGGATGGAGGGCGAGGAAGC  3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3661  GACCATTCAAGGACCAGAGCCACAAGGGCGCAGGATGGAGGGCGAGGAAGC  3720

Db   3721  GCGACGCCAGCAAGGAGGATTTAGGTCTCGACGAGGAACTGGACGAGGCGAATGCG  3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3721  GCGACGCCAGCAAGGAGGATTTAGGTCTCGACGAGGAACTGGACGAGGCGAATGCG  3780

Db   3781  AGGAGGGCCCGCTGAGATCATTATTGATCTGTATCATTATTCACACGACGACGAGTATCGATG  3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3781  AGGAGGGCCCGCTGAGATCATTATTGATCTGTATCATTATTCACACGACGACGAGTATCGATG  3840

Db   3841  AATATCCAGCTGATTCGTCGCCCGATTCGTACTACTATTAAGAAATTCCGATCTTAGCCGGTG  3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3841  AATATCCAGCTGATTCGTCGCCCGATTCGTACTACTATTAAGAAATTCCGATCTTAGCCGGTG  3900

Db   3901  ACGATGACTCGCCGTTCTGGCAAGGATGGGGCAATTACGACTGAAAACTTTCAATTAA  3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3901  ACGATGACTCGCCGTTCTGGCAAGGATGGGGCAATTACGACTGAAAACTTTCAATTAA  3960

Db   3961  TTGAAAATAAATATTTGAAACAGCTGTATTCACTCGGTGTTGCTCGAATTCGTGATTTCAGCTT  4020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3961  TTGAAAATAAATATTTGAAACAGCTGTATTCACTCGGTGTTGCTCGAATTCGTGATTTCAGCTT  4020

Db   4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCGGATATATTTTATACTATA  4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCGGATATATTTTATACTATA  4080

Db   4081  TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTAATCAAGTGGTTGGCCCTCG  4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4081  TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTAATCAAGTGGTTGGCCCTCG  4140

Db   4141  GCTTCAAAGTGTACTTCACCAACCGGTGTTGGCTCGATTTCGTGATTTCGTGATTGTCATGGTAT  4200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4141  GCTTCAAAGTGTACTTCACCAACCGGTGTTGGCTCGATTTCGTGATTTCGTGATTGTCATGGTAT  4200

Db   4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGGTGTATTCGTATTCAAGCCTTCAAGACTA  4260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGGTGTATTCGTATTCAAGCCTTCAAGACTA  4260

Db   4261  TGGAACGTTAAGAGCACTGAGACACTACGTCCCGTATGCAGGCACCTACGGTCAGGAGGG  4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4261 TGCGAACGTTAAGAGCACTGAGACCACTACGTGCCACGTGTCCCGTATGCGCATGAGAGGG 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 TCGTCGTTAATGCCGTGGTACAAGCTACGTATACCGTCCATCTTCAAGTGTGGTGTGTC   4380
Qy   4321 TCGTCGTTAATGCCGTGGTACAAGCTACGTATACCGTCCATCTTCAAGTGTGGTGTGTC   4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 TAATATTTTGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTA  4440
Qy   4381 TAATATTTTGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTA  4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 AGTGCGAGGACATGAATGGCACGAAGCTCAGCCACGAGCTCAGCCACCAGCCAATGCCT   4500
Qy   4441 AGTGCGAGGACATGAATGGCACGAAGCTCAGCCACGAGCTCAGCCACCAGCCAATGCCT   4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 GCGAGGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGTAACG   4560
Qy   4501 GCGAGGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGTAACG   4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 CGTATCTGTGCCTTTTCCAAGTGGTGGCCACCTTCAAAGGCTGGATACAAAATCATGAACGATG 4620
Qy   4561 CGTATCTGTGCCTTTTCCAAGTGGTGGCCACCTTCAAAGGCTGGATACAAAATCATGAACGATG 4620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CTATCGATTCACGAGGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680
Qy   4621 CTATCGATTCACGAGGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG   4740
Qy   4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG   4740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 TTATCATTGATATATTTTAATGAGCAAAAGAAAAAGCAGGTGGATCATTAGAAATGTTCA  4800
Qy   4741 TTATCATTGATATATTTTAATGAGCAAAAGAAAAAGCAGGTGGATCATTAGAAATGTTCA  4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT  4860
Qy   4801 TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT  4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
Qy   4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTAACCG 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 ATAAGAAATTCGATATAATCATTTATGTTATTCATTGTCGAACATGTTCACCATGACCC   4980
Qy   4921 ATAAGAAATTCGATATAATCATTTATGTTATTCATTGTCGAACATGTTCACCATGACCC   4980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TCGATCGTTACGATGCGTCGGACACGTATAACCGGTCCTAGACTATCTCAATGCGATAT   5040
Qy   4981 TCGATCGTTACGATGCGTCGGACACGTATAACCGGTCCTAGACTATCTCAATGCGATAT   5040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 TCGTAGTTATTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTACGATATCACTATT    5100
Qy   5041 TCGTAGTTATTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTACGATATCACTATT    5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 TTATTGAGCCATGGAATTCGATATTGTGCTTTATCCATTTATCCATCTTAGGTCTTG     5160
Qy   5101 TTATTGAGCCATGGAATTCGATATTGTGCTTTATCCATTTATCCATCTTAGGTCTTG     5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACCTGTCGGTGCGTG         5220
Qy   5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACCTGTCGGTGCGTG         5220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGGCGAAAGTGGGCCGTGTCCTTCGGCGTGTGGACTACTTCGTCAACATCTGCCTGCTG   5280
Qy   5221 TGGCGAAAGTGGGCCGTGTCCTTCGGCGTGTGGACTACTTCGTCAACATCTGCCTGCTG   5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 TCTTCGCCGTTCGGCCATGTCGCCGCGTCGCCGCCCTCGTCGTTCTTCATGCACGTG     5340
Qy   5281 TCTTCGCCGTTCGGCCATGTCGCCGCGTCGCCGCCCTCGTCGTTCTTCATGCACGTG     5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TCATGTTCATCTTTGGCATTTCTTCATCATGCACGTGAGGAGAAGAGAGCC          5400
Qy   5341 TCATGTTCATCTTTGGCATTTCTTCATCATGCACGTGAGGAGAAGAGAGCC          5400
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Db   5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGAGCATGCATGCTGCTCTTTCAGA 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGAGCATGCATGCTGCTCTTTCAGA 5460
Db   5461 TGTCGACGTCAGCCGGTGGGATGGTGTACTGGACGCCCATTATCAATGAGGAAGCATGCG   5520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5461 TGTCGACGTCAGCCGGTGGGATGGTGTACTGGACGCCCATTATCAATGAGGAAGCATGCG   5520
Db   5521 ATCCACCCGACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACGTTGGAATAA   5580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5521 ATCCACCCGACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACGTTGGAATAA   5580
Db   5581 CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTG  5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5581 CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTG  5640
Db   5641 TCATTCTCGAGAACTATAGTCAGGCACCACCGAGGACGTGCAAGAGGGTCTAACCGACACG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5641 TCATTCTCGAGAACTATAGTCAGGCACCACCGAGGACGTGCAAGAGGGTCTAACCGACACG 5700
Db   5701 ACTACGACATGTACTATGAGATCTGGCAGCAATCGGACATCCGAGGCACCCAGTACATAC  5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5701 ACTACGACATGTACTATGAGATCTGGCAGCAATCGGACATCCGAGGCACCCAGTACATAC  5760
Db   5761 GCTATGATCAGCTGTCCCAATTCCTGACGTACTGGAGCCCGTGCAGATCCACAAAC      5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5761 GCTATGATCAGCTGTCCCAATTCCTGACGTACTGGAGCCCGTGCAGATCCACAAAC      5820
Db   5821 CGAACAAGTACAACATCATATCGATGGACACATACCATCTGTCGCGGTGACCTCATGTACT 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5821 CGAACAAGTACAACATCATATCGATGGACACATACCATCTGTCGCGGTGACCTCATGTACT 5880
Db   5881 GCGGTCGACATCCTGACGCCCTACGACAGACTTCTTTGCGCGGGAAGGCAATCCGATATAG 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5881 GCGGTCGACATCCTGACGCCCTACGACAGACTTCTTTGCGCGGGAAGGCAATCCGATATAG 5940
Db   5941 AGGAGACGGGTGAGATTGGTGGCGTCAGCGTGAGGAGTACTCCGCCCCGCTAATCCAGCACGCCCG 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5941 AGGAGACGGGTGAGATTGGTGGCGTCAGCGTGAGGAGTACTCCGCCCCGCTAATCCAGCACGCCCG 6000
Db   6001 TCTCATCAACGCTGTGCGGCGTCGGCGTGAGGAGTACTCCGCCCCGCTAATCCAGCACGCCT 6060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6001 TCTCATCAACGCTGTGCGGCGTCGGCGTGAGGAGTACTCCGCCCCGCTAATCCAGCACGCCT 6060
Db   6061 GGGCGAAAGCCACACAAGGCGCGGCGGCGCGGCGGAGGTGGGTCCTTTGAGCCGGATACGCATG 6120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6061 GGGCGAAAGCCACACAAGGCGCGGCGGCGCGGCGGAGGTGGGTCCTTTGAGCCGGATACGCATG 6120
Db   6121 GCGATGGCGGTGATCCGGATCCGGATGCCCCGGCGACCCGATGAAGCAACGGACGGCGGATG 6180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6121 GCGATGGCGGTGATCCGGATCCGGATGCCCCGGCGACCCGATGAAGCAACGGACGGCGGATG 6180
Db   6181 CGCCCGCTGGTGGAGTGTTAACGGTAGTGTTAACGGTAGTGTTAACGGTACTGCCGATGCCGATG 6240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6181 CGCCCGCTGGTGGAGTGTTAACGGTAGTGTTAACGGTAGTGTTAACGGTACTGCCGATGCCGATG 6240
Db   6241 AGAGTAATGTAAATAGTCCGGCACGACGGTCCGGAGATGCAGCGGCGGCGGCAGCAGCAG   6300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6241 AGAGTAATGTAAATAGTCCGGCACGACGGTCCGGAGATGCAGCGGCGGCGGCAGCAGCAG   6300
Db   6301 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGACGCGCCCGGGAAGTCCCGGGCGGCGGTAGCGCCACAAGG 6360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6301 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGACGCGCCCGGGAAGTCCCGGGCGGCGGTAGCGCCACAAGG 6360
Db   6361 CCCGCGTTCTCGTGGAGAGCGACGATCACGTCGCCGATCGCCCAGCGATCTGAGCCGGCTCGTCATCC 6420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6361 CCCGCGTTCTCGTGGAGAGCGACGATCACGTCGCCGATCGCCCAGCGATCTGAGCCGGCTCGTCATCC 6420
Db   6421 ACTCCGATGCCGATGTCTTCATGCACGTGAGGAGAAGAGAGCG                   6480
          |||||||||||||||||||||||||||||||||||||||||||
Qy   6421 ACTCCGATGCCGATGTCTTCATGCACGTGAGGAGAAGAGAGCG                   6480
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Db  6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513
         |||||||||||||||||||||||||||||||||
Qy  6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513


RESULT 2
ID  US-08-337-339-7 STANDARD; DNA; UNC; 6513 BP.
AC  xxxxxx
DT
DE  Sequence 7, Application US/08337339
CC  Sequence 7, Application US/08337339
CC  Patent No. 5593864
CC  GENERAL INFORMATION:
CC     APPLICANT: Warmke, Jeffrey W.
CC     APPLICANT: Hall, Linda
CC     APPLICANT: Feng, Gouping
CC     APPLICANT: Van Der Ploeg, Leonardus
CC     TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC     TITLE OF INVENTION: PARA SODIUM CHANNEL
CC     NUMBER OF SEQUENCES: 7
CC     CORRESPONDENCE ADDRESS:
CC        ADDRESSEE: John W. Wallen III
CC        STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC        CITY: Rahway
CC        STATE: New Jersey
CC        COUNTRY: USA
CC        ZIP: 07065-0900
CC     COMPUTER READABLE FORM:
CC        MEDIUM TYPE: Floppy disk
CC        COMPUTER: IBM PC compatible
CC        OPERATING SYSTEM: PC-DOS/MS-DOS
CC        SOFTWARE: PatentIn Release #1.0, Version #1.25
CC     CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER: US/08/337,339
CC        FILING DATE:
CC        CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC        NAME: Wallen III, John W.
CC        REGISTRATION NUMBER: 35,403
CC        REFERENCE/DOCKET NUMBER: 19332
CC     TELECOMMUNICATION INFORMATION:
CC        TELEPHONE: (908) 594-3905
CC        TELEFAX: (908) 594-4720
CC  INFORMATION FOR SEQ ID NO: 7:
CC     SEQUENCE CHARACTERISTICS:
CC        LENGTH: 6513 base pairs
CC        TYPE: nucleic acid
CC        STRANDEDNESS: single
CC        TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA
SQ  SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match   100.0%;  Score 6513;  DB 1;  Length 6513;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db    1 TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCGATGAGGAAGAAC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1 TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCGATGAGGAAGAAC 60

Db   61 GCAGTTTGTTCCGTCCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCATTGCCG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 GCAGTTTGTTCCGTCCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCATTGCCG 120

Db  121 CTGAACATGAAAAGCAGAAGGAGCTGGAAAGAAAGAGAGACCGGCGAGGAGGAGGTGCCGGCGAT 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121 CTGAACATGAAAAGCAGAAGGAGCTGGAAAGAAAGAGAGACCGGCGAGGAGGAGGTGCCGGCGAT 180

Db  181 ATGGTCGCAAGAAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGGTC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 ATGGTCGCAAGAAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGATGAAGGTC 240

Db  241 CACAACCGGATCCTACACTTGAACAGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241 CACAACCGGATCCTACACTTGAACAGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT 300

Db  301 TCCCGCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301 TCCCGCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360

Db  361 TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAA 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  361 TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAA 420

Db  421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTCTAGTGCATC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTCTAGTGCATC 480

Db  481 CATTATTTTCCCATTCATCATCACCACAATTCTCGTCAACTGCATCCTGATGATAATGC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  481 CATTATTTTCCCATTCATCATCACCACAATTCTCGTCAACTGCATCCTGATGATAATGC 540

Db  541 CGACAACGCCCACGGTTGAGTCCACTGAGGTGATAATTCACCGGAATCTACACATTTGAAT 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  541 CGACAACGCCCACGGTTGAGTCCACTGAGGTGATAATTCACCGGAATCTACACATTTGAAT 600

Db  601 CAGCTGTTAAAGTGATGGCACGAGGTTCATTTATGCCCGTTTACGTATCTTAGAGATG 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  601 CAGCTGTTAAAGTGATGGCACGAGGTTCATTTATGCCCGTTTACGTATCTTAGAGATG 660

Db  661 CATGGAATTGGCTGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGTATAGATT 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  661 CATGGAATTGGCTGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGTATAGATT 720

Db  721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCGTTAAAACCGTAGCCA 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCGTTAAAACCGTAGCCA 780

Db  781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGTGAAGAATCGCGCG 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGTGAAGAATCGCGCG 840

Db  841 ATGTGATTATCCTGACCATGTTCTCCCGTGTTCGGTTCGGTTGATGGGCCTACAGATCT 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  841 ATGTGATTATCCTGACCATGTTCTCCCGTGTTCGGTTCGGTTGATGGGCCTACAGATCT 900

Db  901 ATATGGGCGTGCTCACCGAGAAGTGCATCAAGAAGTGCATCAAGAAGTTCCCGCGGTTCCTGGGGCA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  901 ATATGGGCGTGCTCACCGAGAAGTGCATCAAGAAGTGCATCAAGAAGTTCCCGCGGTTCCTGGGGCA 960

Db  961 ATCTGACCGACGAGAACTGGGACTATCACAATCCAATCACAATGGTATTCCAGG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  961 ATCTGACCGACGAGAACTGGGACTATCACAATCCAATCACAATGGTATTCCAGG 1020

Db 1021 ACGAGGGCATCTCATTTCCGTTATGCGGCAATATCCGGTGCGGGCAATGCGACGACG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1021 ACGAGGGCATCTCATTTCCGTTATGCGGCAATATCCGGTGCGGGCAATGCGACGACG 1080

Db 1081 ATTACGTGTGCCTGCGAGGGTTTGGTCCGGAGGGTTTGGTTCGGAATCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1081 ATTACGTGTGCCTGCGAGGGTTTGGTCCGGAGGGTTTGGTTCGGAATCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140

Db 1141 CGTTCGGATGGCTTTCCGTCCGTTCCGTTCCGGCCTTCCGCCTTCCGCTGATGACACGAGGACTTCTGGGAGGATC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1141 CGTTCGGATGGCTTTCCGTCCGTTCCGTTCCGGCCTTCCGCCTTCCGCTGATGACACGAGGACTTCTGGGAGGATC 1200

Db 1201 TGTACCAGCTGGTGTTGCCGCCGCCATGGCACCATGCTGTTCTTATAGTCATCA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1201 TGTACCAGCTGGTGTTGCCGCCGCCATGGCACCATGCTGTTCTTATAGTCATCA 1260

Db 1261 TCTTCCTAGTTCATTCTATCTTGTGAATTTGATTTGCCATGTCGTATG 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1261 TCTTCCTAGTTCATTCTATCTTGTGAATTTGATTTGCCATGTCGTATG 1320

Db 1321 ACGAATTGCAAAGAAGGCCGAAGAAGAGAGGCCGTACGTGAAG 1380
         |||||||||||||||||||||||||||||||||||||||||||
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Left column:

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Qy        ACGAATTGCAAAGGAAGGCCGGAGAAGAGAGGCTGCCGAAGAGGAGGCTGATACGTGAAG  1380

Db  1381  CGGAAGAAGCTGCCGCCCGCCAAACGGCGGCCAAGCTGGAGGAGCGGGCCAATGCGCAGGCTC  1440
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Qy  1381  CGGAAGAAGCTGCCGCCCGCCAAAGCTGGAGGAGCGGGCCAATGCGCAGGCTC  1440

Db  1441  AGGCAGCGAGCGGATGCGGCTGCCGCCGAGAGAGGCTCACTGCACTGGCCAAGA  1500
          |||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441  AGGCAGCGAGCGGATGCGGCTGCCGCCGAGAGAGGCTCACTGCACTGGCCAAGA  1500

Db  1501  GTCCGACGTATTCTTGCATCAGCTATGAGCTATTTGTTGGCGGCGAAGGGCAACGATG  1560
          |||||||||||||||||||||||||||||||||||||||||
Qy  1501  GTCCGACGTATTCTTGCATCAGCTATGAGCTATTTGTTGGCGGCGAAGGGCAACGATG  1560

Db  1561  ACAACAACAAAGAAGAGAATGTCCATTCGGAGGCGTCGAGGCGTCGGAGTCGGTCGGTGAGCG  1620
          |||||||||||||||||||||||||||||||||||||||||||||
Qy  1561  ACAACAACAAAGAAGAGAATGTCCATTCGGAGGCGTCGAGGCGTCGGAGTCGGTCGGTGAGCG  1620

Db  1621  TTATACAAAGACAACCAGCACCTACCACAGCACCACCAAGTTCGTAAAGTGA  1680
          |||||||||||||||||||||||||||||||||||||||||||
Qy  1621  TTATACAAAGACAACCAGCACCTACCACAGCACCACCAAGTTCGTAAAGTGA  1680

Db  1681  GCACGACAATCCTTATCCTGGTTCACCGTTTAACATACGCAGGGGATCACGTAGTT  1740
          |||||||||||||||||||||||||||||||||||||||||||
Qy  1681  GCACGACAATCCTTATCCTGGTTCACCGTTTAACATACGCAGGGGATCACGTAGTT  1740

Db  1741  CTCACAAGTACACGATACGGAACGGACGTGGCCGCTTGGTATACCCGTTAGCCGATCGTA  1800
          ||||||||||||||||||||||||||||||||||||||||||
Qy  1741  CTCACAAGTACACGATACGGAACGGACGTGGCCGCTTGGTATACCCGTTAGCCGATCGTA  1800

Db  1801  AGGCCATTGGTATTGTCAACATATCAGGATGCCCAGCACTTGCCCTATGCCGACGACT  1860
          |||||||||||||||||||||||||||||||||||||||
Qy  1801  AGGCCATTGGTATTGTCAACATATCAGGATGCCCAGCACTTGCCCTATGCCGACGACT  1860

Db  1861  CGAATGCCGTCACCCCGATGTCCGGAGAGAATGGGCGCCATCATAGTGCCCGTGTACTATG  1920
          |||||||||||||||||||||||||||||||||||||||
Qy  1861  CGAATGCCGTCACCCCGATGTCCGGAGAGAATGGGCGCCATCATAGTGCCCGTGTACTATG  1920

Db  1921  GCAATCTAGGCTCCGGCGACACTCATCGATGACGAGTCCCGAATATCGTATACCT  1980
          |||||||||||||||||||||||||||||||||||||
Qy  1921  GCAATCTAGGCTCCGGCGACACTCATCGATGACGAGTCCCGAATATCGTATACCT  1980

Db  1981  CACATGGCGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCGTCCAGACAC  2040
          ||||||||||||||||||||||||||||||||||||
Qy  1981  CACATGGCGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCGTCCAGACAC  2040

Db  2041  GCAAATTGCGCAACCGCAACAACACCACCATCAGTGGCGGCCAACCAATGGCGGCCACCA  2100
          |||||||||||||||||||||||||||||||||||
Qy  2041  GCAAATTGCGCAACCGCAACAACACCACCATCAGTGGCGGCCAACCAATGGCGGCCACCA  2100

Db  2101  CCTGTCTGACACCCAATCACAAGCTCGATCATCGCGACTACGGAAATTGGCCTGAGTGCA  2160
          |||||||||||||||||||||||||||||||||||
Qy  2101  CCTGTCTGACACCCAATCACAAGCTCGATCATCGCGACTACGGAAATTGGCCTGAGTGCA  2160

Db  2161  CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC  2220
          ||||||||||||||||||||||||||||||||||||
Qy  2161  CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC  2220

Db  2221  AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACAATCGCGACTACGGCGCTG  2280
          |||||||||||||||||||||||||||||||||||
Qy  2221  AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACAATCGCGACTACGGCGCTG  2280

Db  2281  GTCGGCACAGTCGGCCAAGCGATCGCGGTCGTCCGTTCAAAGACAAGGCACTCGAAGGCATCG  2340
          |||||||||||||||||||||||||||||||||||
Qy  2281  GTCGGCACAGTCGGCCAAGCGATCGCGGTCGTCCGTTCAAAGACAAGGCACTCGAAGGCATCG  2340

Db  2341  ATGACGAGGATGGCCGCAGTCGTCAAAGACAAGGCACTCGAAGTGAAATTCAGGAGTGGGTATCGC  2400
          |||||||||||||||||||||||||||||||||||
Qy  2341  ATGACGAGGATGGCCGCAGTCGTCAAAGACAAGGCACTCGAAGTGAAATTCAGGAGTGGGTATCGC  2400

Db  2401  ATGTGTTTTGTGTCGTGGGACTGTTGCTGCGGTTGCGTGGGACTGTTGCTGCGGTTGGGTATCCGC  2460
          |||||||||||||||||||||||||||||||||||
Qy  2401  ATGTGTTTTGTGTCGTGGGACTGTTGCTGCGGTTGCGTGGGACTGTTGCTGCGGTTGGGTATCCGC  2460
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Right column:

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Db  2461  TCATCGTCTTCGTCATCCTTCGTCGAGCTCTTCATCACGCGTGCATTGTGGTCAACACGA  2520
          ||||||||||||||||||||||||||||||||||||
Qy  2461  TCATCGTCTTCGTCATCCTTCGTCGAGCTCTTCATCACGCGTGCATTGTGGTCAACACGA  2520

Db  2521  TGTTCATGGCAATGGATCACCGCCACCTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA  2580
          |||||||||||||||||||||||||||||||||||
Qy  2521  TGTTCATGGCAATGGATCACCGCCACCTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA  2580

Db  2581  GCAACTATTTCTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA  2640
          ||||||||||||||||||||||||||||||||||||
Qy  2581  GCAACTATTTCTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA  2640

Db  2641  GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATTCGCTGGCCCTAT  2700
          ||||||||||||||||||||||||||||||||||||
Qy  2641  GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATTCGCTGGCCCTAT  2700

Db  2701  CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTGTCCGTATTTCCTTTCGAT  2760
          |||||||||||||||||||||||||||||||||||
Qy  2701  CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTGTCCGTATTTCCTTTCGAT  2760

Db  2761  TGCTGCGTGTATTCAAACTGGGCCAAGTCTTGGCCCACACTTAATTTCACTTACTCATTTCGATTA  2820
          |||||||||||||||||||||||||||||||||||
Qy  2761  TGCTGCGTGTATTCAAACTGGGCCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTA  2820

Db  2821  TGGGACGGCACCATGGACGGCGGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA  2880
          |||||||||||||||||||||||||||||||||||
Qy  2821  TGGGACGGCACCATGGACGGCGGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA  2880

Db  2881  TCTTTGCGTGATGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCT  2940
          |||||||||||||||||||||||||||||||||||
Qy  2881  TCTTTGCGTGATGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCT  2940

Db  2941  TTCCGGATGGCGACCTGCCGCGTGCCGCGTGGACTTCACCGACTTTATGCACAGCTTCATGATCG  3000
          |||||||||||||||||||||||||||||||||||
Qy  2941  TTCCGGATGGCGACCTGCCGCGTGCCGCGTGGACTTCACCGACTTTATGCACAGCTTCATGATCG  3000

Db  3001  TGTTCCGGGTGCTGCTGCGGAGAATGGATCGAGTGCATGTGGGACTCCATGTAGGCGTGGGCG  3060
          |||||||||||||||||||||||||||||||||||
Qy  3001  TGTTCCGGGTGCTGCTGCGGAGAATGGATCGAGTGCATGTGGGACTCCATGTAGGCGTGGGCG  3060

Db  3061  ATGTCTCGTCGATTCCTTCTTCGTTGTCCAATTTGGCTCATCTAGCTTATCAGCCGCCGACTCG  3120
          |||||||||||||||||||||||||||||||||||
Qy  3061  ATGTCTCGTCGATTCCTTCTTCGTTGTCCAATTTGGCTCATCTAGCTTATCAGCCGCCGACTCG  3120

Db  3121  ACCTTTCTTAGCCTTGCTTTGTTGTCCAATTTGCTCATCTAGCTTATCAGCCGCCGACTG  3180
          |||||||||||||||||||||||||||||||||||
Qy  3121  ACCTTTCTTAGCCTTGCTTTGTTGTCCAATTTGCTCATCTAGCTTATCAGCCGCCGACTG  3180

Db  3181  CCGATAACGATACGAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT  3240
          |||||||||||||||||||||||||||||||||||
Qy  3181  CCGATAACGATACGAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT  3240

Db  3241  GGTTAAGCGTAATATTGCTGATTGTTCAAGTTAATACGTAACAAATCAA  3300
          |||||||||||||||||||||||||||||||||||
Qy  3241  GGTTAAGCGTAATATTGCTGATTGTTCAAGTTAATACGTAACAAATCAA  3300

Db  3301  TAAGTGATCAACCATCAGGTGAGAGGACCAACCAGATCAGTTGGAGCGGAAGAGC  3360
          |||||||||||||||||||||||||||||||||||
Qy  3301  TAAGTGATCAACCATCAGGTGAGAGGACCAACCAGATCAGTTGGAGCGGAAGAGC  3360

Db  3361  ATGGTGACAACGAACTGGAGCTGGGCCACGATCGAGGTGGCCATCGAGGTGGCCATGGAATTCACGA  3420
          |||||||||||||||||||||||||||||||||||
Qy  3361  ATGGTGACAACGAACTGGAGCTGGGCCACGATCGAGGTGGCCATCGAGGTGGCCATGGAATTCACGA  3420

Db  3421  AGGGGATCAAGGAGCGCAACTGCAACTGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA  3480
          |||||||||||||||||||||||||||||||||||
Qy  3421  AGGGGATCAAGGAGCGCAACTGCAACTGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA  3480

Db  3481  TACACGGCGACATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA  3540
          |||||||||||||||||||||||||||||||||||
Qy  3481  TACACGGCGACATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA  3540
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Db  3541  TGATTGGCAACTCAATTAACCACCAAGAACAATAGACTTGAACACGAGCTAAACCATAGAG  3600
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Qy  3541  TGATTGGCAACTCAATTAACCACCAAGAACAATAGACTTGAACACGAGCTAAACCATAGAG  3600

Db  3601  GTTTGTCCTTACAGGACGACGACGACTGCCAGCATTAACTAACTGTAGCCATAGAGAATC  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601  GTTTGTCCTTACAGGACGACGACGACTGCCAGCATTAACTAACTGTAGCCATAGAGAATC  3660

Db  3661  GACCATTCAAGGACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGC  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3661  GACCATTCAAGGACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGC  3720

Db  3721  GCGACGCCAGCAGCAAGGAGATTTAGGTCTCGACAGGAGACTGGACGAGGGGCGAATGCG  3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3721  GCGACGCCAGCAGCAAGGAGATTTAGGTCTCGACAGGAGACTGGACGAGGGGCGAATGCG  3780

Db  3781  AGGAGGGCCCGCTCGACGGTGATATCATTATTCATGCACACGACGAGATATACTCGATG  3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3781  AGGAGGGCCCGCTCGACGGTGATATCATTATTCATGCACACGACGAGATATACTCGATG  3840

Db  3841  AATATCCAGCTGATTGCTGCCCCATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG  3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3841  AATATCCAGCTGATTGCTGCCCCATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTG  3900

Db  3901  ACGATGACTCGCCGTTCTGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCAATTAA  3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3901  ACGATGACTCGCCGTTCTGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCAATTAA  3960

Db  3961  TTGAAAATAAATATTTGAAACAGCTGTATCACTATGATTTAATGAGTAGCTTAGCTT  4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3961  TTGAAAATAAATATTTGAAACAGCTGTATCACTATGATTTAATGAGTAGCTTAGCTT  4020

Db  4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACGTCAGGATATTTTATACTATA  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACGTCAGGATATTTTATACTATA  4080

Db  4081  TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG  4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4081  TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG  4140

Db  4141  GCTTCAAAGTGTACTTCACCAACGCGTGGTGTTGGCTCGATTCGTGATTGTCATGGTAT  4200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4141  GCTTCAAAGTGTACTTCACCAACGCGTGGTGTTGGCTCGATTCGTGATTGTCATGGTAT  4200

Db  4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTGTATTCAAGCCTTCAAGACTA  4260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTGTATTCAAGCCTTCAAGACTA  4260

Db  4261  TGGCAACGTTAAGAGCACTGAGCCACTACGTGCCCATGTCCCGTATGCAGGGCATGAGGG  4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4261  TGGCAACGTTAAGAGCACTGAGCCACTACGTGCCCATGTCCCGTATGCAGGGCATGAGGG  4320

Db  4321  TCGTCGTTAATGGCTGGTGTACAAGCTATACCGTCCATCTTCAATGGTGTGTTGTGTGTC  4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4321  TCGTCGTTAATGGCTGGTGTACAAGCTATACCGTCCATCTTCAATGGTGTGTTGTGTGTC  4380

Db  4381  TAATATTTTGGCTAATTTTGCCATAATGGGTACAGCTTTTTGCTGAAAATATTTTA  4440
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Qy  4381  TAATATTTTGGCTAATTTTGCCATAATGGGTACAGCTTTTTGCTGAAAATATTTTA  4440

Db  4441  AGTGCGAGGACAATGCAAGCTCAGGCGACGACACAAATCCGCAATGCCT  4500
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Qy  4441  AGTGCGAGGACAATGCAAGCTCAGGCGACGACACAAATCCGCAATGCCT  4500

Db  4501  GCGAGAGCGGAGAACTCACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG  4560
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Qy  4501  GCGAGAGCGGAGAACTCACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG  4560

Db  4561  CGTATCTGTGCCTTTCCAAGTGGCCACCTTCAAAGGCTTGGATACAAATCATGAACGATG  4620
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Qy  4561  CGTATCTGTGCCTTTCCAAGTGGCCACCTTCAAAGGCTTGGATACAAATCATGAACGATG  4620

Db  4621  CTATCGATTCACGAGAGGTGGACAAGCAACCATTCGTGAAACGAACATCTACACATGTATT  4680
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Qy  4621  CTATCGATTCACGAGAGGTGGACAAGCAACCATTCGTGAAACGAACATCTACACATGTATT  4680

Db  4681  TATATTTCGTATTCTTCATCATATTTGATCCTTTTCACACTCAATCTGTTCATTGGTG  4740
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Qy  4681  TATATTTCGTATTCTTCATCATATTTGATCCTTTTCACACTCAATCTGTTCATTGGTG  4740

Db  4741  TTATCATTGATATTTTAATGAGCAAAAGAAAAAGCAGTGATCATTAGAAATGTTCA  4800
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Qy  4741  TTATCATTGATATTTTAATGAGCAAAAGAAAAAGCAGTGATCATTAGAAATGTTCA  4800

Db  4801  TGACAAGGATCAGAAAAGTACTATAAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT  4860
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Qy  4801  TGACAAGGATCAGAAAAGTACTATAAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT  4860

Db  4861  TAAAAGCCATTCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCG  4920
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Qy  4861  TAAAAGCCATTCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCG  4920

Db  4921  ATAAGAAATTCGATATAATCATTATGTCTGAACATGTTCACCATGACCC  4980
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Qy  4921  ATAAGAAATTCGATATAATCATTATGTCTGAACATGTTCACCATGACCC  4980

Db  4981  TCGATCGTTACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGATAT  5040
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Qy  4981  TCGATCGTTACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGATAT  5040

Db  5041  TCGTAGTATTTTCAGTTCCGAATGTCATTATTAAAAATATTCGCTTACGATATCACTATT  5100
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Qy  5041  TCGTAGTATTTTCAGTTCCGAATGTCATTATTAAAAATATTCGCTTACGATATCACTATT  5100

Db  5101  TTATTGAGCCATGGAATTTATTTGATGAGTAGTTGTCATTTATCCATCTTAGGTCTTG  5160
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Qy  5101  TTATTGAGCCATGGAATTTATTTGATGAGTAGTTGTCATTTATCCATCTTAGGTCTTG  5160

Db  5161  TACTTAGCGATAATATCGAGAAGTACTTCGTCGTCGCCGACCCTCCCAGTGGTGCGCGTG  5220
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Qy  5161  TACTTAGCGATAATATCGAGAAGTACTTCGTCGTCGCCGACCCTCCCAGTGGTGCGCGTG  5220

Db  5221  TGGCGAAAGTGGGCCGTGTCCTTCGAAGGGAGCCAAGGGCATTCGGACACTGC  5280
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Qy  5221  TGGCGAAAGTGGGCCGTGTCCTTCGAAGGGAGCCAAGGGCATTCGGACACTGC  5280

Db  5281  TCTTCGGTGGTGGCCATGTCGCTGGCCCGTGTTCAACATCGGCCTGCGTGTTCCTGG  5340
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Qy  5281  TCTTCGGTGGTGGCCATGTCGCTGGCCCGTGTTCAACATCGGCCTGCGTGTTCCTGG  5340

Db  5341  TCATGTTCATCTTTGCCATTTTCATGGCAGTGTCTTCATGCACGTGAAGGAGAGAGCG  5400
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Qy  5341  TCATGTTCATCTTTGCCATTTTCATGGCAGTGTCTTCATGCACGTGAAGGAGAGAGCG  5400

Db  5401  GCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGGAGCATGATCCTGCTCTTCAGA  5460
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Qy  5401  GCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGGAGCATGATCCTGCTCTTCAGA  5460

Db  5461  TGTCGCACGTCAGCAACTATAGTCAGGCCACCGGAGACGTCAAGAGGTCTCAACCGACGCG  5520
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Qy  5461  TGTCGCACGTCAGCAACTATAGTCAGGCCACCGGAGACGTCAAGAGGTCTCAACCGACGCG  5520

Db  5521  ATCCACCCGACAGCAGCCACCACAAAGGCTATCCGGGCAATTGTGTTCAGCGGTTGGAATAA  5580
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Qy  5521  ATCCACCCGACAGCAGCCACCACAAAGGCTATCCGGGCAATTGTGTTCAGCGGTTGGAATAA  5580

Db  5581  CGTTTCTCCCTCCATAACCTAGTTATAAGCTTTTGATAGTTATTAATATGTACATTGCTC  5640
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Qy  5581  CGTTTCTCCCTCCATAACCTAGTTATAAGCTTTTGATAGTTATTAATATGTACATTGCTC  5640

Db  5641  TCATTCTCGAGAACTATAGTCAGGCCACCGGAGACGTCAAGAGGGTCTCAACCGACGACG  5700
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Qy  5641  TCATTCTCGAGAACTATAGTCAGGCCACCGGAGACGTCAAGAGGGTCTCAACCGACGACG  5700

Db  5701  ACTACGACATGTACTATGAGATACTGGCAGCAATTCGATCCGAGGGCCAGTACATAC  5760
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Qy 5701 ACTACGACATGACTACTATGAGATCTGGCAGCAATTCGATCCGGAGGCACCCAGTACATAC 5760

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Db 5821 CGAACAAGTACAAGATACATGGACATACCCATCTGTCCGCGTGACCTCATGTACT 5880
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Qy 5821 CGAACAAGTACAAGATCACATGATCATCGATGGACATACCCATCTGTCCGCGTGACCTCATGTACT 5880

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Qy 5881 GCGTCGACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGGCGGAAGGGCAATCCGATAG 5940

Db 5941 AGGAGACGGGTGAGATTGGTGAGCGTGAGGATAGCCGGCCCGCCGGATACGGAGGGCTACGAGCCCG 6000
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Qy 5941 AGGAGACGGGTGAGATTGGTGAGCGTGAGGATAGCCGGCCCGCCGGATACGGAGGGCTACGAGCCCG 6000

Db 6001 TCTCATCAACGCTGTGGCGTCAGCGTGAGGAGTACTGCGCGCCCGGCTAATCCAGCACGCCT 6060
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Qy 6001 TCTCATCAACGCTGTGGCGTCAGCGTGAGGAGTACTGCGCGCCCGGCTAATCCAGCACGCCT 6060

Db 6061 GGCGAAAGCACAAGGCGCGCGGCGGCGGCGGCGGAGGGGAGTGGGTCCTTTGAGCCGGATACGGATCATG 6120
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Qy 6061 GGCGAAAGCACAAGGCGCGCGGCGGCGGCGGCGGAGGGGAGTGGGTCCTTTGAGCCGGATACGGATCATG 6120

Db 6121 GCGATGGCGGTGATCCGGATCCGGGGGACCCGCGCCCCGATGAAGCAACGGACGGCGATG 6180
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Qy 6121 GCGATGGCGGTGATCCGGATCCGGGGGACCCGCGCCCCGATGAAGCAACGGACGGCGATG 6180

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Qy 6181 CGCCCGCTGGTGAGATGGTAGTGTTAACGGTACTCGAGAAGGAGCTGCCGATGCCGATG 6240

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Qy 6241 AGAGTAATGTAAATAGTCGGGTGAGGATGCAGCGGCGGCGGCAGCGAGCAGCAG 6300

Db 6301 CGGCGGCGGCCGGCCACGACGACGGCGGGAGTCCCGAGCCGGTAGCGCCCGGGCGACAGA 6360
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Qy 6301 CGGCGGCGGCCGGCCACGACGACGGCGGGAGTCCCGAGCCGGTAGCGCCCGGGCGACAGA 6360

Db 6361 CCCCGGTTCTCGTGGAGAGCGACGGGTTCGTGACGAGAACGGCCCACAAGGTGGTCATCC 6420
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Db 6421 ACTCGCGATCGCCGAGCATCACGTCGCCGCCCACGGCCGCCGCGCCTCGCCCCCC 6480
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Qy 6421 ACTCGCGATCGCCGAGCATCACGTCGCCGCCCACGGCCGCCGCGCCTCGCCCCCC 6480

Db 6481 CCCTCCAAGATGACGACGCCGAGTATTAGCTCTAGA 6513
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Qy 6481 CCCTCCAAGATGACGACGCCGAGTATTAGCTCTAGA 6513

RESULT 3
ID US-08-724-095-7 STANDARD; DNA; UNC; 6513 BP.
AC xxxxxx
DT
DE Sequence 7, Application US/08724095
CC Sequence 7, Application US/08724095
CC Patent No. 5688917
CC GENERAL INFORMATION:
CC APPLICANT: Warmke, Jeffrey W.
CC APPLICANT: Hall, Linda
CC APPLICANT: Feng, Gouping
CC APPLICANT: Van Der Ploeg, Leonardus
CC TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC TITLE OF INVENTION: PARA SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 7
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
CC STREET: P.O. Box 2000 - 126 E. Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07065-0907
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTseq, Version #1.d5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/724,095
CC FILING DATE:
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hand, J. Mark
CC REGISTRATION NUMBER: 36,545
CC REFERENCE/DOCKET NUMBER: 19332DA
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 6513 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
SQ SEQUENCE 6513 BP: 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match       100.0%;   Score 6513;   DB 1;   Length 6513;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 6513;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Db 1 TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC 60
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Qy 1 TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC 60

Db 61 GCAGTTTGTTCCGTCCCTTTACCCGCGAATCATTGGTCAAATCGAACAACGCATTGCCG 120
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Qy 61 GCAGTTTGTTCCGTCCCTTTACCCGCGAATCATTGGTCAAATCGAACAACGCATTGCCG 120

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Qy 121 CTGAACATGAAAAGCAGAAGGAGCTGGAAAGAAAGAGAGCCGAGGGAGGAGGTGCCGCGAT 180

Db 181 ATGGTCGCAAGAAAAAAACCGATATGATGACGAGGATGAGGATGAAGGTC 240
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Qy 241 CACAACCGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGAATTGCAGGGCAGCT 300

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Qy 301 TCCCGGCCGGAATTGGCCGCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360

Db 361 TGACATTCGTAGTTGTTAAGCAAAGGAAAAAGATATTTTTCGCATTCGCATCAAAAGCAA 420
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Qy 361 TGACATTCGTAGTTGTTAAGCAAAGGAAAAAGATATTTTTCGCATTCGCATCAAAAGCAA 420

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Qy 541 CGACAACGCCCACGGTTGAGTCCACTGAGGTGATATTCACCCGGAATTCACCCGGAATTTGAAT 600

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Db  601  CAGCTGTTAAAGTGATGGCACGAGGTTTCATTTTATGCCCGTTTACGTTTACGTATCTTAGAGATG  660
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Qy  601  CAGCTGTTAAAGTGATGGCACGAGGTTTCATTTTATGCCCGTTTACGTTTACGTATCTTAGAGATG  660

Db  661  CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT  720
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Qy  661  CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT  720

Db  721  TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCGTTAAAACCGTAGCCA  780
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Qy  721  TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCGTTAAAACCGTAGCCA  780

Db  781  TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGGTGAAGAATCTGCCG  840
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Qy  781  TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGGTGAAGAATCTGCCG  840

Db  841  ATGTGATTATCCTGACCATGTCTCCCTGTCGGTTGTCCGTTGATGGGCCTACAGATCT  900
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Qy  841  ATGTGATTATCCTGACCATGTCTCCCTGTCGGTTGTCCGTTGATGGGCCTACAGATCT  900

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Qy  901  ATATGGGCGTGCTCACCGAGAAGTCATCAAGAAGTTCCCGCTGACGGTTCCTGGGGCA  960

Db  961  ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAATTGGTATTCCGAGG  1020
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Qy  961  ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAATTGGTATTCCGAGG  1020

Db  1021 ACGAGGGCCATCTCATTTCCGTTATGCGGCCAATATCCGGTGCGGGCAATGCCAATGCGACG  1080
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Qy  1021 ACGAGGGCCATCTCATTTCCGTTATGCGGCCAATATCCGGTGCGGGCAATGCCAATGCGACG  1080

Db  1081 ATTACGTGCCTGCAGGGTTTGTTCGGACGTTATGGCTACACCAGCTTCGATT  1140
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Db  1141 CGTTCGGATGGGCCTTCCTGTGCCGCCTCCGGCTGATGACACAGGACTTCTGGGAGGATC  1200
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Qy  1201 TGTACCAGCTGGTGTGTTGCGCGCCGCCCAAAGCGGCCATCGGTATTGTGGCCATGCCATCA  1260

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Db  1381 CGGAAGAGCTGCCGCGGCCCAAAGCGGCCAAGCTGGAGGCGGCCCAAGCTGGAGGCTC  1440
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Qy  1381 CGGAAGAGCTGCCGCGGCCCAAAGCGGCCAAGCTGGAGGCGGCCCAAGCTGGAGGCTC  1440

Db  1441 AGGCAGCAGCGGATCGGCTGCCGCGCCGGCTGCCACTCGATCCGGAAATGGCCAAGA  1500
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Qy  1441 AGGCAGCAGCGGATCGGCTGCCGCGCCGGCTGCCACTCGATCCGGAAATGGCCAAGA  1500

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Db  1561 ACAACAACAAGAGAAGAGATGTCCATTCGGAGGCGTCGAGTGGAGTCGGTGAGCG  1620
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Db  1621 TTATACAAAGACAACAACCAACCACTACCACCACACACCAAGCTACCAAAGTTCGTAAAGTGA  1680
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Qy  1621 TTATACAAAGACAACAACCAACCACTACCACCACACACCAAGCTACCAAAGTTCGTAAAGTGA  1680

Db  1681 GCACGACATCCTTATCCTTACCTGTTAACATACGGGGGATCACGTAGTT  1740
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Qy  1681 GCACGACATCCTTATCCTTACCTGTTAACATACGGGGGATCACGTAGTT  1740
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Db  1741 CTCACAAGTACACGATACGGAACGGACGTGGCCCGCTTGGTATACCCGGTAGCGGATCGTA  1800
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Qy  1801 AGCCATTGGTATTGTCAACATATCAGGATGCCCAGCGCACTTGCCTGCCGCCTATGCCGACGACT  1860

Db  1861 CGAATGCCGTCACCCGATGTCCGAAGAGAATGGGCCATCATCATAGTGCCCGTGTACTATG  1920
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Qy  1861 CGAATGCCGTCACCCGATGTCCGAAGAGAATGGGCCATCATCATAGTGCCCGTGTACTATG  1920

Db  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTGCCGATCAGTCCCGAATATCGTATACCT  1980
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Qy  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTGCCGATCAGTCCCGAATATCGTATACCT  1980

Db  1981 CACATGGGATCTACTCGGCGCATGGCCGTCATGGCCGTCAGCAGACAATGACCAAGGAGA  2040
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Qy  1981 CACATGGGATCTACTCGGCGCATGGCCGTCATGGCCGTCAGCAGACAATGACCAAGGAGA  2040

Db  2041 GCAAATTGCCAACCGCAACACACAACAGTGGGCGCCACCAATGCGGCACCA  2100
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Qy  2041 GCAAATTGCCAACCGCAACACACAACAGTGGGCGCCACCAATGCGGCACCA  2100

Db  2101 CCTGTCTGGACACCAAGTCGATCATCACAAGCTCGATCGCGACTACGGACTACGCTGGAGTGCA  2160
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Qy  2101 CCTGTCTGGACACCAAGTCGATCATCACAAGCTCGATCGCGACTACGGACTACGCTGGAGTGCA  2160

Db  2161 CGGACGAAGCTGGCAAGAGTCAAAGACACCTTTTATCGAGCCGTCCAGACAC  2220
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Qy  2161 CGGACGAAGCTGGCAAGAGTCAAAGACACCTTTTATCGAGCCGTCCAGACAC  2220

Db  2221 AAACCGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCGCTG  2280
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Qy  2221 AAACCGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTG  2280

Db  2281 GTCGGCACAGTCGGGCACGCAAGCGATGCGGTGTCTCCGTTACTATTCCCAACAGAGGACG  2340
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Qy  2281 GTCGGCACAGTCGGGCACGCAAGCGATGCGGTGTCTCCGTTACTATTCCCAACAGAGGACG  2340

Db  2341 ATGACGAGGATGGGCCGACGTTCAAAGACACTCGAAGTCGAAGGCATCG  2400
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Db  2401 ATGTGTTTGTGTGTTGGGACTGTTGCTGGGTTGTTGGTGAAATTTCGAGGTGGGTATCGC  2460
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Qy  2401 ATGTGTTTGTGTGTTGGGACTGTTGCTGGGTTGTTGGTGAAATTTCGAGGTGGGTATCGC  2460

Db  2461 TCATCGTCTTCAACATCCCTTCGTCGAACATCTTCGACTTCATCATCGCCGTGCAACACGA  2520
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Qy  2461 TCATCGTCTTCAACATCCCTTCGTCGAACATCTTCGACTTCATCATCGTCGTCAACACGA  2520

Db  2521 TGTTCATGGCAATGAATGACATCACCGACCACCTTTGCCATCGAGGCCACCATGAGCAGAGTG  2580
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Qy  2521 TGTTCATGGCAATGAATGACATCACCGACCACCTTTGCCATCGAGCGCACCATGAGCAGAGTG  2580

Db  2581 GCAACTATTTCTTCACCGCCATTTGTTGCCATCGAGGCCACCATGGCCATGA  2640
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Qy  2581 GCAACTATTTCTTCACCGCCATTTGTTGCCATCGAGGCCACCATGGCCATGA  2640

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Qy  2641 GCCCCAAGTACTATTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGCCCCTAT  2700

Db  2701 CGCTATTGGAACTCGGGACTGTGTCCAGGGTGTCGTGTATTGCGTATTTCGAT  2760
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Qy  2701 CGCTATTGGAACTCGGGACTGTGTCCAGGGTGTCGTGTATTGCGTTCCTTTCGAT  2760

Db  2761 TGCTGCGTGTATTCAAACTGCTGCCACCAGTCATTGGCCACACTTAATTTACTCATTTCGATTA  2820
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Db 3901 ACGATGACTCCGCGTCTCGGCGAAGGATGGGCGAAGTTACGACTGAAAACTTTCAATTAA 3960
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Qy 3901 ACGATGACTCCGCGTCTCGGCGAAGGATGGGCGAAGTTACGACTGAAAACTTTCAATTAA 3960

Db 3961 TTGAAAATAAATATTTGAAACAGCTGTTATCACATGATTTAATGAGTAGCTTAGCTT 4020
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Qy 3961 TTGAAAATAAATATTTGAAACAGCTGTTATCACATGATTTAATGAGTAGCTTAGCTT 4020

Db 4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTATACTATA 4080
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Qy 4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTATACTATA 4080

Db 4081 TGGACAGAATATTACCGGTTATTCTTCTTGGAAATGTAATCAACGTGGTTGGCGCTCG 4140
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Qy 4081 TGGACAGAATATTACCGGTTATTCTTCTTGGAAATGTAATCAACGTGGTTGGCGCTCG 4140

Db 4141 GCTTCAAAGTGTACTTCACCAACGCGTGGTGTGTCGTCGTGTTCGTCGTTCGATTGTCATGGTGTAT 4200
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Db 4321 TCGTCGTTAATGCGCTGGTACAAGCTATACGTCCATCTTCAATGTGCTCATTGGTGTGTC 4380
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Qy 4441 AGTGCGAGGACAATGAATGGCACGTGGGTGAATTCAGCAATTCGGATCATGTAGGTAACG 4500

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Qy 4501 GCGAGAGCGAGAACTACACGTGGGTGGGTGAATTCAGCAATGAATTCGGATCATGTGTAACG 4560

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Db 4621 CTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGATCACATGTATT 4680
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Db 4741 TTATCATTGATAATTTAATGAGCAAAAGAAGAAAAAAGCAGGTGGATCATTAGAAATGTTCA 4800
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Qy 4741 TTATCATTGATAATTTAATGAGCAAAAGAAGAAAAAAGCAGGTGGATCATTAGAAATGTTCA 4800

Db 4801 TGACAGAAGATCAGAAAAGTACTATAATGTGACCAGTGGCGACCAAGCAATGCG 4860
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Qy 2761 TGCTGCGTATTCAAACTGGCTCAAGTCTTGGCCCAACTTAATTTACTCATTCGATTA 2820
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Db 3061 ATGTCTCGTGCAATCCCTTCTCTTGGCCACCGTTGTCATCGGCAATCTTGTGTGGTACTTA 3120

Qy 3061 ATGTCTCGTGCAATCCCTTCTCTTGGCCACCGTTGTCATCGGCAATCTTGTGTGGTACTTA 3120
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Qy 3181 TAAGTGATCAACATCAGGTGAGAGGACCAACCAGATCAGTTGGATTGGAGCGAGAGC 3240
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Qy 3241 CCGATAACGATACGAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTAAAAGTT 3300
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Qy 3421 AGGGGATCAAGGAGCGCAGAGCCAGCGCCGCAGAGGGCAGCGGCGAGGAGAGC 3480
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Qy 3481 TACACGGCGACATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
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Db 3541 TGAATTGGCAACTCAATTAACCACCACCAAGACTGAAACTGAAACCATAGAG 3600

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Qy 3601 GTTTGTCCTTACAGGACGACGACGACTGCCAGCATTCATATGGTAGCCATAAGAATC 3660
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Qy 3781 AGGAGGCCCCCTCGACGCGGTGATATCAGAGATATACTTCGATG 3840
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Db  6061  GGCGAAAGCACAAGGCGCGCGGCGAGGGAGGTGGGTCCTTTGAGCCGGATACGGCGGATCATG  6120
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Qy        GGGATGGCGGTGATCCGATCGAGAGGGAGGTGGGTCCTTTGAGCCGGATGAGCCGATG      6120

Db  6121  GCGATGGCGGTGATCCGATCCGGATGCCGGGCGACCCGGGCCCGATGAGCCAACGGACGGCGATG  6180
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Qy        GCGATGGCGGTGATCCGATCCGGATGCCGGGCGACCCGGGCCCGATGAGCCAACGGACGGCGATG  6180

Db  6181  CGCCCGCTGGTGATGAGTACTGTTAACGGTACTGCGAGAAGGAGCTGCCGATGCCGATG  6240
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Qy        CGCCCGCTGGTGATGAGTACTGTTAACGGTACTGCGAGAAGGAGCTGCCGATGCCGATG  6240

Db  6241  AGAGTAATGTAAATAGTCCGGTGAGGATCGCGGCGGCGCGGCGCAGCAGCAGCAG  6300
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Db  6301  CGGCGGCGGCGGGCACGACGAGTCCGGGAGTCCCGGCGGCGTAGCGCGGGGCGACAGA  6360
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Qy        CGGCGGCGGCGGGCACGACGAGTCCCGGGAGTCCCGGCGGCGTAGCGCGGGGCGACAGA  6360

Db  6361  CGGCCGTTCGTGGAGAGCGACGGGTTCGTGACGAAGAAGAACGGCCACAAGGTGGTCATCC  6420
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Qy        CGGCCGTTCGTGGAGAGCGACGGGTTCGTGACGAAGAAGAACGGCCACAAGGTGGTCATCC  6420

Db  6421  ACTCGGACGATCGCCGAGCATCACGTCGCGCACGACGTCTGAGCCGCGATGTCTGAGCCGCCCC  6480
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Qy        ACTCGGACGATCGCCGAGCATCACGTCGCGCACGACGTCTGAGCCGCGATGTCTGAGCCGCCCC  6480

Db  6481  CCCTCCAAGATGACACGCGAGTATTAGCTCTTAGA  6513
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Qy        CCCTCCAAGATGCACGCGAGTATTAGCTCTTAGA  6513
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RESULT  4
ID  US-08-338-702-7 STANDARD; DNA; UNC; 6513 BP.
AC  xxxxxx
DT
DE  Sequence 7, Application US/08338702
CC  Sequence 7, Application US/08338702
CC  Patent No. 5550049
CC  GENERAL INFORMATION:
CC      APPLICANT:  Warnke, Jeffrey W.
CC      APPLICANT:  Van Der Ploeg, Leonardus
CC      TITLE OF INVENTION:  PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC      TITLE OF INVENTION:  PARA SODIUM CHANNEL
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC          ADDRESSEE:  John W. Wallen III
CC          STREET:  P.O. Box 2000, 126 E. Lincoln Avenue
CC          CITY:  Rahway
CC          STATE:  New Jersey
CC          COUNTRY:  USA
CC          ZIP:  07065-0900
CC      COMPUTER READABLE FORM:
CC          MEDIUM TYPE:  Floppy disk
CC          COMPUTER:  IBM PC compatible
CC          OPERATING SYSTEM:  PC-DOS/MS-DOS
CC          SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER:  US/08/338,702
CC          FILING DATE:
CC          CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC          NAME:  Wallen III, John W.
CC          REGISTRATION NUMBER:  35,403
CC          REFERENCE/DOCKET NUMBER:  19338
CC      TELECOMMUNICATION INFORMATION:
CC          TELEPHONE:  (908) 594-3905
CC          TELEFAX:  (908) 594-4720
CC  INFORMATION FOR SEQ ID NO:  7:
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH:  6513 base pairs
CC          TYPE:  nucleic acid
CC          STRANDEDNESS:  single

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Qy  4981  TCGATCGTTACGATGCGTCGGACACGTATAACGGGTCCTAGACTATCTCAATGCGATAT  5040

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Qy  5161  TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTG  5220

Db  5221  TGGGCAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGAGCAAGGCATTCGGACACTGC  5280
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Qy  5461  TGTCGACGTCAGCCGGTTGGGATGTGTACTGGACGCCCATTATCAATGAGAAGCATGCG  5520

Db  5521  ATCCACCCCGACACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCCGACCGTTGGAATAA  5580
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Qy  5521  ATCCACCCCGACACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCCGACCGTTGGAATAA  5580

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Db  5641  TCATTCTGAGAACTATAGTCAGGCACCAGGACGTCAAGAGGGTCTAACCGACGACG  5700
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Qy  5641  TCATTCTGAGAACTATAGTCAGGCACCAGGACGTCAAGAGGGTCTAACCGACGACG  5700

Db  5701  ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCCACCCAGTACATAC  5760
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Qy  5761  GCTATGATCAGCAGTCTGTCCGAATTCCTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAAC  5820

Db  5821  CGAACAAGTACAAGATCATATCGATGGACATACCCCATCTGTCGCGGTGACCTCATGTACT  5880
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Qy  5821  CGAACAAGTACAAGATCATATCGATGGACATACCCCATCTGTCGCGGTGACCTCATGTACT  5880

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Qy  5881  GCGTCGCACATCCTCGACGGCCCTTACGGAAAGACTTCTTCTTTGCGCGGAAGGGCAATCCGATAG  5940

Db  5941  AGGAGACGGGTGAGATTGGTGAGATAGCGGCCCGGCCCGATACGGAGGGCTACGAGCCCG  6000
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Db  6001  TCTCATCAACGCTGTGGCGTGGCGTCAGCGTGAGGAGTACTGCGCCCGGCTAATCCAGCACGCGCCT  6060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6001  TCTCATCAACGCTGTGGCGTGGCGTCAGCGTGAGGAGTACTGCGCCCGGCTAATCCAGCACGCGCCT  6060

Db  6061  GGCGAAAGCACAAGGCGCGCGGCGAGGGAGGTGGGTCCTTTGAGCCGGATACGGCGGATCATG  6120
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CC    TOPOLOGY: linear
CC    MOLECULE TYPE: cDNA
SQ    SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match       100.08;   Score 6513;  DB 1;  Length 6513;
Best Local Similarity 100.08;  Pred. No. 0.00e+00;
Matches   6513;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1  TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1  TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC   60

Db     61  GCAGTTTGTTCCGTCTCCTTTACCCGCGAATCATTGTGCAAATGCAATTGCCG        120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61  GCAGTTTGTTCCGTCTCCTTTACCCGCGAATCATTGTGCAAATGCAATTGCCG        120

Db    121  CTGAACAATGAAAAGCAGAAGAGGCTGGAAAGAGAAAGAGAGCCGAGGGAGAGGTGCCGCGAT   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121  CTGAACAATGAAAAGCAGAAGAGGCTGGAAAGAGAAAGAGAGCCGAGGGAGAGGTGCCGCGAT   180

Db    181  ATGGTCGCCAAGAAAACAAAAGAAATCCGATATGACGAGGACGAGGACGAGGAGGTC     240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181  ATGGTCGCCAAGAAAACAAAAGAAATCCGATATGACGAGGACGAGGACGAGGAGGTC     240

Db    241  CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGCAGCT    300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241  CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGCAGCT    300

Db    301  TCCCGCCGGAATTGGCCTCCACTCCTCGAGGATATCGATCCCTACTACAGCAATGTAC   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301  TCCCGCCGGAATTGGCCTCCACTCCTCGAGGATATCGATCCCTACTACAGCAATGTAC   360

Db    361  TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTCGCTTTCTGCATCAAAAGCAA   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361  TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTCGCTTTCTGCATCAAAAGCAA   420

Db    421  TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTACATTCTAGTGCATC   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    421  TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTACATTCTAGTGCATC   480

Db    481  CATTATTTTCCCTATTCATCATCACCAATTCTCGTCAACTGCATCCTGATGATAATGC   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    481  CATTATTTTCCCTATTCATCATCACCAATTCTCGTCAACTGCATCCTGATGATAATGC   540

Db    541  CGACAACGCCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    541  CGACAACGCCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT   600

Db    601  CAGCTGTTTAAAGTGATGGCACGAGAGGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATG   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601  CAGCTGTTTAAAGTGATGGCACGAGAGGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATG   660

Db    661  CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATAATGTGACCATGGGTATAGATT   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    661  CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATAATGTGACCATGGGTATAGATT   720

Db    721  TAGGTAATCTAGCAGCCGTTTAGGGTGCTGCGAACGTTTAGGGTGCTGCGAACCGTAGCCA   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721  TAGGTAATCTAGCAGCCGTTTAGGGTGCTGCGAACGTTTAGGGTGCTGCGAACCGTAGCCA   780

Db    781  TTGTGCCAGGCTTGAAGACCATGTGCGGGCGCCCGGTCATCGAGAAGAAGTTCCGCCG    840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781  TTGTGCCAGGCTTGAAGACCATGTGCGGGCGCCCGGTCATCGAGAAGAAGTTCCGCCG    840

Db    841  ATGTGATTATCCGACCATGTGCTTGCCGGTCATCAAGAGTGCATCAAGAGTCTACAGATCT   900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841  ATGTGATTATCCGACCATGTGCTTGCCGGTCATCAAGAGTGCATCAAGAGTCTACAGATCT   900

Db    901  ATATGGGCGTGTCACCGAGAAGTCGTCTCACCGAGAAGTCGTCGACGGTTCCTGGGGCA   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901  ATATGGGCGTGTCACCGAGAAGTCGTCTCACCGAGAAGTCGTCGACGGTTCCTGGGGCA   960

Db    961  ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATATCCGAGG        1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961  ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATATCCGGTGCGGGGCAATGCGACGACG  1020

Db   1021  ACGAGGGCATCTCATTTCCGTTATGGCGCAATATATCCGGTGCGGGGCAATGCGACGACG   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021  ACGAGGGCATCTCATTTCCGTTATGGCGCAATATATCCGGTGCGGGGCAATGCGACGACG   1080

Db   1081  ATTACGTGTGCCTGCCAGGGTTGGTCCGAATCCGAATCCGAATTATGGCTACACCAGCTTCGATT   1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081  ATTACGTGTGCCTGCCAGGGTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT   1140

Db   1141  CGTTCGGATGGGCTTTCGTGTCCGCCTTCCGGCTGTGATGACACAGGACTTCTGGGAGGATC   1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141  CGTTCGGATGGGCTTTCGTGTCCGCCTTCCGGCTGTGATGACACAGGACTTCTGGGAGGATC   1200

Db   1201  TGTACCAGCTGGTGTTGCGCGGCCGCCCGACCATGCGATCGTGTCTTATAGTCATCA   1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201  TGTACCAGCTGGTGTTGCGCGGCCGCCCGACCATGCCATTGTGTCTTATAGTCATCA   1260

Db   1261  TCTTCCTAGGTTCATTCTATCTTGTGAATTGATTTGGCCCATTGTTGCCCATTGTCGTATG   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261  TCTTCCTAGGTTCATTCTATCTTGTGAATTGATTTGGCCCATTGTTGCCCATTGTCGTATG   1320

Db   1321  ACGAATTGCAAAGGAAGGCCGAAGAGGCCGGAAGAGGAGCCGGCCGGCCAATGCCCAGGCTC   1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321  ACGAATTGCAAAGGAAGGCCGAAGAGGAGCCGGCCAATGCCCAGGCTC   1380

Db   1381  CGGAAGAAGCTGCCGCCCGCCAAGCGGCCGGCCAATGCCCAGGCTC        1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381  CGGAAGAAGCTGCCGCCCGCCAAGCGGCCGGCCAATGCCCAGGCTC        1440

Db   1441  AGGCAGCAGCGGATGCGGCTGCCGCCGCCAGTATTGTTGGCGCGCTATTGTTGGCGGCAACGATG   1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441  AGGCAGCAGCGGATGCGGCTGCCGCCGCCAGTATTGTTGGCGCGCAGAGAAATGCCCAAGA   1500

Db   1501  GTCCGACGTATTCTTGCATCAGTGAGCTATTGTTGGCGGCAACGATG        1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501  GTCCGACGTATTCTTGCATCAGTGAGCTATTGTTGGCGGCAACGATG        1560

Db   1561  ACAACAACAAAGAAGAAGATGTCCATTCGAGACGTCGAGTCGGTGAGGTGTGAGCG   1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1561  ACAACAACAAAGAAGAAGATGTCCATTCGAGACGTCGAGTCGGTGAGGTGTGAGCG   1620

Db   1621  TTATACAAAGACAACCAGCAACCAGCAACTGCATCAGGATGCCAAGTTCGTAAAGTGAA   1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1621  TTATACAAAGACAACCAGCAACCAGCAACTGCATCAGGATGCCAAGTTCGTAAAGTGAA   1680

Db   1681  GCACGACAATCCTATCCTTCACCGTTTAACATACGCAGGGGATCACGTAGTT   1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1681  GCACGACAATCCTATCCTTCACCGTTTAACATACGCAGGGGATCACGTAGTT   1740

Db   1741  CTCACAAGTACACGATACGGAACGACGTGGCCGCTTTGGTATACCCGGTAGCCGATCGTA   1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1741  CTCACAAGTACACGATACGGAACGACGTGGCCGCTTTGGTATACCCGGTAGCCGATCGTA   1800

Db   1801  AGCCATTGTATTGTCAACATATCAGGATGCCGCCATATGCCCCTGTGCCCTATGCCGCGACT   1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1801  AGCCATTGTATTGTCAACATATCAGGATGCCGCCATATGCCCCTGTGCCCTATGCCGCGACT   1860

Db   1861  CGAATGCCGTCACCCGATGTCCGAAGAGAATGGGCCATCATAGTGCCCGTGTACTATG   1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1861  CGAATGCCGTCACCCGATGTCCGAAGAGAATGGGCCATCATAGTGCCCGTGTACTATG   1920

Db   1921  GCAATCTAGGCTCCGACCATGTTCCCGACTCATCAGTGCCCGAATCGTGTAACC   1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1921  GCAATCTAGGCTCCGACCATGTTCCCGACTCATCAGTGCCCGAATCGTGTAACC   1980

Db   1981  CACATGGCCGATCTACTCGGCGATCTCGGCGATCATCAATGGGGCCATGGCGGTTCCTGGGGCA   2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1981  CACATGGCCGATCTACTCGGCGATCTCGGCGATCATCAATGGGGCCACAAATGACCAAGGAGA   2040

Db   2041  GCAAATTGCGCAACGACGTATCACAACACGCCAATCAATCAGTGGGCGCCACCA   2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2041 GCAAATTGCGCAACCGCCACACACGCAATCAATCAGTGGGCGCCACCAATGGCCGGCACCA 2100

Db   2101 CCTGTCTGGACACCAACCAATCACAAGCTCGATCATCGGACTACGAAATTGGCCTGAGTGCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2101 CCTGTCTGGACACCAACCAATCACAAGCTCGATCATCGGACTACGAAATTGGCCTGAGTGCA 2160

Db   2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC 2220

Db   2221 AAACGGTGGTTGATATGAAAGATGATGTCCTGAATGACATCATCATCGAACAGCCGCGTG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2221 AAACGGTGGTTGATATGAAAGATGATGTCCTGAATGACATCATCATCGAACAGCCGCGTG 2280

Db   2281 GTCGGCACAGTCGGGCAAGCGATCCGGTGTCTCGAGCTCTTCAAAGACACTCGAAGTGATC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2281 GTCGGCACAGTCGGGCAAGCGATCCGGTGTCTCGAGCTCTTCAAAGACACTCGAAGTGATC 2340

Db   2341 ATGACGAGGATGGGCGCACGTTCAAAGACAAGGCACTCGAAGTGATCTCGAAGGCATCG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2341 ATGACGAGGATGGGCGCACGTTCAAAGACAAGGCACTCGAAGTGATCTCGAAGGCATCG 2400

Db   2401 ATGTGTTTGTGTGGGACTGTTGCTGGTTGGTTGCTGGGTATTTCAGGAGTGGGTATCGC 2460
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Qy   2401 ATGTGTTTGTGTGGGACTGTTGCTGGTTGGTTGCTGGGTATTTCAGGAGTGGGTATCGC 2460

Db   2461 TCATCGTCTTCGATCCCTTCGTCTCGAGCTCTTCATTGTGGTCAACACGACTCAACGA 2520
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Qy   2461 TCATCGTCTTCGATCCCTTCGTCTCGAGCTCTTCATTGTGGTCAACACGACTCAACGA 2520

Db   2521 TGTTCATGGCAATGGACTCGGAGCTGTCCAGGGTCTGTCCGTATTCGTTCCTTTCGAT 2580
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Qy   2521 TGTTCATGGCAATGGACTCGGAGCTGTCCAGGGTCTGTCCGTATTCGTTCCTTTCGAT 2580

Db   2581 GCAACTATTCTTCACCGCCACCTTGCCATCGAGGCCATGAAGCTAATGGCGCCATGA 2640
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Qy   2581 GCAACTATTCTTCACCGCCACCTTGCCATCGAGGCCATGAAGCTAATGGCGCCATGA 2640

Db   2641 GCCCCAAGTACTATTCCGAGGGCTGGAACATCTTCGACTTCATTATCGTGTGGCCCTAT 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2641 GCCCCAAGTACTATTCCGAGGGCTGGAACATCTTCGACTTCATTATCGTGTGGCCCTAT 2700

Db   2701 CGCTATTGGAACTGGACTCGAGGGTGTCCAGGGTCTGTCCGTATTGCGTTCCTTTCGAT 2760
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Qy   2701 CGCTATTGGAACTGGACTCGAGGGTGTCCAGGGTCTGTCCGTATTGCGTTCCTTTCGAT 2760

Db   2761 TGCTGCGTGTATTCAAACTGGCCAGCTGAACTGCTGGCAAGTCTTAATTACTCATTCGATTA 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2761 TGCTGCGTGTATTCAAACTGGCCAGCTGAACTGCTGGCAAGTCTTAATTACTCATTCGATTA 2820

Db   2821 TGGGACGCACCATGGCCATGGGCTTTGGTAATCTGACATTGTACTTTGCATTATCATCTTCA 2880
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Qy   2821 TGGGACGCACCATGGCCATGGGCTTTGGTAATCTGACATTGTACTTTGCATTATCATCTTCA 2880

Db   2881 TCTTATTGCGGTGATGGGAATGCAACTGTTCCGGAAAGAATTCATGATCACAAGACCGGCT 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2881 TCTTATTGCGGTGATGGGAATGCAACTGTTCCGGAAAGAATTCATGATCACAAGACCGGCT 2940

Db   2941 TTCCGGATGGCGACCTGCGCCGCCGGGAATGCGCCTTCACCGGACTTCATGCACAGCTTCA 3000
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Qy   2941 TTCCGGATGGCGACCTGCGCCGCCGGGAATGCGCCTTCACCGGACTTCATGCACAGCTTCA 3000

Db   3001 TGTTCCGGGTGCTCTGCGGAGAATGATCGGATCCATGTGGACTACGTGGGGCG 3060
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Qy   3001 TGTTCCGGGTGCTCTGCGGAGAATGATCGGATCCATGTGGACTACGTGGGGCG 3060

Db   3061 ATGTCTCGTGCATTCCTTCTTCCGTCATCGGCAATCTTGTGTGGTACTTA 3120
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Qy   3061 ATGTCTCGTGCATTCCTTCTTCCGTCATCGGCAATCTTGTGTGGTACTTA 3120

Db   3121 ACCTTTTCTTAGCCTTGCTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCCGCCGACTG 3180
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Qy   3121 ACCTTTTCTTAGCCTTGCTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCCGCCGACTG 3180


Db   3181 CCGATAACGATACGATAAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3181 CCGATAACGATACGATAAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT 3240

Db   3241 GGGTTAAGCGTAATATTGCTGATTGTTCAAGTTATACGTAACAAATTGACAAATCAAA 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3241 GGGTTAAGCGTAATATTGCTGATTGTTCAAGTTATACGTAACAAATTGACAAATCAAA 3300

Db   3301 TAAGTGATCAACCATCAGTGAGAGGACCAACCAGATCAGTGGATTTGGAGCGAAGAGC 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3301 TAAGTGATCAACCATCAGTGAGAGGACCAACCAGATCAGTGGATTTGGAGCGAAGAGC 3360

Db   3361 ATGGTGACAACGAACTGGAGCTGGCCACGAGAGCTCCGCCGACGCGACTCATCATCAAGA 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3361 ATGGTGACAACGAACTGGAGCTGGCCACGAGAGCTCCGCCGACGCGACTCATCATCAAGA 3420

Db   3421 AGGGGATCAAGGAGCAGAGACCAACGCAACTGGAGTGTGGCCATCGGGGATCGGAATTCACGA 3480
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Qy   3421 AGGGGATCAAGGAGCAGAGACCAACGCAACTGGAGTGTGGCCATCGGGGATCGGAATTCACGA 3480

Db   3481 TACACGGCGACATGAAGAACAGCAGCCGAAGAAATCCAAATATCTAAATAACGCCAACGA 3540
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Qy   3481 TACACGGCGACATGAAGAACAGCAGCCGAAGAAATCCAAATATCTAAATAACGCCAACGA 3540

Db   3541 TGATTGGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCGTAAACCATAGAG 3600
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Qy   3541 TGATTGGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCGTAAACCATAGAG 3600

Db   3601 GTTTGTTCCTTACGACGACGACACTGCCAGCACTAACTCATATGTAGCCATAAGAAATC 3660
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Qy   3601 GTTTGTTCCTTACGACGACGACACTGCCAGCACTAACTCATATGTAGCCATAAGAAATC 3660

Db   3661 GACCATTCAAGGACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGC 3720
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Qy   3661 GACCATTCAAGGACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGC 3720

Db   3721 GCGACGCCAGCAAGAAGAGGATTTAGTGTCTCGACGAGGAACTGGACGAGGAGGGCGAATGCG 3780
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Qy   3721 GCGACGCCAGCAAGAAGAGGATTTAGTGTCTCGACGAGGAACTGGACGAGGAGGGCGAATGCG 3780

Db   3781 AGGAGGCCCGCCCTCGACGCGTGATATCATTATTGAAACAGCTGTTATCACTGATTTTAATGAATC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3781 AGGAGGCCCGCCCTCGACGCGTGATATCATTATTGAAACAGCTGTTATCACTGATTTTAATGAATC 3840

Db   3841 AATATCCAGCTGATTGCTGCCCCGATTCGTACTATCGCCCAAAGACCCATACTGCAGGATATTTTATACTATA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3841 AATATCCAGCTGATTGCTGCCCCGATTCGTACTATCGCCCAAAGACCCATACTGCAGGATATTTTATACTATA 3900

Db   3901 ACGATGACTCGCCGTCGCCGTTCTGGCAAGGGCAATTCACGATCTTACGGGTTAATCAAGTTTTCAATTAA 3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3901 ACGATGACTCGCCGTCGCCGTTCTGGCAAGGGCAATTCACGATCTTACGGGTTAATCAAGTTTTCAATTAA 3960

Db   3961 TTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTT 4020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3961 TTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTT 4020

Db   4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTTATACTATA 4080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTTATACTATA 4080

Db   4081 TGGACAGAATATTACGGTTATATTCTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4081 TGGACAGAATATTACGGTTATATTCTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140

Db   4141 GCTTCAAAGTGTACTTCACCACGCGGTGTTGGCTCGATTGCTCGATTGTCATGGTAT 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4141 GCTTCAAAGTGTACTTCACCACGCGGTGTTGGCTCGATTGCTCGATTGTCATGGTAT 4200

Db   4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTATTCAAGCCTTCAAGACTA 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTATTCAAGCCTTCAAGACTA 4260
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Db 4261 TGCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGAGGGCATGAGGG 4320
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Qy 4261 TGCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGAGGGCATGAGGG 4320

Db 4321 TCGTCGTTAATGCCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTGTC 4380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4321 TCGTCGTTAATGCCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTGTC 4380

Db 4381 TAAATATTTTGGCTAATTTTGCCATAATGGGTACAGCTTTTTGCTGAAAATATTTTA 4440
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Qy 4381 TAAATATTTTGGCTAATTTTGCCATAATGGGTACAGCTTTTTGCTGAAAATATTTTA 4440

Db 4441 AGTGCGAGGACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATCGCAATGCCT 4500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4441 AGTGCGAGGACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATCGCAATGCCT 4500

Db 4501 GCGAGAGCGAGGAACTACACGTGGGTGAATTCAGCAATTTCGATCATGTAGGTAACG 4560
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Qy 4501 GCGAGAGCGAGGAACTACACGTGGGTGAATTCAGCAATTTCGATCATGTAGGTAACG 4560

Db 4561 CGTATCTGTGCCTTTTCCAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620
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Qy 4561 CGTATCTGTGCCTTTTCCAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG 4620

Db 4621 CTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACACATATT 4680
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Qy 4621 CTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACACATATT 4680

Db 4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG 4740
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Qy 4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG 4740

Db 4741 TTATCATTGATAATTTTAATGACAAAGAAAAAGCAGGTGGATCATTAGAAATGTTCA 4800
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Db 4801 TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860
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Qy 4801 TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860

Db 4861 TAAAAGCCATTCCAAGACCAAGGTGGCCACCACAAGCTATAACGGTATAGTAGTAACCG 4920
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Qy 4861 TAAAAGCCATTCCAAGACCAAGGTGGCCACCACAAGCTATAACGGTATAGTAGTAACCG 4920

Db 4921 ATAAGAAATTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTCACCATGACCC 4980
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Qy 4921 ATAAGAAATTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTCACCATGACCC 4980

Db 4981 TCGATCGTTACGATGCGTCGGACACGTCGGACCGTCCTAGACTATCTCAATGCGATAT 5040
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Qy 4981 TCGATCGTTACGATGCGTCGGACACGTCGGACCGTCCTAGACTATCTCAATGCGATAT 5040

Db 5041 TCGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGGAGCATTGCTTGCTGGACACTGC 5100
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Qy 5041 TCGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGGAGCATTGCTTGCTGGACACTGC 5100

Db 5101 TTATTGAGCCATGGAATTTATTTGATGTAGTAGTGTCATTTGTCATTTATCCATCTTAGGTCTTG 5160
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Qy 5101 TTATTGAGCCATGGAATTTATTTGATGTAGTAGTGTCATTTGTCATTTATCCATCTTAGGTCTTG 5160

Db 5161 TACTTAGCGATATTATCGAGAGTACTTCGTGTCGCCGACCGTCTCCGAGTGGTGCGTG 5220
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Db 5221 TGGCGAAAGTGGGGCCGTGTCCTTCGACTGGTGAAGGGAGCATTGCCAAGGGCATTCGGACACTGC 5280
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Qy 5221 TGGCGAAAGTGGGGCCGTGTCCTTCGACTGGTGAAGGGAGCATTGCCAAGGGCATTCGGACACTGC 5280

Db 5281 TCTTCGCGTTGGCCATGTCGCCTGCCCGGCCCTGTTCAACATCTGCCTGCTTGTTCCTGG 5340
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Db 5341 TCAATGTTCATCTTTGCCATTTCGGCATGTCGTTCTTCACGTCGTTCATGCACGTGAAGGAGAAGAGCG 5400
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Db 5341 TCATGTTCATCTTTGCCATTTCGGCATGTCGTTCTTCACGTCGTTCATGCACGTGAAGGAGAAGAGCG 5400
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Qy 5341 ... 5400

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Qy 5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGACCATGATGTCGTTCTTCAGA 5460

Db 5461 TGTCGACGTCAGCGTCGGTTGGGATGGTGTACTGGACGGGCCATTATCAATGAGAAGCATGCG 5520
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Qy 5461 TGTCGACGTCAGCGTCGGTTGGGATGGTGTACTGGACGGGCCATTATCAATGAGAAGCATGCG 5520

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Qy 5521 ATCCACCCGACACGCGACAAAGGTATCCGGCAATTGTGGTTCAGCGACCGTTGGAATAA 5580

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Db 5641 TCATTCTCGAGAACTATAGTCAGGCCACCGAGGACGTTGCAAGAGGGTCTAACCGACGACG 5700
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Qy 5701 ACTACGACATGTACTATCAGATCTGGCAGCAATTCGATCCGGAGCCGTGCTGGCCCGAGATCCACATAC 5760

Db 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGACGTGCCAGACGCGTGCCAGATCCACAAAC 5820
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Qy 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGACGTGCCAGACGCGTGCCAGATCCACAAAC 5820

Db 5821 CGAACAAGTACAAGATCATATCATGATGACCATACCCATCGTGTCGCGGTGACCTCATGTACT 5880
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Qy 5821 CGAACAAGTACAAGATCATATCATGATGACCATACCCATCGTGTCGCGGTGACCTCATGTACT 5880

Db 5881 GCGTCGACATCCTCCGAGCGCCCTTACGAAAGACTTCTTTGCGCGGCCCGAAGGGCAATCCGATAG 5940
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Qy 5881 GCGTCGACATCCTCCGAGCGCCCTTACGAAAGACTTCTTTGCGCGGCCCGAAGGGCAATCCGATAG 5940

Db 5941 AGGAGACGGGTGAGATTGGTGCGGTCAGCGTGAGGTACTGCGCCGGCTAATCCAGCACGCGCCT 6000
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Qy 5941 AGGAGACGGGTGAGATTGGTGCGGTCAGCGTGAGGTACTGCGCCGGCTAATCCAGCACGCGCCT 6000

Db 6001 TCTCATCAACGCTGTGCGGCGTCAGCGTCAGCCGTGAGGGAGGTACTGCGCCGGCTAATCCAGCACGCGCCT 6060
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Qy 6001 TCTCATCAACGCTGTGCGGCGTCAGCGTCAGCCGTGAGGGAGGTACTGCGCCGGCTAATCCAGCACGCGCCT 6060

Db 6061 GGGCGAAAGCACAAGGCGCGGCGCCCGGCGAGGGGACCCCGGCGATGAAGCAACGGACGGCGGATCATG 6120
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Qy 6061 GGGCGAAAGCACAAGGCGCGGCGCCCGGCGAGGGGACCCCGGCGATGAAGCAACGGACGGCGGATCATG 6120

Db 6121 GCGATGGCGGTGATCCGGATCCGGACGCGGGCGAAGTCCCGGGACCCCGGCGTAGCCGGGGTAGCGGCGATG 6180
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Qy 6121 GCGATGGCGGTGATCCGGATCCGGACGCGGGCGAAGTCCCGGGACCCCGGCGTAGCCGGGGTAGCGGCGATG 6180

Db 6181 CGCCCGGTTCGTGGAGAGTAGTGTTAACGGTACTGCCGATGCCGATGCCGATGCCGATGCCGATGCTG 6240
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Qy 6181 CGCCCGGTTCGTGGAGAGTAGTGTTAACGGTACTGCCGATGCCGATGCCGATGCCGATGCCGATGCTG 6240

Db 6241 AGAGTAATGTAAAATAGTCCGGGTGAGGATGCCGGCGGCGCGCGGGCGCGGCAGCAGCAGCAGCAG 6300
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Qy 6241 AGAGTAATGTAAAATAGTCCGGGTGAGGATGCCGGCGGCGCGCGGGCGCGGCAGCAGCAGCAGCAG 6300

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Qy 6301 CGGCGGCAGGCGGGGCACGACGACGCGGGCCACGACGACGGCTACCCGAGCGGCGGTAGCCGGCGACAGA 6360

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Db 6421 ACTCGCGGCGATCGCCGAGCCATCACGTCGTTCTTCATCGCCACGCCGATGCTCTGCAGCCGGCCTCGCCCCCC 6480
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Qy   6421 ACTCGGCGATCGCCGAGCATCACGTCGCGCGGAGTATTAGCTCTAGA 6480
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Db   6481 CCCTCCAAGATGCGACGCGGAGTATTAGCTCTAGA 6513
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Qy   6481 CCCTCCAAGATGCGACGCGGAGTATTAGCTCTAGA 6513

RESULT 5
ID   PCT-US95-14262-7 STANDARD; DNA; UNC; 6513 BP.
AC   xxxxxx
DT
DE   Sequence 7, Application PCT/US9514262
CC   Sequence 7, Application PCT/US9514262
CC   GENERAL INFORMATION:
CC     APPLICANT: Warmke, Jeffrey W.
CC     APPLICANT: Van Der Ploeg, Leonardus
CC     TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC     TITLE OF INVENTION: PARA SODIUM CHANNEL
CC     NUMBER OF SEQUENCES: 7
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Jack L. Tribble
CC       STREET: P.O. Box 2000, 126 E. Lincoln Avenue
CC       CITY: Rahway
CC       STATE: New Jersey
CC       COUNTRY: USA
CC       ZIP: 07065-0907
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, Version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: PCT/US95/14262
CC       FILING DATE:
CC       CLASSIFICATION:
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Tribble, Jack L.
CC       REGISTRATION NUMBER: 32,633
CC     REFERENCE/DOCKET NUMBER: 19338 PCT
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (908) 594-5321
CC       TELEFAX: (908) 594-4720
CC   INFORMATION FOR SEQ ID NO: 7:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 6513 base pairs
CC       TYPE: nucleic acid
CC       STRANDEDNESS: single
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA
SQ   SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match             100.0%;  Score 6513;  DB 2;  Length 6513;
Best Local Similarity   100.0%;  Pred. No. 0.00e+00;
Matches  6513;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 TCTAGACGTTGGCCGCCATAGACAGACAATGACAGAAGATTCCGACTCCGATATCTGAGGAAGAAC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 TCTAGACGTTGGCCGCCATAGACAGACAATGACAGAAGATTCCGACTCCGATATCTGAGGAAGAAC 60

Db     61 GCAGTTGTTCGTCCCTTTACCCGCCGAATCATTGGTCAAATCGAACAACGCATTGCCG 120
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Qy     61 GCAGTTGTTCGTCCCTTTACCCGCCGAATCATTGGTCAAATCGAACAACGCATTGCCG 120

Db    121 CTGAACATGAAAAGCAGGAGGAGTCGGAAAGAAAGAGAGAGCCGGAGGAGAGGTGCCGCGAT 180
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Qy    121 CTGAACATGAAAAGCAGGAGGAGTCGGAAAGAAAGAGAGAGCCGGAGGAGAGGTGCCGCGAT 180

Db    181 ATGGTCGCAAGAAAACAAAAAGAAAACAAAAACAAACATCCGATATGATGACGAGGAGGAAGGTC 240
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Qy    181 ATGGTCGCAAGAAAACAAAAAGAAAACAAAAACAAACATCCGATATGATGACGAGGAGGAAGGTC 240

Db    241 CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT 300

Db    301 TCCCGCCGGAATTGGCCTCCACTCCTCCTCTCGAGGATATCGATCCTACTACAGCAATGTAC 360
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Qy    301 TCCCGCCGGAATTGGCCTCCACTCCTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360

Db    361 TGACATTCGTAGTTGTAAGCAAGATAGTATTTTTCGCTTTCTGCATCAAAAGCAA 420
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Qy    361 TGACATTCGTAGTTGTAAGCAAAGATAGTATTTTTCGCTTTCTGCATCAAAAGCAA 420

Db    421 TGTGGATGCTGCGATCCATCAATCCGATACGTCGTGTGGCCATTACAATTCTAGTGCATC 480
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Qy    421 TGTGGATGCTGCGATCCATTCAATCCGATACGTCGTGGCCATTACAATTCTAGTGCATC 480

Db    481 CATTATTTCCCTATTCATCATCACCACAATCTCGTCAACTGCATCCTGATGATAATGC 540
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Qy    481 CATTATTTCCCTATTCATCATCATCACCACAATCTCGTCAACTGCATCCTGATGATAATGC 540

Db    541 CGACAACGCCCACGTTGAGTCCACTGAGTGATATTCACCGGAATTCTACACATTTGAAT 600
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Qy    541 CGACAACGCCCACGTTGAGTCCACTGAGTGATATTCACCGGAATCTACACATTTGAAT 600

Db    601 CAGCTGTTAAAGTGATGGCACGAGGTTTCATTTATGCCCGTTTACGTATCTTAGAGATG 660
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Qy    601 CAGCTGTTAAAGTGATGGCACGAGGTTTCATTTATGCCCGTTTACGTATCTTAGAGATG 660

Db    661 CATGGAATTGCTGAGCTTCGTAGTAATAGCTTTAGTTATGTGACCATGGTATAGATT 720
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Qy    661 CATGGAATTGCTGAGCTTCGTAGTAATAGCTTTAGTTATGTGACCATGGTATAGATT 720

Db    721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCGTGCTGCGAGCCA 780
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Qy    721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCGTGCTGCGAGCCA 780

Db    781 TTGTGCCAGGCTTGAAGACCATCGTCGGCCCGTCATCGAATCGGTGAAGAATCTGCCG 840
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Qy    781 TTGTGCCAGGCTTGAAGACCATCGTCGGCCCGTCATCGAATCGGTGAAGAATCTGCCG 840

Db    841 AGTGATTATCCTGACCATGTTCTCCCGTGTCGGTTGTCGGTTGATGGGCCTACAGATCT 900
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Qy    841 AGTGATTATCCTGACCATGTTCTCCCGTGTCGGTTGTCGGTTGATGGGCCTACAGATCT 900

Db    901 ATATGGGCGTGCTCACCGAGAGTGCATCAAGAAGTCCCGCTGCACGGTTCCTGGGGCA 960
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Qy    901 ATATGGGCGTGCTCACCGAGAGTGCATCAAGAAGTCCCGCTGCACGGTTCCTGGGGCA 960

Db    961 ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAATTGGTATTCCGAGG 1020
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Qy    961 ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTCCAATTGGTATTCCGAGG 1020

Db   1021 ACGAGGGCATCTCATTCGGTGCCTGCCAATGCCGGGCAATGCGACGACG 1080
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Qy   1021 ACGAGGGCATCTCATTCGGTGCCTGCCAATGCCGGGCAATGCGACGACG 1080

Db   1081 ATTACGTGTGCCTGCGAATGGGGTTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140
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Qy   1081 ATTACGTGTGCCTGCGAATGGGTTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140

Db   1141 CGTTCGGATGGGCTTTCTCCGCTTCCCGTCGCCGCCTTCCGCGTCCGCCTTCCGCTGGGAGGATC 1200
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Qy   1141 CGTTCGGATGGGCTTTCTCCTGTCCCGTCGCCGCCTTCCGCGTCCGCCTTCCGCTGGGAGGATC 1200

Db   1201 TGTACCAGCTGCGTGTTGCGCGCCGCCGGACCATGGCACATGCGTTCTTTATAGTCATCA 1260
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Qy   1201 TGTACCAGCTGCGTGTTGCGCGCCGCCGGACCATGGCACATGCGTTCTTTATAGTCATCA 1260

Db   1261 TCTTCCTAGGTTCATTCTATCTTGTGAATTTGATTTGGCCATTGTTGCCATGTCGTATG 1320
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Qy   1261 TCTTCCTAGGTTCATTCTATCTTGTGAATTTGATTTGGCCATTGTTGCCATGTCGTATG 1320

Db   1321 ACGAATTGCAAAGGAAGGCCGAAGAAGAAGAGGCTGCCGAAGAGAGGAGGCCGATACGTGAAG 1380
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Qy   1321 ACGAATTGCAAAGGAAGGCCGAAGAAGAAGAGGCTGCCGAAGAGAGGAGGCCGATACGTGAAG 1380
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Db  1381 CGGAGAAGCTGCGCGCCAAAGCGGCCAAGCTGGAGGAGCGGCCGGCCAATGCGCCAGGCTC 1440
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Qy  1381 CGGAGAAGCTGCGCGCCAAAGCGGCCAAGCTGGAGGAGCGGCCGGCCAATGCGCCAGGCTC 1440

Db  1441 AGGCAGCAGCGGATGCGGCGCTGCCCGCCGAGAGGCTGCACTGCGCACTCCGAAATGGCCAAGA 1500
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Qy  1441 AGGCAGCAGCGGATGCGGCGCTGCCCGCCGAGAGGCTGCACTGCGCACTCCGAAATGGCCAAGA 1500

Db  1501 GTCCGACGTATTCTTGCATCAGCTATGAGCTATTTGTTGGCGGCGTATTGTTGGCGGCAACGATG 1560
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Qy  1501 GTCCGACGTATTCTTGCATCAGCTATGAGCTATTTGTTGGCGGCGTATTGTTGGCGGCAACGATG 1560

Db  1561 ACAACACAAAGAGAAGATGTCCATTCGGAGGCGTCGAGGTGGAGTCGGTCGGTGAGCG 1620
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Db  1621 TTATACAAAGACAACCAGCACTTACACCACCAAGCTACCAAAGTTCGTAAAGTGA 1680
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Qy  1621 TTATACAAAGACAACCAGCACTTACACCACCAAGCTACCAAAGTTCGTAAAGTGA 1680

Db  1681 GCACGACAATCCTATCCTTACCTGGTTCACCGTTTAAACATACGCAGGGGATCACGTAGTT 1740
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Qy  1681 GCACGACAATCCTATCCTTACCTGGTTCACCGTTTAAACATACGCAGGGGATCACGTAGTT 1740

Db  1741 CTCACAAGTACACGATACGGAACGACGTGCCCGCTTTGGTATACCCGGTAGCCGATCGTA 1800
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Qy  1741 CTCACAAGTACACGATACGGAACGACGTGCCCGCTTTGGTATACCCGGTAGCCGATCGTA 1800

Db  1801 AGCCATTGGTATTGTCAACATATCAGGATGCCCAGCACTTGCCCTATGCCGACGACT 1860
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Qy  1801 AGCCATTGGTATTGTCAACATATCAGGATGCCCAGCACTTGCCCTATGCCGACGACT 1860

Db  1861 CGAATGCCGTCACCCGATGTCCCGACACTCATCGTATACCTCAGTCCCGAATATCGTATACCT 1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861 CGAATGCCGTCACCCGATGTCCCGACACTCATCGTATACCTCAGTCCCGAATATCGTATACCT 1920

Db  1921 GCAATCTTAGGGTCCCCGGATCTACTCGGCGGCCATCGTATCAGTGGGCGTCAGACCAAGGAGA 1980
         |||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 GCAATCTTAGGGTCCCCGGATCTACTCGGCGGCCATCGTATCAGTGGGCGTCAGACCAAGGAGA 1980

Db  1981 CACATGGCGATCTACTCGGCGGCGATGCCGTCATGGGCGTCAGACGCAATGGCGGCCACCA 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 CACATGGCGATCTACTCGGCGGCGATGCCGTCATGGGCGTCAGACGCAATGGCGGCCACCA 2040

Db  2041 GCAAATTGGCAACGCAACACGCCAATCAATCACAACGCGATTAAACATCATGACAACAC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041 GCAAATTGGCAACGCAACACGCCAATCAATCACAACGCGATTAAACATCATGACAACAC 2100

Db  2101 CCTGTCTGACAACAGTCGGCGGCGATCATCGCGACTACGGACTACGGCCTGGAGTGCA 2160
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Qy  2101 CCTGTCTGACAACAGTCGGCGGCGATCATCGCGACTACGGACTACGGCCTGGAGTGCA 2160

Db  2161 CGGACGAAGCTGGCAAGATTAAACATCCTTTATCGAGCCGTCCAGACAC 2220
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Qy  2161 CGGACGAAGCTGGCAAGATTAAACATCCTTTATCGAGCCGTCCAGACAC 2220

Db  2221 AAACGGTGGTTGATATGAAAGATGTCCTGAATGACATCATCGAACATCATCGAACAGCCCGTG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 AAACGGTGGTTGATATGAAAGATGTCCTGAATGACATCATCGAACATCATCGAACAGCCCGTG 2280

Db  2281 GTCGGCACAGTCGGCGATCGGCGCGTGTCTCCGTTTACTATTTCCCAACAGAGGACG 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281 GTCGGCACAGTCGGCGATCGGCGCGTGTCTCCGTTTACTATTTCCCAACAGAGGACG 2340

Db  2341 ATGACGAGGATGGGCGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCG 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341 ATGACGAGGATGGGCGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCG 2400

Db  2401 ATGTGTTTGTGTGGACTGTTGCTGGACTGTTGCTGGGTTTGGTTGGGTTTGGTTTGGGTGGTTATCGC 2460
         |||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401 ATGTGTTTGTGTGGACTGTTGCTGGACTGTTGCTGGGTTTGGTTGGGTTTGGTTTGGGTGGTTATCGC 2460


Db  2461 TCATCGTCTTCGATCCTTCGCTGAGCTCTTCATCACGCGTGTCGCATTGTGGTCAACACGA 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461 TCATCGTCTTCGATCCTTCGCTGAGCTCTTCATCACGCGTGTCGCATTGTGGTCAACACGA 2520

Db  2521 TGTTCATGGCAATGACTCACCACGATGAACAAGGAGATGGAACGCGTGCTCAAGAGTG 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521 TGTTCATGGCAATGACTCACCACGATGAACAAGGAGATGGAACGCGTGCTCAAGAGTG 2580

Db  2581 GCAACTATTTCTTCACCGCACCTTTGCCATCGAGCGCCACCATGAGCTAATGGCCATGA 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581 GCAACTATTTCTTCACCGCACCTTTGCCATCGAGCGCCACCATGAGCTAATGGCCATGA 2640

Db  2641 GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2641 GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 2700

Db  2701 CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTGTCCGGGGTGTCCAGGGTGTCCTTTCGAT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701 CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTGTCCGGGGTGTCCAGGGTGTCCTTTCGAT 2760

Db  2761 TGCTGCGTGTATTCAAACTGGCCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTA 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2761 TGCTGCGTGTATTCAAACTGGCCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTA 2820

Db  2821 TGGGACGGCACCATGGGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821 TGGGACGGCACCATGGGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA 2880

Db  2881 TCTTTGCGTGATGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCCT 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881 TCTTTGCGTGATGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCCT 2940

Db  2941 TTCCGGATGCGACTGCCGCGCCTGGAACTTCACCGACTTATGCGACTTATGCACTTCATGATCG 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941 TTCCGGATGCGACTGCCGCGCCTGGAACTTCACCGACTTATGCGACTTATGCACTTCATGATCG 3000

Db  3001 TGTTCCGGGTGCTCTGCGGAGAATGGATCGAGTGCATGTACGTGGGCG 3060
         |||||||||||||||||||||||||||||||||||||||||||||
Qy  3001 TGTTCCGGGTGCTCTGCGGAGAATGGATCGAGTGCATGTACGTGGGCG 3060

Db  3061 ATGTCGTGCATCCCATTCCTTCTTCTTGGCTCATCTCAGCTTATCAGCCGACTG 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061 ATGTCGTGCATCCCATTCCTTCTTCTTGGCTCATCTCAGCTTATCAGCCGACTG 3120

Db  3121 ACCTTTCTTAGCCTTGCTTTGTCCAATTTTGGCTCATCTAGCTTAATGGCCGTTAAAAGTT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121 ACCTTTCTTAGCCTTGCTTTGTCCAATTTTGGCTCATCTAGCTTAATGGCCGTTAAAAGTT 3180

Db  3181 CCGATAACGATACGAATAAAATAGCCGAGGCCTTCAATGCAATTGCCGATTAAAAGTT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181 CCGATAACGATACGAATAAAATAGCCGAGGCCTTCAATGCAATTGCCGATTAAAAGTT 3240

Db  3241 GGGTTAAGCGTAATATTGCTGATTGTTCAAGTTAATACGTAACAAATCAA 3300
         ||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241 GGGTTAAGCGTAATATTGCTGATTGTTCAAGTTAATACGTAACAAATCAA 3300

Db  3301 TAAGTGATCAACCATCAGTGAGAGGACCAACCAGCATCAGTTGGATTTGGAGCGGAAGAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301 TAAGTGATCAACCATCAGTGAGAGGACCAACCAGCATCAGTTGGATTTGGAGCGGAAGAGC 3360

Db  3361 ATGTGACAACGAACTGGAGCTGGGCCACGACGAGATCCTCGCCGACGGCCTCATCAAGA 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361 ATGTGACAACGAACTGGAGCTGGGCCACGACGAGATCCTCGCCGACGGCCTCATCAAGA 3420

Db  3421 AGGGGATCCAAGGAGCAACTGGAGTTGGCCATCGAGGTTGGCCATCGAGGTTGGCGAATTCCACGA 3480
         |||||||||||||||||||||||||||||||||||||||||||||
Qy  3421 AGGGGATCCAAGGAGCAACTGGAGTTGGCCATCGAGGTTGGCCATCGAGGTTGGCGAATTCCACGA 3480

Db  3481 TACACGGCGACATGAAGAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481 TACACGGCGACATGAAGAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540

Db  3541 TGATTGGCAACTGCAATTAACCACCAAGCAAGACAATAGACTGGAACGACGCTAAACCATAGAG 3600
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Qy  3541  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  3600
Db  3541  TGATTGGCAACTCAATTAACCACCAAGACAATAATGGAACACGACTGGAACCATAGAG  3600

Db  3601  GTTGTCCTTACAGGACGACGAGCACTGCCAGCATTAACTCATATGTGAGCCATAAGAATC  3660
Qy  3601  GTTTGTCCTTACAGGACGACGAGCACTGCCAGCATTAACTCATATGTGAGCCATAAGAATC  3660

Db  3661  GACCATTCAAGGACGACGAGCACCAAGGGCAGCCGCCGAGCGATGGAGGGCGAGGAGAAGC  3720
Qy  3661  GACCATTCAAGGACGACGAGCACCAAGGGCAGCCGCCGAGCGATGGAGGGCGAGGAGAAGC  3720

Db  3721  GCGACGCCCAGCAAGGAGGATTTAGGTCTCGACGAGGAGGGCCGGAATGCG  3780
Qy  3721  GCGACGCCCAGCAAGGAGGATTTAGGTCTCGACGAGGAGGGCCGGAATGCG  3780

Db  3781  AGGAGGGGCCCGCTCGACGGTGATCATTATTCATGCCACGACGAGATACTCGATG  3840
Qy  3781  AGGAGGGGCCCGCTCGACGGTGATCATTATTCATGCCACGACGAGATACTCGATG  3840

Db  3841  AATATCCAGCTGATTGCTGCCCCGATTCGGCAAGGATGGGGCAATTTTCCGATCTTAGCCGGTG  3900
Qy  3841  AATATCCAGCTGATTGCTGCCCCGATTCGGCAAGGATGGGGCAATTTTCCGATCTTAGCCGGTG  3900

Db  3901  ACGATGACTCGCCCTTCTTCGGCAAGGATGGGGCAATTTTACGGTTATATTTCCAATTAA  3960
Qy  3901  ACGATGACTCGCCCTTCTTCGGCAAGGATGGGGCAATTTTACGGTTATATTTCCAATTAA  3960

Db  3961  TTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTT  4020
Qy  3961  TTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTT  4020

Db  4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTCGAGGATATTTTATACTATA  4080
Qy  4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTCGAGGATATTTTATACTATA  4080

Db  4081  TGGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTTGGTTGGCGCTCG  4140
Qy  4081  TGGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTTGGTTGGCGCTCG  4140

Db  4141  GCTTCAAAGTTGTACTTCACCAAGCGTGGTGTTGGCTCGATTGTTGGTCTCATGGTAT  4200
Qy  4141  GCTTCAAAGTTGTACTTCACCAAGCGTGGTGTTGGCTCGATTGTTGGTCTCATGGTAT  4200

Db  4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGCTGGAGCTGGTGTATTCAAGCCTTCAAGGACTA  4260
Qy  4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGCTGGAGCTGGTGTATTCAAGCCTTCAAGGACTA  4260

Db  4261  TGGCAACGTTAAGAGCACATGAGACTACGTGCCCATGTCCCGTATGCCAGGGCATGAGGG  4320
Qy  4261  TGGCAACGTTAAGAGCACATGAGACTACGTGCCCATGTCCCGTATGCCAGGGCATGAGGG  4320

Db  4321  TCGTCGTTAATGCGCTGGTACAACGTCCATCTTCAATGCTGTCATTGGTGTC  4380
Qy  4321  TCGTCGTTAATGCGCTGGTACAACGTCCATCTTCAATGCTGTCATTGGTGTC  4380

Db  4381  TAATATTTTGGCTAATTTTTGCCATAAATGGGTTTTTGCTGGAAAATATTTTA  4440
Qy  4381  TAATATTTTGGCTAATTTTTGCCATAAATGGGTTTTTGCTGGAAAATATTTTA  4440

Db  4441  AGTGCGGAGGACATGAATGGCACGTGGGTGAATTCAGCTCAGCGAATCATACCAAATGCCT  4500
Qy  4441  AGTGCGGAGGACATGAATGGCACGTGGGTGAATTCAGCTCAGCGAATCATACCAAATGCCT  4500

Db  4501  CGTATCTGTGCCTTTCTTCGGCCACCTTCAAGTGGATACAAATCGAATTCAGCATCATGTAGGTAACG  4560
Qy  4501  CGTATCTGTGCCTTTCTTCGGCCACCTTCAAGTGGATACAAATCGAATTCAGCATCATGTAGGTAACG  4560

Db  4561  CGTATCTGTGCCTTTCCAAGTGGCCACCTTCAAAAGCTGGATACAAATCGAATCATGAACGATG  4620
Qy  4561  CGTATCTGTGCCTTTCCAAGTGGCCACCTTCAAAAGCTGGATACAAATCGAATCATGAACGATG  4620

Db  4621  CTATCGATTCACGAGAGGTGGACAAGCACCAATTCGTGAAACGAACATCTACATGTATT  4680
Qy  4621  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  4621  CTATCGATTCACGAGAGGTGGACAAGCACCAATTCGTGAAACGAACATCTACATGTATT  4680
Db  4681  TATATTTCGTATTCTTCATCATATTGGATCCTTTTCACTCAATCTGTTCATTGGTG  4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4681  TATATTTCGTATTCTTCATCATATTGGATCCTTTTCACTCAATCTGTTCATTGGTG  4740

Db  4741  TTATCATTGATAATTTAATGAGCAAAAAGCAGGTGGATCATTAGAAATGTTCA  4800
Qy  4741  TTATCATTGATAATTTAATGAGCAAAAAGCAGGTGGATCATTAGAAATGTTCA  4800

Db  4801  TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAGAATGGGCTCTAAAAAACCAT  4860
Qy  4801  TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAGAATGGGCTCTAAAAAACCAT  4860

Db  4861  TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTGAAATAGTAACCG  4920
Qy  4861  TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTGAAATAGTAACCG  4920

Db  4921  ATAAGAAATTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTCAACATGTCGATAT  4980
Qy  4921  ATAAGAAATTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTCAACATGTCGATAT  4980

Db  4981  TCGATCGTTACGATGCGTCGGCACACGCGGTCCTAGACTATAACGGTCTATCTCAATGCGATATCACTATT  5040
Qy  4981  TCGATCGTTACGATGCGTCGGCACACGCGGTCCTAGACTATAACGGTCTATCTCAATGCGATATCACTATT  5040

Db  5041  TCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTACGATATCACTATT  5100
Qy  5041  TCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTACGATATCACTATT  5100

Db  5101  TTAATTGAGCCATGGAATTTATTTGATGTAGTAGTGTCATTTTATCCATCTTAGGTCTTG  5160
Qy  5101  TTATTGAGCCATGGAATTTATTTGATGTAGTAGTGTCATTTTATCCATCTTAGGTCTTG  5160

Db  5161  TACTTAGCGATATATCGTCCCGTCCTGCTCCGTCCCCTGCTCTCCGAGTGGTGCGTG  5220
Qy  5161  TACTTAGCGATATATCGTCCGAAGAAGTACTTCGTCGTCGTCCTGCTCCCGTCCCCTGCTCTCCGAGTGGTGCGTG  5220

Db  5221  TGGCGAAAGTGGGCCGTGTCCTGTGTCTTGGCTCACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGC  5280
Qy  5221  TGGCGAAAGTGGGCCGTGTCCTGTGTCTTGGCTCACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGC  5280

Db  5281  TCTTCGCGTTGCCATGTGCCATGTGGCTCGCTGCTCCGCCTGCTCTCAACATCTCGCCTCGTGTCCTGG  5340
Qy  5281  TCTTCGCGTTGCCATGTGCCATGTGGCTCGCTGCTCCGCCTGCTCTCAACATCTCGCCTCGTGTCCTGG  5340

Db  5341  TCATGTTCATCTTTGCCATTTGCTCCATTTCGGCAGGCATGGGGTATGCTCCGCATGCTGAGGG  5400
Qy  5341  TCATGTTCATCTTTGCCATTTGCTCCATTTCGGCAGGCATGGGGTATGCTCCGCATGCTGAGGG  5400

Db  5401  GCATTAACGACGTCTACAACTTCAAGACCTTGGCCAGATCCTCCTCTTCAGA  5460
Qy  5401  GCATTAACGACGTCTACAACTTCAAGACCTTGGCCAGATCCTCCTCTTCAGA  5460

Db  5461  TGTCGACGTCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGCG  5520
Qy  5461  TGTCGACGTCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGCG  5520

Db  5521  ATCCACCCGACGACAAAGGCTATCCGGGCAATTGGTGTTCAGCGACCGTTGGAATAA  5580
Qy  5521  ATCCACCCGACGACAAAGGCTATCCGGGCAATTGGTGTTCAGCGACCGTTGGAATAA  5580

Db  5581  CGTTTCTCCTCTCGAGAACTATAGTCAGTTATTTTGATAGTTATTAATATGTACATTGCTG  5640
Qy  5581  CGTTTCTCCTCTCGAGAACTATAGTCAGTTATTTTGATAGTTATTAATATGTACATTGCTG  5640

Db  5641  TCATTCTCGAGAACTTCAGGCCACCGACGACGTGCAAGAGGGTCTAACCGACGACG  5700
Qy  5641  TCATTCTCGAGAACTATAGTCAGGCCACCGACGACGTGCAAGAGGGTCTAACCGACGACG  5700

Db  5701  ACTACGACATGTACTATGAGATCGGCAGCAATTCGGCAATTCGGCAGCAATTCGATCCCGAGGCACCCAGTACATAC  5760
Qy  5701  ACTACGACATGTACTATGAGATCGGCAGCAATTCGGCAATTCGGCAGCAATTCGATCCCGAGGCACCCAGTACATAC  5760
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Db   5761  GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCCCGTGCGAGATCCCACAAAC  5820
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Qy   5761  GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCCCGTGCGAGATCCCACAAAC  5820

Db   5821  CGAACAAGTACAAGATCATATCGATGGACATACCCATCGTCCGCGGTGACCTCATGTACT   5880
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Qy   5821  CGAACAAGTACAAGATCATATCGATGGACATACCCATCGTCCGCGGTGACCTCATGTACT   5880

Db   5881  GCGGTCGACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAG  5940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5881  GCGGTCGACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAG  5940

Db   5941  AGGAGACGGGTGAGATTGGTGAGATAGGGCCCGCCCGGATACGGAGGGCTACGAGCCCG   6000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5941  AGGAGACGGGTGAGATTGGTGAGATAGGGCCCGCCCGGATACGGAGGGCTACGAGCCCG   6000

Db   6001  TCTCATCAACGCTGTGGCGTCAGCGTGAGGAGTACTGCCCGGCTAATCCAGCACGCCT   6060
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Qy   6001  TCTCATCAACGCTGTGGCGTCAGCGTGAGGAGTACTGCCCGGCTAATCCAGCACGCCT   6060

Db   6061  GGCGAAAGCACAAGGCGCGCGGAGGGAGTGGGTCCTTTGAGCCGGATACGGATCATG   6120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6061  GGCGAAAGCACAAGGCGCGCGGAGGGAGTGGGTCCTTTGAGCCGGATACGGATCATG   6120

Db   6121  GCGATGGCCGGTGATCCGGATGCCCGGGGACCCGCGCCGATGAAGCAACGACGGCGATG  6180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6121  GCGATGGCGGGTGATCCGGATGCCCGGGGACCCGCGCCGATGAAGCAACGACGGCGATG  6180

Db   6181  CGCCCCCTGTGGAGATGGTAGTGTTAAACGTACTGCAGAAGGAGCTGCCGATGCCGATG  6240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6181  CGCCCGCTGTGGAGATGGTAGTGTTAAACGTACTGCAGAAGGAGCTGCCGATGCCGATG  6240

Db   6241  AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCGGCGGCCAGCAGCAGCAGCAGCAG   6300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6241  AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCGGCGGCCAGCAGCAGCAGCAGCAG   6300

Db   6301  CGGCGGCGGCGGCGGCGCACGACGACGGCCGGAAGTCCCCGGAAGTGGCGCCGGGGACAGA  6360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6301  CGGCGGCGGCGGCGGCGCACGACGACGGCCGGAAGTCCCCGGAAGTGGCGCCGGGGACAGA  6360

Db   6361  CCGCCGGTTCTCGTGGAGAGCCACGGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC  6420
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Qy   6361  CCGCCGGTTCTCGTGGAGAGCCACGGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC  6420

Db   6421  ACTCGCGGATCGCCGAGCATCACGTCCGCGCACGCGCGATGTCTGAGCCGTCTGCGCCCCC  6480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   6421  ACTCGCGGATCGCCGAGCATCACGTCCGCGCACGCGCGATGTCTGAGCCGTCTGCGCCCCC  6480

Db   6481  CCCTCCAAGATGCACGCGGAGTATTAGCTCTAGA  6513
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Qy   6481  CCCTCCAAGATGCACGCGGAGTATTAGCTCTAGA  6513
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RESULT   6
ID    US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC    xxxxxx
DT
DE    Sequence 14, Application US/08232463
CC    Sequence 14, Application US/08232463
CC    Patent No. 5670367
CC    GENERAL INFORMATION:
CC    APPLICANT: DORNER, F.
CC    APPLICANT: SCHEFLINGER, F.
CC    APPLICANT: FALKNER, F. G.
CC    TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC    NUMBER OF SEQUENCES: 52
CC    CORRESPONDENCE ADDRESS:
CC    ADDRESSEE: Foley & Lardner
CC    STREET: 1800 Diagonal Road, Suite 500
CC    CITY: Alexandria
CC    STATE: VA
CC    COUNTRY: USA

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CC    ZIP: 22313-0299
CC    COMPUTER READABLE FORM:
CC    MEDIUM TYPE: Floppy disk
CC    COMPUTER: IBM PC compatible
CC    OPERATING SYSTEM: PC-DOS/MS-DOS
CC    SOFTWARE: PatentIn Release #1.0, Version #1.25
CC    CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER: US/08/232,463
CC    FILING DATE:
CC    CLASSIFICATION: 435
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: US/07/935,313
CC    FILING DATE:
CC    APPLICATION NUMBER: EP 91 114 300.6
CC    FILING DATE: 26-AUG-1991
CC    ATTORNEY/AGENT INFORMATION:
CC    NAME: BENT, Stephen A.
CC    REGISTRATION NUMBER: 29,768
CC    REFERENCE/DOCKET NUMBER: 30472/114 IMMU
CC    TELECOMMUNICATION INFORMATION:
CC    TELEPHONE: (703)836-9300
CC    TELEFAX: (703)683-4109
CC    TELEX: 899149
CC    INFORMATION FOR SEQ ID NO: 14:
CC    SEQUENCE CHARACTERISTICS:
CC    LENGTH: 7218 base pairs
CC    TYPE: nucleic acid
CC    STRANDEDNESS: single
CC    TOPOLOGY: linear
CC    IMMEDIATE SOURCE:
CC    CLONE: pTZgpt-F1s
SQ    SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

Query Match        1.7%;  Score 110;  DB 1;  Length 7218;
Best Local Similarity   1.9%;  Pred. No. 3.29e-59;
Matches    7;  Conservative   237;  Mismatches   134;  Indels    0;  Gaps    0;

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Db   1056  GAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  1115
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Cp   3794  GAGCCGGCCCTCGCCATTCGCCCTCCGTCGTCCGAGACCTAAATCCTC  3735

Db   1116  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  1175
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Cp   3734  CTTGCTGGCGTCGCGGCCTTCTCCTCGCCCATCGTCTCGGCGCCTGCCCTTGTGGCTCTC  3675

Db   1176  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  1235
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Cp   3674  GTCCTTGAATGGTCGATTCTTATGCTACCATATGAGTTAATGCTGGCAGTGTCGTCGTC  3615

Db   1236  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  1295
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Cp   3614  CTGTAAGGACAAACCTCTATGTGTTTAGCTCGTGTCTCTGGTGTGGTTAAT  3555

Db   1296  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  1355
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Cp   3554  TGAGTTGCCAATCATCGTTGCGTTATTTAGATATTGGATTTCTTCGGCTTGTTGTTCTT  3495

Db   1356  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY  1415
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Cp   3494  CATGTCGCCGTGTATCGTGAATTCCATCCGATCCCGATGCGCCACCTCCAGTTGCGTCTG  3435

Db   1416  YYYYYYYYYYYYYYY  1433
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Cp   3434  CTCCTTGATCCCTTCTT  3417
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RESULT   7
ID    US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC    xxxxxx
DT
DE    Sequence 14, Application US/08232463
CC    Sequence 14, Application US/08232463
CC    Patent No. 5670367

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CC    GENERAL INFORMATION:
CC       APPLICANT: DORNER, F.
CC       APPLICANT: SCHEFLINGER, F.
CC       APPLICANT: FALKNER, F. G.
CC       TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC       NUMBER OF SEQUENCES: 52
CC       CORRESPONDENCE ADDRESS:
CC          ADDRESSEE: Foley & Lardner
CC          STREET: 1800 Diagonal Road, Suite 500
CC          CITY: Alexandria
CC          STATE: VA
CC          COUNTRY: USA
CC          ZIP: 22313-0299
CC       COMPUTER READABLE FORM:
CC          MEDIUM TYPE: Floppy disk
CC          COMPUTER: IBM PC compatible
CC          OPERATING SYSTEM: PC-DOS/MS-DOS
CC          SOFTWARE: PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER: US/08/232,463
CC          FILING DATE:
CC          CLASSIFICATION: 435
CC       PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER: US/07/935,313
CC          FILING DATE:
CC          APPLICATION NUMBER: EP 91 114 300.6
CC          FILING DATE: 26-AUG-1991
CC       ATTORNEY/AGENT INFORMATION:
CC          NAME: BENT, Stephen A.
CC          REGISTRATION NUMBER: 29,768
CC          REFERENCE/DOCKET NUMBER: 30472/114 IMMU
CC       TELECOMMUNICATION INFORMATION:
CC          TELEPHONE: (703)836-9300
CC          TELEFAX: (703)683-4109
CC          TELEX: 899149
CC    INFORMATION FOR SEQ ID NO: 14:
CC       SEQUENCE CHARACTERISTICS:
CC          LENGTH: 7218 base pairs
CC          TYPE: nucleic acid
CC          STRANDEDNESS: single
CC          TOPOLOGY: linear
CC       IMMEDIATE SOURCE:
CC          CLONE: pTZgpt-F1s
SQ    SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

   Query Match     0.9%;  Score 60;  DB 1;  Length 7218;
   Best Local Similarity  1.7%;  Pred. No. 4.19e-23;
   Matches    6;  Conservative 197;  Mismatches 143;  Indels  0;  Gaps  0;

Db 1061 TGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1120
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Qy 5033 TGCGGATATCCGTAGTTATTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTTACGATA 5092

Db 1121 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1180
         ::: :::::: :::  :::: ::: :: :::: ::: :::: :::::: ::::
Qy 5093 TCACTATTTTATTGAGCCATGGAATTATTTGATGTAGTAGTTGTCATTTTATCCATCTT 5152

Db 1181 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1240
         ::: ::::: ::::: :::: ::::: :::::::: :::: :::: :
Qy 5153 AGGTCTTGTACTTAGCGATATTATCGAGAGAGTACTTCGTGTCGCCGACCCTGCTCCGAGT 5212

Db 1241 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1300
         :::::::: :: ::::: :::::::::: :::::: :
Qy 5213 GGTGCGTGTGGCGAAAGTGGGCGCCGTGTCCTTCGACTGGTGAAGGGAGCCAAGGCATTCG 5272

Db 1301 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1360
         ::::::::: :: ::::: :: :::::::::::: :::::
Qy 5273 GACACTGCCTCTTCGCGTTGGCCATGTGCCGCCGCCCCTGTTCAACATCTGCCTGCTGCT 5332

Db 1361 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1406
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Qy 5333 GTTCCTGGTCATGTCATGTTCATCTTGCCATTTTCGGCCATGTGTCGTTCTTC 5378
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RESULT  8
ID   US-08-238-163-5  STANDARD; DNA; UNC; 215 BP.
AC   xxxxxx
DT
DE   Sequence 5, Application US/08238163
CC   Sequence 5, Application US/08238163
CC   Patent No. 5569830
CC   GENERAL INFORMATION:
CC      APPLICANT: BENNETT, Alan
CC      APPLICANT: LABAVITCH, John M.
CC      APPLICANT: POWELL, Ann
CC      APPLICANT: STOTZ, Henrik
CC      TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC      TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
CC      NUMBER OF SEQUENCES: 24
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE: Townsend and Townsend Khourie and Crew
CC         STREET: Steuart Street Tower, One Market Plaza
CC         CITY: San Francisco
CC         STATE: California
CC         COUNTRY: US
CC         ZIP: 94105-1493
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE: Floppy disk
CC         COMPUTER: IBM PC compatible
CC         OPERATING SYSTEM: PC-DOS/MS-DOS
CC         SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER: US/08/238,163
CC         FILING DATE: 03-MAY-1994
CC         CLASSIFICATION: 800
CC      ATTORNEY/AGENT INFORMATION:
CC         NAME: Bastian, Kevin L.
CC         REGISTRATION NUMBER: 34,774
CC         REFERENCE/DOCKET NUMBER: 2307E-540
CC      TELECOMMUNICATION INFORMATION:
CC         TELEPHONE: (415) 543-9600
CC         TELEFAX: (415) 543-5043
CC   INFORMATION FOR SEQ ID NO: 5:
CC      SEQUENCE CHARACTERISTICS:
CC         LENGTH: 215 base pairs
CC         TYPE: nucleic acid
CC         STRANDEDNESS: single
CC         TOPOLOGY: unknown
CC      MOLECULE TYPE: protein
CC      FEATURE:
CC         NAME/KEY: misc_feature
CC         LOCATION: 1..215
CC         OTHER INFORMATION:  /standard_name= "Deduced amino acid
CC         OTHER INFORMATION: sequence of PGIP from bean."
SQ   SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.

   Query Match     0.6%;  Score 41;  DB 1;  Length 215;
   Best Local Similarity 15.6%;  Pred. No. 1.53e-10;
   Matches   30;  Conservative 77;  Mismatches 83;  Indels  2;  Gaps  2;

Db   22 AKKDGNTTSSWTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAKTHYY 81
          : |:  |  ::  | : |  :||::  ::|::| || :
Qy 1257 ATCATCTTCCTAGGTTCATTCTATCTTGTGAATTTGATTTTGGCCATTGTGCCATGTCG 1316

Db   82 THTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTA-MTSRNRTGKTANNA 140
          ::|:: | :::  :  :  :  |::: ::  ::|  | |  :|  :
Qy 1317 TATGACGAATTGCAAAGAAGGAGCCGAAGAAGAAGAGGCTGCCGAAGAGGAGGCGGATACGT 1376

Db  141 VDSRMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSNVSNCGGGNKRD 200
          :  |:|:|:::|  : |: : |: :|::|  | |  :  :|
Qy 1377 GAAGGCGGAAGAAGCTGCCGCCGCCAAGCCGCCAAGCTGGAG-GAGCGGGCCAATGCGCA 1435

Db  201 VSSYANNKCCGS 212
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Qy 1436 GGCTCAGGCAGC 1447
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RESULT 9
ID    US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC    xxxxxx
DT
DE    Sequence 5, Application US/08238163
DE    Sequence 5, Application US/08238163
CC    Patent No. 5569830
CC    GENERAL INFORMATION:
CC       APPLICANT: BENNETT, Alan
CC       APPLICANT: LABAVITCH, John M.
CC       APPLICANT: POWELL, Ann
CC       APPLICANT: STOTZ, Henrik
CC       TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC       TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC       NUMBER OF SEQUENCES: 24
CC       CORRESPONDENCE ADDRESS:
CC          ADDRESSEE: Townsend and Townsend Khourie and Crew
CC          STREET: Steuart Street Tower, One Market Plaza
CC          CITY: San Francisco
CC          STATE: California
CC          COUNTRY: US
CC          ZIP: 94105-1493
CC       COMPUTER READABLE FORM:
CC          MEDIUM TYPE: Floppy disk
CC          COMPUTER: IBM PC compatible
CC          OPERATING SYSTEM: PC-DOS/MS-DOS
CC          SOFTWARE: PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER: US/08/238,163
CC          FILING DATE: 03-MAY-1994
CC          CLASSIFICATION: 800
CC       ATTORNEY/AGENT INFORMATION:
CC          NAME: Bastian, Kevin L.
CC          REGISTRATION NUMBER: 34,774
CC          REFERENCE/DOCKET NUMBER: 2307E-540
CC       TELECOMMUNICATION INFORMATION:
CC          TELEPHONE: (415) 543-9600
CC          TELEFAX: (415) 543-5043
CC    INFORMATION FOR SEQ ID NO: 5:
CC       SEQUENCE CHARACTERISTICS:
CC          LENGTH: 215 base pairs
CC          TYPE: nucleic acid
CC          STRANDEDNESS: single
CC          TOPOLOGY: unknown
CC       MOLECULE TYPE: protein
CC       FEATURE:
CC          NAME/KEY: misc_feature
CC          LOCATION: 1..215
CC          OTHER INFORMATION: /standard_name= "Deduced amino acid
CC          OTHER INFORMATION: sequence of PGIP from bean."
SQ    SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.

Query Match         0.6%;   Score 36;   DB 1;   Length 215;
Best Local Similarity 16.9%;   Pred. No. 1.83e-07;
Matches   27;   Conservative   61;   Mismatches 72;   Indels  0;   Gaps   0;

Db    1 MTNVTMSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNK 60
         :|:|:: :: |::: | | |:: :::: | | |:: ::|:::
Cp  233 ATCCTCGTCTCCGTCATCATATCGGATTTCTTTTGTTTTTCTTGCGACCATATCGCGG 174

Db   61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKIVTDSVNASGTSSSNGGTDGNRSGADSY 120
         : |:::| | |:|::|:|| |:::: :|::: :|:: |
Cp  173 CACCTCTCCCTCGGCCTCTTTTCTTTCCAGCTCCTTCTGCTTTTCATGTTCAGCGGCAAT 114

Db  121 GSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKH 160
         |:::| |:: |:| | | |:::: : ::| :::
Cp  113 GCGTTGTTCGATTTGCACCAATGATTCGCGGGTAAAGGGA 74

RESULT 10
ID    PCT-US95-11869-1 STANDARD; DNA; UNC; 1809 BP.
AC    xxxxxx
DT
DE    Sequence 1, Application PC/TUS9511869
DE    Sequence 1, Application PC/TUS9511869
CC    GENERAL INFORMATION:
CC       APPLICANT:
CC       TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
CC       TITLE OF INVENTION: Thereto
CC       NUMBER OF SEQUENCES: 5
CC       COMPUTER READABLE FORM:
CC          MEDIUM TYPE: Floppy disk
CC          COMPUTER: IBM PC compatible
CC          OPERATING SYSTEM: PC-DOS/MS-DOS
CC          SOFTWARE:
CC       CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER: PCT/US95/11869
CC          FILING DATE: 19-SEP-1995
CC       ATTORNEY/AGENT INFORMATION:
CC          NAME: Vincent, Matthew P.
CC          REGISTRATION NUMBER: 36,709
CC          REFERENCE/DOCKET NUMBER: HMI-011CPPC
CC       TELECOMMUNICATION INFORMATION:
CC          TELEPHONE: (617) 227-7400
CC          TELEFAX: (617) 227-5941
CC    INFORMATION FOR SEQ ID NO: 1:
CC       SEQUENCE CHARACTERISTICS:
CC          LENGTH: 1809 base pairs
CC          TYPE: nucleic acid
CC          STRANDEDNESS: both
CC          TOPOLOGY: linear
CC       MOLECULE TYPE: cDNA
CC       FEATURE:
CC          NAME/KEY: CDS
CC          LOCATION: 265..891
CC       FEATURE:
CC          NAME/KEY: 5'UTR
CC          LOCATION: 1..264
CC       FEATURE:
CC          NAME/KEY: 3'UTR
CC          LOCATION: 892..1809
CC       FEATURE:
CC          NAME/KEY: sig_peptide
CC          LOCATION: 255..324
SQ    SEQUENCE 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 OTHER.

Query Match         0.6%;   Score 36;   DB 2;   Length 1809;
Best Local Similarity 80.0%;   Pred. No. 1.83e-07;
Matches   48;   Conservative    0;   Mismatches 12;   Indels  0;   Gaps   0;

Db  260 GGGCCATGGCGCCCGCCAGCGCCCGCTGCGCGCCTGCGCTGCTGCGCGCTGCGCGCTGC 319
         || || |||| |||| | |||| || | ||||| || |||||||||||||||||||||||
Cp 6335 GGGACTTCCCGCGCTCGTCGTGCCCGCCGCCGCCGCCGCCTGCGTCGCTGCTGCGCCCGC 6276

RESULT 11
ID    US-07-745-206A-6 STANDARD; DNA; UNC; 5904 BP.
AC    xxxxxx
DT
DE    Sequence 6, Application US/07745206A
DE    Sequence 6, Application US/07745206A
CC    Patent No. 5429921
CC    GENERAL INFORMATION:
CC       APPLICANT: Harpold, Michael
CC       APPLICANT: Ellis, Steven
CC       APPLICANT: Williams, Mark
CC       APPLICANT: McCue, Ann
CC       APPLICANT: Feldman, Daniel
CC       TITLE OF INVENTION: Human Calcium Channel Compositions and
CC       TITLE OF INVENTION: Methods
CC       NUMBER OF SEQUENCES: 32
CC       CORRESPONDENCE ADDRESS:
CC          ADDRESSEE: Fitch, Even, Tabin & Flannery
CC          STREET: 135 S. LaSalle
CC          CITY: Chicago

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CC     STATE: Illinois
CC     COUNTRY: U.S.A.
CC     ZIP: 60603
CC     COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.25
CC     CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/07/745,206A
CC     FILING DATE: 19910815
CC     CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC     NAME: Feder, Scott B
CC     REFERENCE/DOCKET NUMBER: 51504
CC     TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: 312-372-7842
CC     INFORMATION FOR SEQ ID NO: 6:
CC     SEQUENCE CHARACTERISTICS:
CC     LENGTH: 5904 base pairs
CC     TYPE: NUCLEIC ACID
CC     STRANDEDNESS: unknown
CC     TOPOLOGY: unknown
CC     MOLECULE TYPE: DNA (genomic)
SQ     SEQUENCE 5904 BP; 1353 A; 1717 C; 1544 G; 1260 T; 30 OTHER.

Query Match       0.6%;   Score 39;  DB 1;  Length 5904;
Best Local Similarity 60.3%;   Pred. No. 2.69e-09;
Matches   114;  Conservative    0;  Mismatches  75;  Indels   0;  Gaps   0;

Db   3759 CATCCTGCTCAACACCATCTGCCTGGCCATGAGCACTACGGCCAGAGAGCTGCCTGTTCAA 3818
          ||| |||||||| ||| |||||  |||||| |||| ||| | |  | |||| ||||| |||
Qy   2504 CATTGTGGTCAACACGATGTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGA 2563

Db   3819 AATCGCCATGAACATCTCCAACATGTCTTCACGGCCTCCTTCACCGTGGAGATGATCCT 3878
          | | |||||| |||  || |  |||||||| | | ||||||||||||| | | ||  |
Qy   2564 ACCGTGCTCAAGAGTGGCAACTATTCTTCACCGCCACCTTTGCCATCGAGGCCACCAT 2623

Db   3879 GAAGCTCATTGCCTTCAAACCCAAGGGTACTTTAGTGATCCCTGGAATGTTTTTGACTT 3938
          | |||| | ||| || |  ||| |  || || | |||  ||||| | ||||| ||||||
Qy   2624 GAAGCTAATGGCCATGAGCCCCAAGTACTACTATTTCCAGGAGGGCTGGAACATCTTCGACTT 2683

Db   3939 CCTCATCGT 3947
          | | |||||
Qy   2684 CATTATCGT 2692


RESULT 12
ID     5386025-5  STANDARD; DNA; UNC; 6459 BP.
AC     xxxxxxx
DT     01-JAN-1900
DE     Patent No. 5386025.
CC     Patent No. 5386025
CC     APPLICANT: JAY, SCOTT D.;ELLIS, STEVEN B.;HARPOLD, MICHAEL
CC     M.;CAMPBELL, KEVIN P.
CC     TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CC     NUMBER OF SEQUENCES: 9
CC     CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/07/482,384
CC     FILING DATE: 20-FEB-1990
CC     SEQ ID NO:5:
CC     LENGTH: 5962
SQ     Sequence 6459 BP; 1280 A; 1835 C; 1691 G; 1156 T; 497 other;

Query Match       0.6%;   Score 37;  DB 3;  Length 5962;
Best Local Similarity 65.0%;   Pred. No. 4.54e-08;
Matches   80;  Conservative    0;  Mismatches  43;  Indels   0;  Gaps   0;

Db   3862 CTGCTGAGTCGGGCGGCCGAGGGCGTGCCGCACGCTGCTGTGGACGTTCATCAAGTCCTTCCAG 3921
          ||| ||| ||||  || |||||||||| ||  | |||| | |||| ||| |||||||| |
Qy   5247 CTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGGACTGCTTCGCCGTCGGCTGCCG 5306

Db   3922 GCCCTGCCCTACGTGGCCCTGCTCATCGTCATCTACCGCCGTCATCGGC 3981
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Qy   5307 GCCCTGTTCAACATCTGCCTGCTGCTGTTCCTGGTCATGTCATCTTTGCCATTTCGGC 5366
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Db   3982 ATG 3984
          |||
Qy   5367 ATG 5369


RESULT 13
ID     US-08-336-257A-3  STANDARD; DNA; UNC; 5975 BP.
AC     xxxxxxx
DT
DE     Sequence 3, Application US/08336257A
CC     Sequence 3, Application US/08336257A
CC     Patent No. 5726035
CC     GENERAL INFORMATION:
CC     APPLICANT: Jay, Scott D
CC     APPLICANT: Ellis, Steven B.
CC     APPLICANT: Harpold, Michael M.
CC     APPLICANT: Campbell, Kevin P.
CC     TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CC     NUMBER OF SEQUENCES: 8
CC     CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Brown, Martin, Haller & McClain
CC     STREET: 1660 Union Street
CC     CITY: San Diego
CC     STATE: CA
CC     COUNTRY: USA
CC     ZIP: 92101-2926
CC     COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Diskette
CC     COMPUTER: IBM Compatible
CC     OPERATING SYSTEM: DOS
CC     SOFTWARE: FastSEQ Version 1.5
CC     CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/336,257A
CC     FILING DATE: 07-NOV-1994
CC     CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC     NAME: Seidman, Stephanie L.
CC     REGISTRATION NUMBER: 33,779
CC     REFERENCE/DOCKET NUMBER: 54898
CC     TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (619) 238-0999
CC     TELEFAX: (619) 238-0062
CC     INFORMATION FOR SEQ ID NO: 3:
CC     SEQUENCE CHARACTERISTICS:
CC     LENGTH: 5975 base pairs
CC     TYPE: nucleic acid
CC     STRANDEDNESS: not relevant
CC     TOPOLOGY: not relevant
CC     MOLECULE TYPE: Genomic DNA
CC     FEATURE:
CC     NAME/KEY: Coding Sequence
CC     LOCATION: 79..5700
CC     OTHER INFORMATION: \product= "Alpha-1 subunit of animal calcium
CC     OTHER INFORMATION: channel"
SQ     SEQUENCE 5975 BP; 1291 A; 1832 C; 1694 G; 1158 T; 0 OTHER.

Query Match       0.6%;   Score 37;  DB 1;  Length 5975;
Best Local Similarity 65.0%;   Pred. No. 4.54e-08;
Matches   80;  Conservative    0;  Mismatches  43;  Indels   0;  Gaps   0;

Db   3814 CTGCTGAGTCGGGCGGCCGAGGGCGTGCCACCCGCTGTGGACGTTCATCAAGTCCTTCCAG 3873
          ||| ||| ||||  || |||||||||| ||||||| |||| |||| ||| |||||||| ||
Qy   5247 CTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGGACTGCTTCGCCGTCGGCTGCCGCGG 5306

Db   3874 GCCCTGCCCTACGTGGCCCTGCTCATCGTCGTTCTTCATCTACCGCCGTCATCGGC 3933
          |||||| ||| | ||| | ||| |||| ||  |||| |||||| | | |||||| |
Qy   5307 GCCCTGTTCAACATCTGCCTGCTGCTGTTCCTGGTCATGTCATCTTTGCCATTTCGGC 5366

Db   3934 ATG 3936
          |||
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Wed Jul  8 10:16:59 1998

Qy  5367 ATG 5369

RESULT  14
ID   US-08-435-675B-1 STANDARD; DNA; UNC; 5975 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/08435675B
CC   Sequence 1, Application US/08435675B
CC   Patent No. 5710250
CC   GENERAL INFORMATION:
CC     APPLICANT: Ellis, Steven Bradley
CC     APPLICANT: Williams, Mark E.
CC     APPLICANT: Harpold, Michael Miller
CC     APPLICANT: Schwartz, Arnold
CC     APPLICANT: Brenner, Robert
CC     TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CC     NUMBER OF SEQUENCES: 6
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Brown, Martin, Haller & McClain
CC       STREET: 1660 Union Street
CC       CITY: San Diego
CC       STATE: CA
CC       COUNTRY: USA
CC       ZIP: 92101-2926
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Diskette
CC       COMPUTER: IBM Compatible
CC       OPERATING SYSTEM: DOS
CC       SOFTWARE: FastSEQ Version 1.5
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/435,675B
CC       FILING DATE: 05-MAY-1995
CC       CLASSIFICATION: 435
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 08/314,083
CC       FILING DATE: 28-SEP-1994
CC       APPLICATION NUMBER: US 07/914,231
CC       FILING DATE: 13-JUL-1992
CC       APPLICATION NUMBER: US 07/603,751
CC       FILING DATE: 08-NOV-1990
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Seidman, Stephanie L
CC       REGISTRATION NUMBER: 33,779
CC       REFERENCE/DOCKET NUMBER: 6362-53193
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: 619-238-0999
CC       TELEFAX: 619-238-0062
CC       TELEX:
CC     INFORMATION FOR SEQ ID NO: 1:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH: 5975 base pairs
CC         TYPE: nucleic acid
CC         STRANDEDNESS: single
CC         TOPOLOGY: linear
CC       MOLECULE TYPE: cDNA
CC       FEATURE:
CC         NAME/KEY: Coding Sequence
CC         LOCATION: 79...5700
CC       OTHER INFORMATION:
SQ   SEQUENCE 5975 BP; 1291 A; 1832 C; 1695 G; 1157 T; 0 OTHER.

Query Match          0.6%;   Score 37;  DB 1;  Length 5975;
Best Local Similarity 65.0%;  Pred. No. 4.54e-08;
Matches   80;  Conservative   0;  Mismatches 43;  Indels   0;  Gaps   0;

Db  3814 CTGCTGAGTCGGGCCGAGGGCGTGCGCACGCTGCTGGACGTTCATCAAGTCCTTCCAG 3873
          ||| |||   | |||| ||||| |||||| ||  ||| | || |||||||||| ||||
Qy  5247 CTGGTGAAGGGAGCCAAGGGCATTCGGACACTGTCTTCATCATCACGCCGTCATCGGC 5306

Db  3874 GCCCTGCCCTACGTGGCCCTGCTCATCGTCATCGTTCTTCATCTACGCCGGTCATCGGC 3933
          |||  |||||| ||  ||||| || | ||||||| | ||| |||| |  |  || ||||
Qy  5307 GCCCTGTTCAACATCTGCCCGCTGCTGTTCCTGGTCATGTTCATCTTTGCCATTTTCGGC 5366

RESULT  15
ID   US-08-404-354B-1 STANDARD; DNA; UNC; 5975 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/08404354B
CC   Sequence 1, Application US/08404354B
CC   Patent No. 5618720
CC   GENERAL INFORMATION:
CC     APPLICANT: Ellis, Steven Bradley
CC     APPLICANT: Williams, Mark E.
CC     APPLICANT: Harpold, Michael Miller
CC     APPLICANT: Schwartz, Arnold
CC     APPLICANT: Brenner, Robert
CC     TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
CC     NUMBER OF SEQUENCES: 3
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Brown, Martin, Haller & McClain
CC       STREET: 1660 Union Street
CC       CITY: San Diego
CC       STATE: CA
CC       COUNTRY: USA
CC       ZIP: 92101-2926
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Diskette
CC       COMPUTER: IBM Compatible
CC       OPERATING SYSTEM: DOS
CC       SOFTWARE: FastSEQ Version 1.5
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/404,354B
CC       FILING DATE: 15-FEB-1995
CC       CLASSIFICATION: 435
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 08/314,083
CC       FILING DATE: 28-SEP-1994
CC       APPLICATION NUMBER: US 07/914,231
CC       FILING DATE: 13-JUL-1992
CC       APPLICATION NUMBER: US 07/603,751
CC       FILING DATE: 08-NOV-1990
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Seidman, Stephanie L
CC       REGISTRATION NUMBER: 33,779
CC       REFERENCE/DOCKET NUMBER: 6362-53192
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: 619-238-0999
CC       TELEFAX: 619-238-0062
CC       TELEX:
CC     INFORMATION FOR SEQ ID NO: 1:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH: 5975 base pairs
CC         TYPE: nucleic acid
CC         STRANDEDNESS: single
CC         TOPOLOGY: linear
CC       MOLECULE TYPE: cDNA
CC       FEATURE:
CC         NAME/KEY: Coding Sequence
CC         LOCATION: 79...5700
CC       OTHER INFORMATION:
SQ   SEQUENCE 5975 BP; 1291 A; 1832 C; 1695 G; 1157 T; 0 OTHER.

Query Match          0.6%;   Score 37;  DB 1;  Length 5975;
Best Local Similarity 65.0%;  Pred. No. 4.54e-08;
Matches   80;  Conservative   0;  Mismatches 43;  Indels   0;  Gaps   0;

Db  3814 CTGCTGAGTCGGGCCGAGGGCGTGCGCACGCTGCTGGACGTTCATCAAGTCCTTCCAG 3873
          ||| |||   | |||| ||||| |||||| ||  ||| | || |||||||||| ||||
Qy  5247 CTGGTGAAGGGAGCCAAGGGCATTCGGACACTGTCTTCATCATCACGCCGTCATCGGC 5306

Db  3874 GCCCTGCCCTACGTGGCCCTGCTCATCGTCATCGTTCTTCATCTACGCCGGTCATCGGC 3933
          |||  |||||| ||  ||||| || | ||||||| | ||| |||| |  |  || ||||
Qy  5247 CTGGTGAAGGGAGCCAAGGGCATTCGGACACTGTCTTCATCATCACGCCGTCATCGGC

Db  3934 ATG 3936
          |||
Qy  5367 ATG 5369

US-08-554-424-7.rni

:59 1998

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CCTACGTGGCCCTGCTCATCGTCATGCGTCGTTCTTCATCTACGCCGTCATCGGC 3933
  | || |  ||||||| | | ||| ||| |  | |||||||  ||| | |||||
GTTCAACATCTGCCTGCGTGTTCCTGGTCATGTTCATCTTTGCCATTTTCGGC 5366
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G 3936
|||
ATG 5369
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ch completed: Wed Jul  8 01:50:54 1998
time : 708 secs.

Wed Jul 8 10:16

Db 3874 GCCCTGC
Qy 5307 GCCC
Db 3934 A
Qy 536

Sea
Jo

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 __   __  ___   __   ___   __  _  _
|   \ |   |   | |  \ |   | |  \ | |
|   | |   |   | |   ||   | |   ||_|
|   | |   |   | |   ||   | |   |
|   / |   |   | |  / |   | |  /     (TM)
|__/  |__ |___| |_   |___ |_
```

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********************************************************
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                    Distribution rights by Oxford Molecular Ltd
********************************************************

MPsrch_nn   n.a.  -  n.a. database search, using Smith-Waterman algorithm

Run on:        Wed Jul  8 01:51:13 1998;  MasPar time 4842.76 Seconds
                                          1208.554 Million cell updates/sec

Tabular output not generated.

Title:        >US-08-554-424-7
Description:  (1-6513) from US08554424.seq
Perfect Score: 6513
N.A. Sequence:   1 TCTAGACGTTGGCCGCATAG.........ACGGGAGTATTAGTCTGA 6513
Comp:              AGATCTGCAACCGGCGTATC.........TGCGCTCATAATCGAGATCT

Scoring table:  TABLE default
                Gap 6

Nmatch  STD :  Dbase 0:  Query 0

Searched:     1384628 seqs, 449312139 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:     n-pending
              1:P9  2:U6000  3:U6001  4:U6002  5:U6003  6:U6004  7:U6005
              8:U6006  9:U6007 10:U6008 11:U07 12:U80 13:U81 14:U82
             15:U83 16:U84A 17:U84B 18:U85 19:U86 20:U87 21:U88
             22:U89 23:U90A 24:U90B 25:U91 26:NEWU8

Statistics:   Mean 11.817;  Variance 4.148;  scale 2.848

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
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| Result No. | Score | % Query Match | Score | Length | DB | ID | | Description | | Pred. No. |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 6513 | 100.0 | | 6513 | 18 | US-08-554- | Sequence 7, Applicatio | | | 0.00e+00 |
| 2 | 5500 | 84.4 | | 6519 | 21 | US-08-808- | Sequence 24, Applicati | | | 0.00e+00 |
| 3 | 4374 | 67.2 | | 5461 | 11 | US-07-998- | Sequence 7, Applicatio | | | 0.00e+00 |
| 4 | 4374 | 67.2 | | 5461 | 11 | US-07-998- | Sequence 7, Applicatio | | | 0.00e+00 |
| 5 | 3676 | 56.4 | | 6318 | 1 | PCT-US97-2 | Sequence 1, Applicatio | | | 0.00e+00 |
| 6 | 3676 | 56.4 | | 6318 | 21 | US-08-808- | Sequence 1, Applicatio | | | 0.00e+00 |
| 7 | 3664 | 56.3 | | 6315 | 1 | PCT-US97-2 | Sequence 2, Applicatio | | | 0.00e+00 |
| 8 | 3664 | 56.3 | | 6315 | 21 | US-08-808- | Sequence 2, Applicatio | | | 0.00e+00 |
| 9 | 3662 | 56.2 | | 6318 | 19 | US-08-608- | Sequence 2, Applicatio | | | 0.00e+00 |
| 10 | 3660 | 56.2 | | 6318 | 19 | US-08-608- | Sequence 26, Applicati | | | 0.00e+00 |
| 11 | 472 | 7.2 | | 1237 | 21 | US-08-808- | Sequence 1, Applicatio | | | 0.00e+00 |
| 12 | 356 | 5.5 | | 5977 | 23 | US-09-024- | Sequence 1, Applicatio | | | 0.00e+00 |
| 13 | 356 | 5.5 | | 6007 | 23 | US-09-024- | Sequence 2, Applicatio | | | 0.00e+00 |
| 14 | 356 | 5.5 | | 6556 | 23 | US-09-024- | Sequence 7, Applicatio | | | 0.00e+00 |
| 15 | 354 | 5.4 | | 6826 | 23 | US-09-024- | Sequence 8, Applicatio | | | 0.00e+00 |
| 16 | 320 | 4.9 | | 6048 | 19 | US-08-682- | Sequence 9, Applicatio | | | 0.00e+00 |
| 17 | 316 | 4.9 | | 6452 | 21 | US-08-836- | Sequence 9, Applicatio | | | 0.00e+00 |
| 18 | 312 | 4.8 | | 3033 | 15 | US-08-334- | Sequence 1, Applicatio | | | 0.00e+00 |
| 19 | 312 | 4.8 | | 3033 | 21 | US-08-836- | Sequence 1, Applicatio | | | 0.00e+00 |
| 20 | 308 | 4.7 | | 6371 | 21 | US-08-836- | Sequence 13, Applicatio | | | 0.00e+00 |
| 21 | 308 | 4.7 | | 6404 | 21 | US-08-836- | Sequence 14, Applicati | | | 0.00e+00 |
| 22 | 298 | 4.6 | | 6344 | 18 | US-08-511- | Sequence 1, Applicatio | | | 0.00e+00 |
| 23 | 298 | 4.6 | | 6344 | 21 | US-08-843- | Sequence 1, Applicatio | | | 0.00e+00 |
| 24 | 296 | 4.5 | | 6524 | 20 | US-08-775- | Sequence 1, Applicatio | | | 2.65e-301 |
| 25 | 296 | 4.5 | | 6524 | 19 | US-08-669- | Sequence 1, Applicatio | | | 2.65e-301 |
| 26 | 296 | 4.5 | | 6527 | 20 | US-08-775- | Sequence 7, Applicatio | | | 2.65e-301 |
| 27 | 296 | 4.5 | | 6527 | 19 | US-08-669- | Sequence 7, Applicatio | | | 2.65e-301 |
| 28 | 296 | 4.5 | | 7052 | 20 | US-08-775- | Sequence 5, Applicatio | | | 2.65e-301 |
| 29 | 296 | 4.5 | | 7052 | 19 | US-08-669- | Sequence 5, Applicatio | | | 2.65e-301 |
| 30 | 254 | 3.9 | | 5874 | 21 | US-08-843- | Sequence 9, Applicatio | | | 1.63e-251 |
| 31 | 231 | 3.5 | | 2573 | 19 | US-08-669- | Sequence 3, Applicatio | | | 2.09e-224 |
| 32 | 231 | 3.5 | | 2573 | 19 | US-08-669- | Sequence 3, Applicatio | | | 2.09e-224 |
| 33 | 214 | 3.3 | | 930 | 19 | US-08-605- | Sequence 2, Applicatio | | | 1.86e-204 |
| 34 | 204 | 3.1 | | 930 | 19 | US-08-605- | Sequence 21, Applicatio | | | 9.18e-193 |
| 35 | 194 | 3.0 | | 930 | 19 | US-08-605- | Sequence 1, Applicatio | | | 4.18e-181 |
| 36 | 192 | 2.9 | | 930 | 19 | US-08-605- | Sequence 1, Applicatio | | | 8.89e-179 |
| 37 | 177 | 2.7 | | 2279 | 11 | US-07-998- | Sequence 3, Applicatio | | | 2.26e-161 |
| 38 | 177 | 2.7 | | 2279 | 11 | US-07-998- | Sequence 3, Applicatio | | | 2.26e-161 |
| 39 | 171 | 2.6 | | 696 | 23 | US-09-024- | Sequence 5, Applicatio | | | 1.94e-154 |
| 40 | 148 | 2.3 | | 5482 | 15 | US-09-346- | Sequence 2, Applicatio | | | 4.97e-128 |
| 41 | 134 | 2.1 | | 702 | 18 | US-08-511- | Sequence 2, Applicatio | | | 4.07e-112 |
| 42 | 134 | 2.1 | | 702 | 21 | US-08-843- | Sequence 3, Applicatio | | | 4.07e-112 |
| 43 | 119 | 1.8 | | 5389 | 15 | US-08-346- | Sequence 3, Applicatio | | | 3.07e-95 |
| 44 | 110 | 1.7 | | 7218 | 17 | US-08-466- | Sequence 14, Applicati | | | 3.23e-85 |
| 45 | 103 | 1.6 | | 568 | 11 | US-07-998- | Sequence 10, Applicati | | | 1.74e-77 |

c

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                              ALIGNMENTS

RESULT 1
ID    US-08-554-424-7 STANDARD; DNA; UNC; 6513 BP.
AC    xxxxxx
DT
DE    Sequence 7, Application US/08554424
CC    Sequence 7, Application US/08554424
CC    GENERAL INFORMATION:
CC      APPLICANT:  Warmke, Jeffrey W.
CC      APPLICANT:  Van Der Ploeg, Leonardus
CC      TITLE OF INVENTION:  PROCESS FOR FUNCTIONAL EXPRESSION OF THE
CC      TITLE OF INVENTION:  PARA SODIUM CHANNEL
CC      NUMBER OF SEQUENCES:  7
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Jack L. Tribble
CC        STREET:  P.O. Box 2000, 126 E. Lincoln Avenue
CC        CITY:  Rahway
CC        STATE:  New Jersey
CC        COUNTRY:  USA
CC        ZIP:  07065-0907
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Floppy disk
CC        COMPUTER:  IBM PC compatible
CC        OPERATING SYSTEM:  PC-DOS/MS-DOS
CC        SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/554,424
CC        FILING DATE:
CC        CLASSIFICATION:  424
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Tribble, Jack L.
CC        REGISTRATION NUMBER:  32,633
CC        REFERENCE/DOCKET NUMBER:  19338DA
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (908) 594-5321
CC        TELEFAX:  (908) 594-4720
CC      INFORMATION FOR SEQ ID NO:  7:
CC        SEQUENCE CHARACTERISTICS:
CC        LENGTH:  6513 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
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CC   MOLECULE TYPE: cDNA
SQ   SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.

Query Match      100.0%; Score 6513; DB 18; Length 6513;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db        1 TCTAGACGTTGGCGCCGATAGACAATGACAGAGAATTCCGACTCGATATCTGAGGAGAAC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        1 TCTAGACGTTGGCGCCGATAGACAATGACAGAGAATTCCGACTCGATATCTGAGGAGAAC 60

Db       61 GCAGTTGTTCCGTCCCTTACCCGCCGGAATCATTGGTGCAAATCGAACAACGCCATTGCCG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       61 GCAGTTGTTCCGTCCCTTACCCGCCGGAATCATTGGTGCAAATCGAACAACGCCATTGCCG 120

Db      121 CTGAACATGAAAAGCAGAAGAGAGCTGGAAAGAAAGAGAGCCGGAGGAGGTGCCGCGAT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      121 CTGAACATGAAAAGCAGAAGAGAGCTGGAAAGAAAGAGAGCCGGAGGAGGTGCCGCGAT 180

Db      181 ATGGTCGCAAGAAACAAAAGACAAAGAAATCCGATATGAATGATGAGGACGAGGATGAAGGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      181 ATGGTCGCAAGAAACAAAAGACAAAGAAATCCGATATGAATGATGAGGACGAGGATGAAGGTC 240

Db      241 CACAACCGGATCCTACACTTGAACAGGTGTGCCAATACCTGTTCGATTGCAGGGGCAGCT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      241 CACAACCGGATCCTACACTTGAACAGGTGTGCCAATACCTGTTCGATTGCAGGGGCAGCT 300

Db      301 TCCCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      301 TCCCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 360

Db      361 TGACATTCGTAGTTGTGAAGCAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      361 TGACATTCGTAGTTGTGAAGCAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAA 420

Db      421 TGTGGATGCTCGATCCATTCAATCGAGGTGTCACTGAGGTGATATTCACCGGAATCTAGTGCATC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      421 TGTGGATGCTCGATCCATTCAATCGAGGTGTCACTGAGGTGATATTCACCGGAATCTAGTGCATC 480

Db      481 CATTATTTTCCCTATTCATCATCACCACAATTTCGCTTTTCGCTTTTCTGCATCCTGATGATAATGC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      481 CATTATTTTCCCTATTCATCATCACCACAATTTCGCTTTTCGCTTTTCTGCATCCTGATGATAATGC 540

Db      541 CGACAACGCCCACGGTTGAGTCGAGGTGAGTTCACCGGAATCTCAACTGACACATTTGAAT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      541 CGACAACGCCCACGGTTGAGTCGAGGTGAGTTCACCGGAATCTCAACTGACACATTTGAAT 600

Db      601 CAGCTGTTAAAGTGATGGCACGAGTTCATTTATGCCCGTTACGTATCTTAGAGATG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      601 CAGCTGTTAAAGTGATGGCACGAGTTCATTTATGCCCGTTACGTATCTTAGAGATG 660

Db      661 CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTATGTGACCATGGTATAGATT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      661 CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTATGTGACCATGGTATAGATT 720

Db      721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAACGCGTTAAAACCGTAGCCA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAACGCGTTAAAACCGTAGCCA 780

Db      781 TTGTGCCAGGCTTGAAGACCATCGTCGCGGCCGTTCGCGCGGAAGAATCTGCGCG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      781 TTGTGCCAGGCTTGAAGACCATCGTCGCGGCCGTTCGCGCGGAAGAATCTGCGCG 840

Db      841 ATGTGATTATCCTGACCATGTTCTCCCCTGTTCGCGTTCGCGTCGGTGATGGCCTTACAGATCT 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      841 ATGTGATTATCCTGACCATGTTCTCCCCTGTTCGCGTTCGCGTCGGTGATGGCCTTACAGATCT 900

Db      901 ATATGGGCGTGCTCACCGGAAGTGCATCAAGAAGTTCCGCCGCGGTTCCCGCGCTGGACGGTTCCCAATTGGTATTCCGAGG 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      901 ATATGGGCGTGCTCACCGGAAGTGCATCAAGAAGTTCCGCCGCGGTTCCCGCGCTGGACGGTTCCCAATTGGTATTCCGAGG 1020

Qy      961 ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATAGCTTCAATTGGTATTCCGAGG 1020

Db     1021 ACGAGGGCATCTCATTCCGTTATGCGGCAATATATCCGGTGCGGGCAATGCGACGACG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1021 ACGAGGGCATCTCATTCCGTTATGCGGCAATATATCCGGTGCGGGCAATGCGACGACG 1080

Db     1081 ATTACGTGTGCCTGCAGGGGTTGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1081 ATTACGTGTGCCTGCAGGGGTTGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140

Db     1141 CGTTCCGATGGGCTTTCCTGTCCGCTGCCTTCCGCTGATGACACAGGACTTCTGGAGGATC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1141 CGTTCCGATGGGCTTTCCTGTCCGCTGCCTTCCGCTGATGACACAGGACTTCTGGAGGATC 1200

Db     1201 TGTACCAGCTCGTGTTGCGCCGCCCGGACCATGGCACATGCGACACGTCTGTTCTTTATAGTCATCA 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1201 TGTACCAGCTCGTGTTGCGCCGCCCGGACCATGGCACATGCGACACGTCTGTTCTTTATAGTCATCA 1260

Db     1261 TCTTCCTAGGTTCATTCTATCTGTGAATTTGATTTTGGCCATTGTTGCCATGTCGTATG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1261 TCTTCCTAGGTTCATTCTATCTGTGAATTTGATTTTGGCCATTGTTGCCATGTCGTATG 1320

Db     1321 ACGAATTGCAAAGGAAGGCCGAAGAAGAGAAGGCTGCCGAGAGAGGAGCGGCGGCCAATGCGCAGGCTC 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1321 ACGAATTGCAAAGGAAGGCCGAAGAAGAGAAGGCTGCCGAGAGAGGAGCGGCGGCCAATGCGCAGGCTC 1380

Db     1381 CGGAAGAAGCTGCGCGCCCAAAGCGGCCAAGCGGGCCAATGCGGAGGAGCGGCGGCCAATGCGCAGGCTC 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1381 CGGAAGAAGCTGCGCGCCCAAAGCGGCCAAGCGGGCCAATGCGGAGGAGCGGCGGCCAATGCGCAGGCTC 1440

Db     1441 AGGCAGCAGCGGATGCGGCGTGCGCTGCCACTGCATCCGGAAATGGCCAAGA 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1441 AGGCAGCAGCGGATGCGGCGTGCGCTGCCACTGCATCCGGAAATGGCCAAGA 1500

Db     1501 GTCCGACGTATTCTTGCATCAGCTATGAGCTATTTGTTGGCGCGAGAGGGCAACGATG 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1501 GTCCGACGTATTCTTGCATCAGCTATGAGCTATTTGTTGGCGCGAGAGGGCAACGATG 1560

Db     1561 ACAACAACAAGACAACACCACCTTACCTGGAGTGCGTTAACATACCAGGGGATCACGTAGTT 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1561 ACAACAACAAGACAACACCACCTTACCTGGAGTGCGTTAACATACCAGGGGATCACGTAGTT 1620

Db     1621 TTATACAAAGACAACACCACCTTACCACGTCAACATACCAGGATGCCCATTGCCCTATGCCGACACT 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1621 TTATACAAAGACAACACCACCTTACCACGTCAACATACCAGGATGCCCATTGCCCTATGCCGACACT 1680

Db     1681 GCACGACATCCTTATCCTTACGTGTTCACCGTTAACATACCAGGGGATCACCAGGGGATCACTGTACTGTT 1740
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Qy     1681 GCACGACATCCTTATCCTTACGTGTTCACCGTTAACATACCAGGGGATCACCAGGGGATCACTGTACTGTT 1740

Db     1741 CTCACAAGTACGACGATACCTTGGTATACCGGTGTATCCGTAGCGATCGTA 1800
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Db     1801 AGCCATTGGTATTGTCAACATATCGCCGCACTTGCCCTATGCCCGTGTACTCGTA 1860
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Qy     1801 AGCCATTGGTATTGTCAACATATCGCCGCACTTGCCCTATGCCCGTGTACTCGTA 1860

Db     1861 CGAATGCCGTCACCCGATGTCCGAAGAATGGGCCATCATGTGCCCATCATATGCCCGTGTACTCGTATATG 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1861 CGAATGCCGTCACCCGATGTCCGAAGAATGGGCCATCATGTGCCCATCATATGCCCGTGTACTCGTATATG 1920

Db     1921 GCAATCTAGGCTCCGACACTCATCGTATACCTCGCAGTCCCGAATATCGTATACCT 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1921 GCAATCTAGGCTCCGACACTCATCGTATACCTCGCAGTCCCGAATATCGTATACCT 1980

Db     1981 CACATGCCGATCTACTCGGCGCATGGGCGCATCAGTGGCGTCAGCAGCAATAATCAGT 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1981 CACATGCCGATCTACTCGGCGCATGGGCGCATCAGTGGCGTCAGCAGCAATAATCAGT 2040

Db     2041 GCAAATGCGCAACCGCCCAACCGGCAACACACCGCAATCAATCAGTGGGCGCCACCA 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     2041 GCAAATGCGCAACCGCCCAACCGGCAACACACCGCAATCAATCAGTGGGCGCCACCA 2100
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Db  2101  CCTGTCTGGACACCAATCACAGAGCTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCA  2160
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Qy  2101  CCTGTCTGGACACCAATCACAGAGCTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCA  2160

Db  2161  CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC    2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161  CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC    2220

Db  2221  AAACGGTGGTTGATATGAAAGATGTGATGTCCTGAATGACATCATCGAACAGGGCCGCTG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221  AAACGGTGGTTGATATGAAAGATGTGATGTCCTGAATGACATCATCGAACAGGGCCGCTG  2280

Db  2281  GTCCGGACAGTGCGGGCAAGGCGGATCGCGGTGTCCGGTGTCCCGTTACTATTCCCAACAGAGGACG  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281  GTCCGGACAGTGCGGGCAAGGCGGATCGCGGTGTCCGGTGTCCCGTTACTATTCCCAACAGAGGACG  2340

Db  2341  ATGACGAGGATGGGCCACGTTCAAAGACAAGGCACTCGAAGTGATCCTCGAAAGGCATCG  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341  ATGACGAGGATGGGCCACGTTCAAAGACAAGGCACTCGAAGTGATCCTCGAAAGGCATCG  2400

Db  2401  ATGTGTTTTGTGTGGGACTGTGTGGTTGAATTTCAGGAGTGGGTATCGC  2460
          ||||||||||||||||||||||||||||||||||||||||||||
Qy  2401  ATGTGTTTGTGTGTGGGACTGTGTGGTTGAATTTCAGGAGTGGGTATCGC  2460

Db  2461  TCATCGTCTTCGATCCCTTCGTGCGAGCTCTGCAGCATCTGTGCATTGTGTGTCAACACGA  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461  TCATCGTCTTCGATCCCTTCGTGCGAGCTCTGCAGCATCTGTGCATTGTGTGTCAACACGA  2520

Db  2521  TGTTCATGGCAATGGACTCGAGGGTGTCCAGGGCTCGTGTCCGTATTGCGTTCCTTTCGAT  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521  TGTTCATGGCAATGGACTCGAGGGTGTCCAGGGCTCGTGTCCGTATTGCGTTCCTTTCGAT  2580

Db  2581  GCAACTATTTCTTCACCGCCACCTTTGCCACTCTTGGCCAAGCTAATGGCCATGA  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581  GCAACTATTTCTTCACCGCCACCTTTGCCACTCTTGGCCAAGCTAATGGCCATGA  2640

Db  2641  GCCCCAAGTACTATTTCCAGGAGGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2641  GCCCCAAGTACTATTTCCAGGAGGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT  2700

Db  2701  CGCTATTGGAACTGGACTCGAGGGTGTCCAGGGTCGTCCGTATTCCGTTCCTTTCGAT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701  CGCTATTGGAACTGGACTCGAGGGTGTCCAGGGTCGTCCGTATTCCGTTCCTTTCGAT  2760

Db  2761  TGCTGCCGTGATTCAAACTGTTGGGAATGCAACTGTTGGGAATTATCAATTTACTCATTTGCGATTA  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2761  TGCTGCCGTGATTCAAACTGTTGGGAATGCAACTGTTGGGAATTATCAATTTACTCATTTGCGATTA  2820

Db  2821  TGGGACGCACCACCATGGCGCTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821  TGGGACGCACCACCATGGCGCTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA  2880

Db  2881  TCTTTGGGTGATGGGAATGCAACTGTTGGGAATTATCATGATCACAAGGACCGCT  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881  TCTTTGGGTGATGGGAATGCAACTGTTGGGAATTATCATGATCACAAGGACCGCT  2940

Db  2941  TTCGGGCTGATTCAAACTGTTGGGAACTTCACCGACTTCATGATCACAGCTTCATGATCG  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941  TTCGGGCTGATTCAAACTGTTGGGAACTTCACCGACTTCATGATCACAGCTTCATGATCG  3000

Db  3001  TGTTCCCGGGTGCTCTGCGGGAGAATGCGGAGAGTGAGTTCGCATGTGGGTACGTGGGCG  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001  TGTTCCCGGGTGCTCTGCGGGAGAATGCGGAGAGTGAGTTCGCATGTGGGTACGTGGGCG  3060

Db  3061  ATGTCTGTGCATTCCCTTCTTCTTCTTGCGATATCGGCAATCTTGTGGGTACTTA  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061  ATGTCTGTGCATTCCCTTCTTCTTCTTGCGATATCGGCAATCTTGTGGGTACTTA  3120

Db  3121  ACCTTTTCTTCTTGCTTTTGTCCAATTTTGGCCTCATCGGCTTATCAGCGCCCGACTG   3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121  ACCTTTTCTTCTTGCTTTTGTCCAATTTTGGCCTCATCGGCTTATCAGCGCCCGACTG   3180
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Db  3181  CCGATAACGGATACGGATAAAAATAGCCGAGGCCTTCAATCGATGAATTGCCGATTAAAGGTT  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181  CCGATAACGGATACGGATAAAAATAGCCGAGGCCTTCAATCGATGAATTGCCGATTAAAGGTT  3240

Db  3241  GGGTTAAGCGTTAATATTGCTGATTGTTCAAGTTAATACGTAACAAATTGACAAATCAAA  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241  GGGTTAAGCGTTAATATTGCTGATTGTTCAAGTTAATACGTAACAAATTGACAAATCAAA  3300

Db  3301  TAAGTGATCAACCATCAGTGAGAGGACCAACCAGATCAGTTGGAGTTGGAGCGAAGAGC  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301  TAAGTGATCAACCATCAGTGAGAGGACCAACCAGATCAGTTGGAGTTGGAGCGAAGAGC  3360

Db  3361  ATGGTGACAACGAACTGGAGCTGGCCACGAGACGAGATCCTCGCCGACGCGCTCATCAAGA  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361  ATGGTGACAACGAACTGGAGCTGGCCACGAGACGAGATCCTCGCCGACGCGCTCATCAAGA  3420

Db  3421  AGGGGATCAAGGAGCAGAGCGCAACTGGAGTGTGGCCATCGGGGATCGGATGGAATTCACGA  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421  AGGGGATCAAGGAGCAGAGCGCAACTGGAGTGTGGCCATCGGGGATCGGATGGAATTCACGA  3480

Db  3481  TACACGGCGACATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA  3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481  TACACGGCGACATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA  3540

Db  3541  TGATTGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAACTAAACCATAGAG  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3541  TGATTGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAACTAAACCATAGAG  3600

Db  3601  GTTTGTCCTTACGGACGACGCCACTGCCAGCATTATTATTATTATGTGTAGCCATTAAGAATC  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601  TGATTGTCCTTACGGACGACGCCACTGCCAGCATTATTATTATTATGTGTAGCCATTAAGAATC  3660

Db  3661  GACCATTCAAGGACGAGAGCCACAGCCGCCACAAGGGCAGCGCCGAGACGATGGAGGGGAGGAAGC  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3661  GACCATTCAAGGACGAGAGCCACAGCCGCCACAAGGGCAGCGCCGAGACGATGGAGGGGAGGAAGC  3720

Db  3721  GCGACGCCAGCAAGGAGGATTAGGTCTGACGAGGAACTGACGAGGAGGCGAATGCG  3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3721  GCGACGCCAGCAAGGAGGATTAGGTCTGACGAGGAACTGACGAGGAGGCGAATGCG  3780

Db  3781  AGGAGGCCCCGCTCGACGCGTGATATCATTCATTATTCATGCATGATATACTCGATG  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3781  AGGAGGCCCCGCTCGACGCGTGATATCATTCATTATTCATGCATGATATACTCGATG  3840

Db  3841  AATATCCAGCTGCTGCCCGATTCGTACTATTGTACTACTCCGATCGTACTATAAGAAAATTCCGATCCTAGCCGGT  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3841  AATATCCAGCTGCTGCCCGATTCGTACTATTGTACTACTCCGATCGTACTATAAGAAAATTCCGATCCTAGCCGGTG  3900

Db  3901  ACGATGACTCGCCGTTCTGGCAAGGATGGGCCAATTTCTTCTTGGAAATTGTAATCAGCTGGTTGGCGCTCG  3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3901  ACGATGACTCGCCGTTCTGGCAAGGATGGGCCAATTTCTTCTTGGAAATTGTAATCAGCTGGTTGGCGCTCG  3960

Db  3961  TTGAAAATAAATATTTGAAACAGCTGTATCACTATGATTTTAATGAGTAGCTTAGCTT  4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3961  TTGAAAATAAATATTTGAAACAGCTGTATCACTATGATTTTAATGAGTAGCTTAGCTT  4020

Db  4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTACTGCAGGATATTTTATACTATA  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTACTGCAGGATATTTTATACTATA  4080

Db  4081  TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG  4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4081  TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG  4140

Db  4141  GCTTCAAAGTGACTTCCACCACGCGTGGCTCGATTTCGTGATTGTCATGGTAT  4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4141  GCTTCAAAGTGACTTCCACCACGCGTGGCTCGATTTCGTGATTGTCATGGTAT  4200

Db  4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGCGGTATTCAAGCCTTCAAGACTA  4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4201  CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGCGGTATTCAAGCCTTCAAGACTA  4260

Db  4261  TGCGAACGTTAAGAGCACTGAGACCACTACGTGCCATCTCCCGTATGCCAGGGCATGAGGG  4320
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Qy  4261 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261 TGGCGAACGTTAAGAGCACTGAGACCACTACGTGCCCATGTGCCATGTCCGTATGGGGCATGAGGG 4320

Qy  4321 TCGTCGTTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380
Db  4321 TCGTCGTTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380

Qy  4381 TAATATTTTGGCTAATTTTGCCATAATGGTGTACAGCTTTTGCTGAAAATATTTTA 4440
Db  4381 TAATATTTTGGCTAATTTTGCCATAATGGTGTACAGCTTTTGCTGAAAATATTTTA 4440

Qy  4441 AGTGCCGAGGACATGAATGGCACGAAGCTCAGCCACGACGAGATCATACCAAATCGCAATGCCT 4500
Db  4441 AGTGCCGAGGACATGAATGGCACGAAGCTCAGCCACGACGAGATCATACCAAATCGCAATGCCT 4500

Qy  4501 GCGAGAGCGAGAACTACACGTGGTGAATTCAGCAATTTCGATCATGTAGGTAACG 4560
Db  4501 GCGAGAGCGAGAACTACACGTGGTGAATTCAGCAATTTCGATCATGTAGGTAACG 4560

Qy  4561 CGTATCTGTGCCTTTTCCAAGTGGCCACCTTCAAAGGCTCAAATCATGAACGATG 4620
Db  4561 CGTATCTGTGCCTTTTCCAAGTGGCCACCTTCAAAGGCTCAAATCATGAACGATG 4620

Qy  4621 CTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACCATCACATCTACATGTATT 4680
Db  4621 CTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACCATCACATCTACATGTATT 4680

Qy  4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG 4740
Db  4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG 4740

Qy  4741 TTATCATTGATAATTTTAATGAGCAAAAGAAAAAAAGCAGGTGATGATCATTAGAAATGTTCA 4800
Db  4741 TTATCATTGATAATTTTAATGAGCAAAAGAAAAAAAGCAGGTGATGATCATTAGAAATGTTCA 4800

Qy  4801 TGACAGAAGATCAGAAAAGTACTATAATGCTATGTGGCGCACCAAGCAATAGTAGTAACCG 4860
Db  4801 TGACAGAAGATCAGAAAAGTACTATAATGCTATGTGGCGCACCAAGCAATAGTAGTAACCG 4860

Qy  4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTTAACCAT 4920
Db  4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTTAACCAT 4920

Qy  4921 ATAAGAAATTCGATATAATCATTATTGTTATTCATTGTGTCATTTTATCCATCTTAGGTCTTG 4980
Db  4921 ATAAGAAATTCGATATAATCATTATTGTTATTCATTGTGTCATTTTATCCATCTTAGGTCTTG 4980

Qy  4981 TCGATCGGTTACGATGCGTCGGACAGTACTTCGTGTCGCCGACCCTGCTGCCGAGTCGTGCGTG 5040
Db  4981 TCGATCGGTTACGATGCGTCGGACAGTACTTCGTGTCGCCGACCCTGCTGCCGAGTCGTGCGTG 5040

Qy  5041 TCGTAGTTATTTCAGTTCCGAATGTCTCATTAAAATATTCGCTTTACGATATCACTATT 5100
Db  5041 TCGTAGTTATTTCAGTTCCGAATGTCTCATTAAAATATTCGCTTTACGATATCACTATT 5100

Qy  5101 TTATTGAGCCATGGAATTTATTTGATGTAGTAGTTGTCATTTATCCATCTTAGGTCTTG 5160
Db  5101 TTATTGAGCCATGGAATTTATTTGATGTAGTAGTTGTCATTTATCCATCTTAGGTCTTG 5160

Qy  5161 TACTTAGCGAAAGTGGGCCGTGTTCGTCGTGCCGACCGCCGGCATTGCCAAGGGGCGTG 5220
Db  5161 TACTTAGCGAAAGTGGGCCGTGTTCGTCGTGCCGACCGCCGGCATTGCCAAGGGGCGTG 5220

Qy  5221 TGGCGAAAGTGGGCCGTGTTCGTCGTGCCGACCGCCGGCATTCAACATCTCGCTGCTTCCGG 5280
Db  5221 TGGCGAAAGTGGGCCGTGTTCGTCGTGCCGACCGCCGGCATTCAACATCTCGCTGCTTCCGG 5280

Qy  5281 TCTTCGCCATGTCGTCGTTCTTGCTCTTTCCTGG 5340
Db  5281 TCTTCGCCATGTCGTCGTTCTTGCTCTTTCCTGG 5340

Qy  5341 TCATGTTCATCTTTGCCATTTCGGCATGTCGTCTTCTTCATGCACGTCAGCATGATCCTGCTTCTTCAGA 5400
Db  5341 TCATGTTCATCTTTGCCATTTCGGCATGTCGTCTTCTTCATGCACGTCAGCATGATCCTGCTTCTTCAGA 5400

Qy  5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGCCGCCAGAGCAATGATCCTGCTTCTTCAGA 5460
Db  5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGCCGCCAGAGCAATGATCCTGCTTCTTCAGA 5460

Qy  5461 TGTCGACGTCAGCCGGTTGGGATGGTGTTACTGGACGCCATTATCAATGAGGAAGCATGCG 5520
Db  5461 TGTCGACGTCAGCCGGTTGGGATGGTGTTACTGGACGCCATTATCAATGAGGAAGCATGCG 5520

Qy  5521 ATCCACCCGACAGCGACAAAGGCTATCCGGCAATTGGTGTTCAGCGACCGTTGGAATAA 5580
Db  5521 ATCCACCCGACAGCGACAAAGGCTATCCGGCAATTGGTGTTCAGCGACCGTTGGAATAA 5580

Qy  5581 CGTTTCTCCCTCATACCTAGTTATTAAGCTTTTTGATAGTTATTAATATGTACATTGCTG 5640
Db  5581 CGTTTCTCCCTCATACCTAGTTATTAAGCTTTTTGATAGTTATTAATATGTACATTGCTG 5640

Qy  5641 TCATTCTCGAGAACTATAGTCAGGCACGTGCAAGACGTGCAAGAGGGTCTAACCGACGACG 5700
Db  5641 TCATTCTCGAGAACTATAGTCAGGCACGTGCAAGACGTGCAAGAGGGTCTAACCGACGACG 5700

Qy  5701 ACTACGACATGTACTATGAGATCTGGACAATTCGATCGGAGGCCCGCTGCAGTACACATAC 5760
Db  5701 ACTACGACATGTACTATGAGATCTGGACAATTCGATCGGAGGCCCGCTGCAGTACACATAC 5760

Qy  5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTGGAGCCCGCCGCTGCAGATCCCACAAAC 5820
Db  5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTGGAGCCCGCCGCTGCAGATCCCACAAAC 5820

Qy  5821 CGAACAAGTACAAGATCATATCGATGACTACACCCATCGTCGGCGTGACCTCATGTACT 5880
Db  5821 CGAACAAGTACAAGATCATATCGATGACTACACCCATCGTCGGCGTGACCTCATGTACT 5880

Qy  5881 GCGTCGACAATCCGACGCGTGAGATTGGTGAGATACGGCGCCCGCCGGAAGGGCAATCCGATAG 5940
Db  5881 GCGTCGACAATCCGACGCGTGAGATTGGTGAGATACGGCGCCCGCCGGAAGGGCAATCCGATAG 5940

Qy  5941 AGGAGACGGGTGAGATTGGTGAGATACGGCGCCCGCCGGAAGGGCAATCCGATACGGCCCCG 6000
Db  5941 AGGAGACGGGTGAGATTGGTGAGATACGGCGCCCGCCGGAAGGGCAATCCGATACGGCCCCG 6000

Qy  6001 TCTCATCAACGCTGTGCGTCAGCGTGAGGAGTACTGCGGCCCGGCTAATCCAGCACGCCCT 6060
Db  6001 TCTCATCAACGCTGTGCGTCAGCGTGAGGAGTACTGCGGCCCGGCTAATCCAGCACGCCCT 6060

Qy  6061 GGCGAAAGCCACAGGGCGCGCGAGGGCAGGGGAAGCACAGGGCGCGCGAGGGGATCATG 6120
Db  6061 GGCGAAAGCCACAGGGCGCGCGAGGGCAGGGGAAGCACAGGGCGCGCGAGGGGATCATG 6120

Qy  6121 GCGATGGCGGTGATCCGGGACGCCGGCGCCGGCGATGAAGCAACGACGACGGCGGATG 6180
Db  6121 GCGATGGCGGTGATCCGGGACGCCGGCGCCGGCGATGAAGCAACGACGACGGCGGATG 6180

Qy  6181 CGCCCGCTGGTGGTGAGTGGTGTTAACGGTGTTAACGGCGGCGCGAGCGAGCGCCGATGCCGATG 6240
Db  6181 CGCCCGCTGGTGGTGAGTGGTGTTAACGGTGTTAACGGCGGCGCGAGCGAGCGCCGATGCCGATG 6240

Qy  6241 AGAGTAATGTAAATAGTCCGGGATGCAGCGGCGGCGCCGGAGCAGCAGCAG 6300
Db  6241 AGAGTAATGTAAATAGTCCGGGATGCAGCGGCGGCGCCGGAGCAGCAGCAG 6300

Qy  6301 CGGCGGGTCTCGTCGTTGGAGAGCCACGACACGCGGGGAAGTCCCGGAGCCGGGGCGGGACAGA 6360
Db  6301 CGGCGGGTCTCGTCGTTGGAGAGCCACGACACGCGGGGAAGTCCCGGAGCCGGGGCGGGACAGA 6360

Qy  6361 CCGGCGGGTTCGTGACGGCGGACACGGTCTCAGCCGGACCCAAGGTTGGTCATCC 6420
Db  6361 CCGGCGGGTTCGTGACGGCGGACACGGTCTCAGCCGGACCCAAGGTTGGTCATCC 6420

Qy  6421 ACTCGGCGATCGCCGCGCGATCACGTGGAGCCGAGCATCACGTGGAGCCGAGCCTCGCCCCC 6480
Db  6421 ACTCGGCGATCGCCGCGCGATCACGTGGAGCCGAGCATCACGTGGAGCCGAGCCTCGCCCCC 6480

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Db  6481 CCCTCCAAGATGACGCGCGGAGTATTAGCTCTAGA 6513
          |||||||||||||||||||||||||||||||||||
Qy  6481 CCCTCCAAGATGACGCGCGGAGTATTAGCTCTAGA 6513

RESULT 2
ID   US-08-808-793-24 STANDARD; DNA; UNC; 6519 BP.
AC   xxxxxx
DT
DE   Sequence 24, Application US/08808793
CC   Sequence 24, Application US/08808793
CC   GENERAL INFORMATION:
CC      APPLICANT: Soderlund, David M.
CC      APPLICANT: Ingles, Patricia J.
CC      TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
CC      TITLE OF INVENTION: AND USE THEREOF
CC      NUMBER OF SEQUENCES: 32
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC         STREET: Clinton Square, P.O. Box 1051
CC         CITY: Rochester
CC         STATE: New York
CC         COUNTRY: USA
CC         ZIP: 14603
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE: Floppy disk
CC         COMPUTER: IBM PC compatible
CC         OPERATING SYSTEM: PC-DOS/MS-DOS
CC         SOFTWARE: PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER: US/08/808,793
CC         FILING DATE:
CC         CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: US 60/034,361
CC         FILING DATE: 24-DEC-1996
CC         CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: US 60/012,649
CC         FILING DATE: 01-MAR-1996
CC         CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC         NAME: Braman, Susan J.
CC         REGISTRATION NUMBER: 34,103
CC         REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
CC      TELECOMMUNICATION INFORMATION:
CC         TELEPHONE: 716-263-1636
CC         TELEFAX: 716-263-1600
CC   INFORMATION FOR SEQ ID NO: 24:
CC      SEQUENCE CHARACTERISTICS:
CC         LENGTH: 6519 base pairs
CC         TYPE: nucleic acid
CC         STRANDEDNESS: single
CC         TOPOLOGY: linear
CC      MOLECULE TYPE: cDNA
SQ   SEQUENCE 6519 BP; 1707 A; 1544 C; 1698 G; 1570 T; 0 OTHER.

Query Match            84.48%;  Score 5500;  DB 21;  Length 6519;
Best Local Similarity  97.7%;  Pred. No. 0.00e+00;
Matches 6337;  Conservative 0;  Mismatches 9;  Indels 138;  Gaps 3;

Db    1 ATGACAGAAGATTCCGACTCGATATCTGAGGAAGAACGCAGTTTGTTCCGTCCCTTACC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   24 ATGACAGAAGATTCCGACTCGATATCTGAGGAAGAACGCAGTTTGTTCCGTCCCTTACC 83

Db   61 CGGGAATCATTGGTGCAAATCGAACAACGCATTGCCGCTGAACATGAAAAGCAGAAGGAG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   84 CGGGAATCATTGGTGCAAATCGAACAACGCATTGCCGCTGAACATGAAAAGCAGAAGGAG 143

Db  121 CTGGAAAGAAAGAGAGCCGAGGGAGGAGGTGCCGCGATATGGTCGCAAGAAAAACAAAAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  144 CTGGAAAGAAAGAGAGCCGAGGGAGGAGGTGCCGCGATATGGTCGCAAGAAAAACAAAAA 203
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Db  181 GAAATCCGATATGATGATGACGAGGACGAGGATGAGGTCCACAACCGGATCCTACACTTGAA 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  204 GAAATCCGATATGATGATGACGAGGACGAGGATGAGGTCCACAACCGGATCCTACACTTGAA 263

Db  241 CAGGGTGTGCCAATACCTGTTCGATTCGAGGCAGCTTCCCGTCCGCCGGAATTGGCCTCCACT 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  264 CAGGGTGTGCCAATACCTGTTCGATTCGAGGCAGCTTCCCGTCCGCCGGAATTGGCCTCCACT 323

Db  301 CCTCTCGAGATATCGATCCTACTACAGCAATGTACTACAGCAATTCGTAGTTGTAAGCAAA 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  324 CCTCTCGAGATATCGATCCTACTACAGCAATGTACTACAGCAATTCGTAGTTGTAAGCAAA 383

Db  361 GGAAAAGATATTTTCGCTTTTCGCTTTTCTGCATCAAAAGCAATGTGGATGCTCGATCCATTCAAT 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  384 GGAAAAGATATTTTCGCTTTTCGCTTTTCTGCATCAAAAGCAATGTGGATGCTCGATCCATTCAAT 443

Db  421 CCGATACGTCGTGTGGCCATTACATTCTAGTGCATCATTATTTTCCCTATTCATCATCATC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  444 CCGATACGTCGTGTGGCCATTACATTCTAGTGCATCATTATTTTCCCTATTCATCATC 503

Db  481 ACCACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCCACGGTTGAGTCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  504 ACCACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCCACGGTTGAGTCC 563

Db  541 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  564 ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGA 623

Db  601 GGTTTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTA 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  624 GGTTTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTA 683

Db  661 GTAATAGCTTAGCTTATGTGACCATGGGTATAGATTTAGGTAATCTAGCAGCCCCTGCGA 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  684 GTAATAGCTTAGCTTATGTGACCATGGGTATAGATTTAGGTAATCTAGCAGCCCCTGCGA 743

Db  721 ACGTTTAGGGTGCTGCGAGCGCTTAAAACCGTAGCCATTGTGCCAGGCTTGAAGACCATC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  744 ACGTTTAGGGTGCTGCGAGCGCTTAAAACCGTAGCCATTGTGCCAGGCTTGAAGACCATC 803

Db  781 GTCGGGCGCGTCATCGAATCGGTGAAGAATCTGCCGCGATCGATTGATTATCCTGACCATGTTC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  804 GTCGGGCGCGTCATCGAATCGGTGAAGAATCTGCCGCGATCGATTGATTATCCTGACCATGTTC 863

Db  841 TCCCTGTGTTCGCGGTTGATGGGCCTACAGATCTATATGGGCGTGCTCACCGAGAAG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  864 TCCCTGTGTTCGCGGTTGATGGGCCTACAGATCTATATGGGCGTGCTCACCGAGAAG 923

Db  901 TGCATCAAGAAGTTCCCGTCCTGGACGGTTCCTGGGCAATCTGACCGGCAATCGGGGAC 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  924 TGCATCAAGAAGTTCCCGTCCTGGACGGTTCCTGGGCAATCTGACCGGCAATCGGGGAC 983

Db  961 TATCAAATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGGACGAGGACATCTCATTTCCGTTA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  984 TATCAAATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGGACGAGGACATCTCATTTCCGTTA 1043

Db 1021 TGCGGCAATATATCCGGTCGGGGGCAATGCGACGACGATTACGTGTGCCTGCAGGGGTTT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1044 TGCGGCAATATATCCGGTCGGGGGCAATGCGACGACGATTACGTGTGCCTGCAGGGGTTT 1103

Db 1081 GGTCCGGAATCCGAATTAGGCTACACCAGCTTCGATTCGTTCGGATGGGCCTTCCTGTCC 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1104 GGTCCGGAATCCGAATTAGGCTACACCAGCTTCGATTCGTTCGGATGGGCCTTCCTGTCC 1163

Db 1141 GCCTTCCGGTCTGATGACAGAGACTTCTGGGAGGATCTGTACCAGCTGGTGTTGCCGCGCC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1164 GCCTTCCGGTCTGATGACAGAGACTTCTGGGAGGATCTGTACCAGCTGGTGTTGCCGCGCC 1223

Db 1201 GCCGGACCATGGCACATGCTGTTCTTTTATAGTCATCATCTTCCTAGGTTCATTCATTCT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1224 GCCGGACCATGGCACATGCTGTTCTTTTATAGTCATCATCTTCCTAGGTTCATTCATTCT 1283
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Db  1261  GTGAATTGATTTGGCCATTGTGCCATGTCGTATGACGAATTGCAAAGGAAGGCCGAA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1284  GTGAATTGATTTGGCCATTGTGCCATGTCGTATGACGAATTGCAAAGGAAGGCCGAAA 1343

Db  1321  GAAGAGAGGCTGCCGAAGAGAGGCGATACGTGGGCGAAGCGGAAGAGCTGCCGCCCAAA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1344  GAAGAGAGGCTGCCGAAGAGAGGCGATACGTGGGCGAAGCGGAAGAGCTGCCGCCCAAA 1403

Db  1381  GCGGCCAAGTCGGAGGAGGCGGCCAATGCGCAGCAGCGGATGCGGCTGCC  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1404  GCGGCCAAGTCGGAGGAGGCGGCCAATGCGCAGCAGCGGATGCGGCTGCC  1463

Db  1441  GCCGGAGAGGCTGCGACTGCGATCCGACGAGTTCGGACGCTATTCTTCCATCAGC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1464  GCCGGAGAGGCTGCGACTGCGATCCGACGAGTTCGGACGCTATTCTTCCATCAGC  1523

Db  1501  TATGAGCTATTTGTTGGCGGCGAGAAGGCGCAACATGACAACAACAGAGAAGATGTCC  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1524  TATGAGCTATTTGTTGGCGGCGAGAAGGCGCAACATGACAACAACAGAGAAGATGTCC  1583

Db  1561  ATTCCGGAGCGTCGAGTCGAGTCGGATACCGTATACAAAGACAACCAGCACCT  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1584  ATTCCGGAGCGTCGAGTCGAGTCGGATACCGTATACAAAGACAACCAGCACCT  1643

Db  1621  ACCACAGCACCAAGTTCGTAAAGTGAGCACGACACATCCTATCCTTACCT  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1644  ACCACAGCACCAAGTTCGTAAAGTGAGCACGACACATCCTATCCTTACCT  1703

Db  1681  GGTTCACCGTTTAAACATACGCAGGGGATCACGTAGTTCTCACAAGTACGATACGGAAC  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1704  GGTTCACCGTTTAAACATACGCAGGGGATCACGTAGTTCTCACAAGTACGATACGGAAC  1763

Db  1741  GGACGTGCGGCCGCTTGGTATACCCGGTATCCGATCGTAAGGCCGATCGTCACAATAT  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1764  GGACGTGCGGCCGCTTGGTATACCCGGTATCCGATCGTAAGGCCGATCGTCACAATAT  1823

Db  1801  CAGGATGCCCAGCAGCACTTGCCCTATGCCGACGACTCGATGCCGTCACCCGATGTCC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1824  CAGGATGCCCAGCAGCACTTGCCCTATGCCGACGACTCGATGCCGTCACCCGATGTCC  1883

Db  1861  GAGAGAATGGGCGTCATGAGCCGTGTACTATGGCAATCTAGGCTCCCGACACTCA  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1884  GAGAGAATGGGCGTCATGAGCCGTGTACTATGGCAATCTAGGCTCCCGACACTCA  1943

Db  1921  TCGTATACCCGCCACAGTCGTATACGTATAACCTTCACATGGCCGATCTACTCGGCGGC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1944  TCGTATACCCGCCACAGTCGTATACGTATAACCTTCACATGGCCGATCTACTCGGCGGC  2003

Db  1981  ATGGCCGTCATGGGCGTCAGCAATGACCAAGGAGCAAATTGCGCAACCGCAACACA  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2004  ATGGCCGTCATGGGCGTCAGCAATGACCAAGGAGCAAATTGCGCAACCGCAACACA  2063

Db  2041  CGCAATCAATCAGTGGGCGGCCATCAATGGCGCCACCGTGTCTGGACCAATCACAAG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Qy  2064  CGCAATCAATCAGTGGGCGGCCATCAATGGCGCCACCGTCTGGACCAATCACAAG-  2123

Db  2101  CTCGATCATCGGACGTT--------  2160
          ||||||
Qy  2124  CTCGATCATCGGACGTT-------  2183

Db  2161  CATCATGACAAATCCTTTATCGCCTCAGATCGTTTCCCACAGAGGACGATACGGGCGATT  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2184  CATCATGACAAATCCTTTATCGCCTCAGATCGTTTCCCACAGAGGACGATACGGGCGATT  2243

Db  2221  GTGATGGTCCTGAATGACATCATCGAACAGATCATCGGGCAGTTGGGCAAGCCGAT  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2244  GTGATGGTCCTGAATGACATCATCGAACAGATCATCGGGCAGTTGGGCAAGCCGAT  2303

Db  2281  CGCGGGTG------  2316
          ||||||
Qy  2304  CGCGGGTGTCTCCGGTTACTATTTCCCACAGAGGACGATACGGGCGACGTTC  2363

Db  2317  AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGCGTTTTGTGTGGGGACTGT  2376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2364  AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTGTTTTGTGTGGGGACTGT  2423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2377  TGCTGGGTTTGGTTGAAATTTCGAGAGTGGGTATCGCTCATGCGTCTTCGATCCTTCGTC  2436

Qy  2424  TGCTGGGTTTGGTTGAAATTTCGAGAGTGGGTATCGCTCATCGTCTTCGATCCTTCGTC  2483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2437  GAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGATGTTCATGGCAATGGATCACCAC  2496

Qy  2484  GAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGATGTTCATGGCAATGGATCACCAC  2543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2497  GATATGAACAAGAGGATGGAACGCGTGCTCAAGAGTGGCAACTATTCTTCACCGCCACC  2556

Qy  2544  GATATGAACAAGAGGATGGAACGCGTGCTCAAGAGTGGCAACTATTCTTCACCGCCACC  2603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2557  TTTGCCATCGAGGCCACCATGAAGCTAATGGCCCAAGTACTATTCCAGGAG  2616

Qy  2604  TTTGCCATCGAGGCCACCATGAAGCTAATGGCCCAAGTACTATTCCAGGAG  2663
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2617  GGCTGGAACATCTTCGACTTCATTATTCGTGCGCTATCGCGTATTCAAAACTGCGCC  2676

Qy  2664  GGCTGGAACATCTTCGACTTCATTATTCGTGCGCTATCGCGTATTCAAAACTGCGAG  2723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2677  GGTGTCCAGGGTCTGTCCGTATTGCGTGCGTTCCTTTCGATTGCTGCTGTATTCAAAACTGGCC  2736

Qy  2724  GGTGTCCAGGGTCTGTCCGTATTGCGTGCGTTCCTTTCGATTGCTGCTGTATTCAAACTGCCC  2783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2737  AAGTCTTGGCCCACACTTAATTACTCATTCGATTATGGGACGCACCATGGGGCGCTTTG  2796

Qy  2784  AAGTCTTGGCCCACACTTAATTACTCATTCGATTATGGGACGCACCATGGGGCGCTTTG  2843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2797  GGTAATCTGACATTTGTACTTTGCCATTATCATCTTCATCTTTGCGGTGTGATGGGAATGCAA  2856

Qy  2844  GGTAATCTGACATTTGTACTTTGCCATTATCATCTTTCATCTTTGCGGTGTGATGGGAATGCAA  2903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2857  CTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGCGGACCTGCCGCGC  2916

Qy  2904  CTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGCGGACCTGCCGCGC  2963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2917  TGGAACTTCACCGACTTTATGCGACAGCTTCATGATCGTCGTTCGTGTTCTCGGGAGAA  2976

Qy  2964  TGGAACTTCACCGACTTTATGCGACAGCTTCATGATCGTCGTTCGTGTTCTCGGGAGAA  3023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2977  TGGATCGAGTCCATGTGGGACTGCATGCGACGTGGGCGATGTCTCGTGCAATCCCTTCTTC  3036

Qy  3024  TGGATCGAGTCCATGTGGGACTGCATGCGACGTGGGCGATGTCTCGTGCAATCCCTTCTTC  3083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3037  TTGGCCACCGTTGTCATCGGCAATCTTGTGGTACTTAACCTTTTCTTAGCCTTTGCTTTTG  3096

Qy  3084  TTGGCCACCGTTGTCATCGGCAATCTTGTGGTACTTAACCTTTTCTTAGCCTTTGCTTTTG  3143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3097  TCCAATTTTTGGCTCATCTAGCTTATCAGCGCGACTGGCCGATAACGATACGAATAAAATA  3156

Qy  3144  TCCAATTTTTGGCTCATCTAGCTTATCAGCGCGACTGGCCGATAACGATACGAATAAAATA  3203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3157  GCCGAGGCCTTCAATCGAATTGGGCCGATTTAAAAGTTGGGTTAAGCGTAATATTGCTGAT  3216

Qy  3204  GCCGAGGCCTTCAATCGAATTGGGCCGATTTAAAAGTTGGGTTAAGCGTAATATTGCTGAT  3263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3217  TGTTTCAAGTTAATACGTAACAAATTGACAAATCAAATAAGTGATCAACCATCAG-----  3271

Qy  3264  TGTTTCAAGTTAATACGTAACAAATTGACAAATCAAATAAGTGATCAACCATCAGGTGAG  3323
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3272  ----------------------------AGCAATGTGACAACGACTGGAGCTG  3297

Qy  3324  AGACCAACCACCAGTCAGTTGGATTTGGAGCGAAGACGACTGGAGCTG  3383
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  3298  GGCCACCAACGACGATCCTCGCCAAGCACCCATCAAGAGGGATCAAGGAGGAGCAGCGCAA  3357

Qy  3384  GGCCACCAACGACGATCCTCGCCAAGCACCCATCAAGAGGGATCAAGGAGGAGCAGCGCAA  3443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3358  CTGGAGTGGCCATCGGGGGATGGGGATGCGGAATTCAAAGGCACTCAAAGGCACTCGAAGTGAAGAACAAC  3417
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Qy  3444 CTGGAGGTGGCCATCGGGGATCGGATGAATTCACGGATACACGGCGACATGAAGAACAAC 3503
         
Db  3418 AAGCCGAAGAAATCCAAATATCTAAATACGCAACG---------                  3453
         |||||||||||||||||||||||||||||||||
Qy  3504 AAGCCGAAGAAATCCAAATATCTAAATACGCAACGATGATTGGCAACTCAATTAACCAC  3563

Db  3454 -------------------------------------GACGACGAC                3462
                                              |||||||||
Qy  3564 CAAGACAATAGACTGGAACACGACTAAACCATAGAGGTTGTCCTTACGGACGACGAC    3623

Db  3463 ACTGCCAGCATTAACTCATATGGTAGCCATTAAGAATCGACCATTCAAGGACGAGAGCCAC 3522
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3624 ACTGCCAGCATTAACTCATATGGTAGCCATTAAGAATCGACCATTCAAGGACGAGAGCCAC 3683

Db  3523 AAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGGCCGCACGGCCAGCAGGGATTA       3582
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3684 AAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGGCCGCACGGCCAGCAGGGATTA       3743

Db  3643 ATCATTATTCACTACGACGAGGATATACTCGATGAATATCCAGCTGATTGCTGCCCCC    3702
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3744 ATCATTATTCACTACGACGAGGATATACTCGATGAATATCCAGCTGATTGCTGCCCCC    3803

Db  3703 GATTCGTACTATAAGAAATTCCGATCTTAGCCGTGACGATGACTCGCCGTTCTGGCAA    3762
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3864 GATTCGTACTATAAGAAATTCCGATCTTAGCCGTGACGATGACTCGCCGTTCTGGCAA    3923

Db  3763 GGATGGGCGCAATTGTAATCAAGTTTTCGATTAAATTGAGGATAAATATTTGAAACA    3822
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3924 GGATGGGCGCAATTGTAATCAAGTTTTCGATTAAATTGAGGATAAATATTTGAAACA    3983

Db  3823 GCTGTTATCACTACGATGATTTAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTG 3882
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3984 GCTGTTATCACTACGATGATTTAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTG 4043

Db  3883 CCACAAAGACCCATCTGCAGGATATATTTTGCTGGAAAATATTTACGGTTATA       3942
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4044 CCACAAAGACCCATCTGCAGGATATATTTTGCTGGAAAATATTTACGGTTATA       4103

Db  3943 TTCTTCTTGGAAATGTTAATCAAGTTGGTCGCCTCGGCTTCAAAGTGTACTTGACCAAC   4002
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4104 TTCTTCTTGGAAATGTTAATCAAGTTGGTCGCCTCGGCTTCAAAGTGTACTTCACCAAC   4163

Db  4003 GCGTGGTGTTGGCTCGATTCGTCATGTGTCTATTGGTGTCTATAATATTTGGCTAATTTTTGCC 4062
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4164 GCGTGGTGTTGGCTCGATTCGTCATGTGTCTATTGGTGTCTATAATATTTGGCTAATTTTTGCC 4223

Db  4063 CTTGTTGGAGCTGGTTATTCAAGCCTTCAAGACTATGCGAACGTTAAGAGCACTGAGA   4122
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4224 CTTGTTGGAGCTGGTTATTCAAGCCTTCAAGACTATGCGAACGTTAAGAGCACTGAGA   4283

Db  4123 CCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGGTCGTCGTTAATGCGCTGGTACAA 4182
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4284 CCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGGTCGTCGTTAATGCGCTGGTACAA 4343

Db  4183 GCTATACCGTCCATCTTCAATGTGCTATTGGTGTCTATAATTGGTCTAATATTTGGCTAATTTTTGCC 4242
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4344 GCTATACCGTCCATCTTCAATGTGCTATTGGTGTCTATAATTGGTCTAATATTTGGCTAATTTTTGCC 4403

Db  4243 ATAATGGGTGTACAGCTTTTGCTGGAAAATATTTAAGTGCGAGGACATGAATGGCACG    4302
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4404 ATAATGGGTGTACAGCTTTTGCTGGAAAATATTTAAGTGCGAGGACATGAATGGCACG    4463

Db  4303 AAGCTTCAGCCACGAGATCATACCACCAATCGCAATCGCAATCGGCAGAGCTCAACGTG   4362
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4464 AAGCTTCAGCCACGAGATCATACCACCAATCGCAATCGCAATCGGCAGAGCTCAACGTG   4523

Db  4363 GTGAATTCAGCAATGAATGAATTTCGATCATGTAGGTAACGCGTATCTGTGCCTTTTCCAAGTG 4422
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4524 GTGAATTCAGCAATGAATGAATTTCGATCATGTAGGTAACGCGTATCTGTGCCTTTTCCAAGTG 4583
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Db  4423 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATCGATTCACGAGAGGTGGAC 4482
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Qy  4584 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATCGATTCACGAGAGGTGGAC 4643

Db  4483 AAGCAACCAATTCGTGAAACGAACATCTACACGTTATTATATTCGTATTCTTCATCATA 4542
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4644 AAGCAACCAATTCGTGAAACGAACATCTACACGTTATTATATTCGTATTCTTCATCATA 4703

Db  4543 TTTGGATCATTTTCACACTCAATCTGTTCATTGTGTTATCATTGATAATTTTAATGAG 4602
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4704 TTTGGATCCTTTTCACACTCAATCTGTTCATTGTGTTATCATTGATAATTTTAATGAG 4763

Db  4603 CAAAAGAAAAAAGCAGGTGGATCATTAGAAAATGTTCATGACAGAGATCAGAAAAAGTAC 4662
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Qy  4764 CAAAAGAAAAAAGCAGGTGGATCATTAGAAAATGTTCATGACAGAGATCAGAAAAAGTAC 4823

Db  4663 TATAGTGCTATGAAAAAGATGGGCTCTAAAAAAACCATTAAAAAGCCATTCCAAGACCAAGG 4722
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Qy  4824 TATAATGCTATGAAAAAGATGGGCTCTAAAAAAACCATTAAAAAGCCATTCCAAGACCAAGG 4883

Db  4723 TGGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATT 4782
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4884 TGGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATT 4943

Db  4783 ATGTTATTCATTGGTCGTCGAACATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGAC 4842
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4944 ATGTTATTCATTGGTCGTCGAACATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGAC 5003

Db  4843 ACGTATAACGCGGTCCTAGACTATCTCAATGCGATATCGTAGTTATTTTCAGTTCCGAA 4902
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5004 ACGTATAACGCGGTCCTAGACTATCTCAATGCGATATCGTAGTTATTTTCAGTTCCGAA 5063

Db  4903 TGTCTATTAAAAATATTCGCTTACGATATCACTATTTTATTGAGCCATGGAATTTATTT 4962
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5064 TGTCTATTAAAAATATTCGCTTACGATATCACTATTTTATTGAGCCATGGAATTTATTT 5123

Db  4963 GATGTAGTAGTTGTCATTTATCCATCTTAGGTCTTAGCTAGCGATATTATCGAGAAG 5022
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5124 GATGTAGTAGTTGTCATTTATCCATCTTAGGTCTTAGCTAGCGATATTATCGAGAAG 5183

Db  5023 TACTTCGTGTCGCCACCCTGCTGCGTGTGGCGAAAGTGGGCCGTGTCCTTT 5082
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5184 TACTTCGTGTCGCCACCCTGCTGCGTGTGGCGAAAGTGGGCCGTGTCCTT 5243

Db  5083 CGACTGGTGAAGGAGCCAAGGGCATTCCTGCTGCTCTTCGCGTGTGGCCATGTCGCTG 5142
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5244 CGACTGGTGAAGGAGCCAAGGGCATTCCTGCTGCTCTTCGCGTGTGGCCATGTCGCTG 5303

Db  5143 CCGGCCCTGTTCAACATGCCTGCTGCGTGTTCCTGGTCATGTCATCTTGCCATTTTC 5202
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5304 CCGGCCCTGTTCAACATGCCTGCTGCGTGTTCCTGGTCATGTCATCTTGCCATTTTC 5363

Db  5203 GGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCGGCATTAACGACGTCTACAACTTC 5262
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Qy  5364 GGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCGGCATTAACGACGTCTACAACTTC 5423

Db  5263 AAGACCTTTGGCCAGAGCATGATCCTGCTCTTCAGATGTCGACGTCAGCCGGTTGGGAT 5322
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5424 AAGACCTTTGGCCAGAGCATGATCCTGCTCTTCAGATGTCGACGTCAGCCGGTTGGGAT 5483

Db  5323 GGTGTACTGGACGCGACCATTATCAATGACGCGATCCGAACGACAACGACAAAGGC 5382
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5484 GGTGTACTGGACGCGACCATTATCAATGACGCGATCCGAACGACAACGACAAAGGC 5543

Db  5383 TATCCGGGCAATTGGTTCAGCGACCGTTGGAATAACGTTCTCCTCTCATACCTAGTT 5442
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5544 TATCCGGGCAATTGGTTCAGCGACCGTTGGAATAACGTTCTCCTCTCATACCTAGTT 5603

Db  5443 ATAAGCTTTTGATAGTATTATTAAATATGCTGTCATTCTCGAGAACTATAGTCAG 5502
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Qy  5604 ATAAGCTTTTGATAGTATTATTAAATATGCTGTCATTCTCGAGAACTATAGTCAG 5663
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CC    NUMBER OF SEQUENCES: 40
CC    CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Darby & Darby PC
CC       STREET: 805 Third Avenue
CC       CITY: New York
CC       STATE: New York
CC       COUNTRY: US
CC       ZIP: 10022
CC    COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, Version #1.30
CC    CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/07/998,289B
CC       FILING DATE: 30-DEC-1992
CC       CLASSIFICATION: 435
CC    ATTORNEY/AGENT INFORMATION:
CC       NAME: Robinson, Joseph R
CC       REGISTRATION NUMBER: 33,448
CC       REFERENCE/DOCKET NUMBER: 0646/0A939
CC    TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: 212-527-7700
CC       TELEFAX: 212-753-6237
CC       TELEX: 236687
CC    INFORMATION FOR SEQ ID NO: 7:
CC       SEQUENCE CHARACTERISTICS:
CC          LENGTH: 5461 base pairs
CC          TYPE: nucleic acid
CC          STRANDEDNESS: single
CC          TOPOLOGY: linear
CC       MOLECULE TYPE: DNA (genomic)
SQ    SEQUENCE 5461 BP; 1425 A; 1259 C; 1374 G; 1403 T; 0 OTHER.

Query Match             67.2%;  Score 4374;  DB 11;  Length 5461;
Best Local Similarity   96.7%;  Pred. No. 0.00e+00;
Matches  5445;  Conservative    0;  Mismatches    9;  Indels  177;  Gaps  3;
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Db     1 ATGACAGAAGATTCCGACTCGATATCTGAGGAAGAACGCAGTTTGTTCCGTCCCTTTACC  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    24 ATGACAGAAGATTCCGACTCGATATCTGAGGAAGAACGCAGTTTGTTCCGTCCCTTTACC  83

Db    61 CGGGAATCATTGGTGCAAATCGAACAACCATTCGCGCTGAAACATGAAAAGCAGAAGGAG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    84 CGCGAATCATTGGTGCAAATCGAACAACCATTCGCGCTGAAACATGAAAAGCAGAAGGAG 143

Db   121 CTGGAAAGAAAGAGAGCCGAGGGAGGAGGTGCCGCGATGGTCGCCAAGAAAAAACAAAAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   144 CTGGAAAGAAAGAGAGCCGAGGGAGGAGGTGCCGCGATGGTCGCCAAGAAAAAACAAAAA 203

Db   181 GAAATCCGATATGACGAGGACGAGGATGAAGGTCCAAACCGGATCCTACACTTGAA 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   204 GAAATCCGATATGACGAGGACGAGGATGAAGGTCCAAACCGGATCCTACACTTGAA 263

Db   241 CAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCTTCCGCGGAATTGGCCTCCACT 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   264 CAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCTTCCGCGGAATTGGCCTCCACT 323

Db   301 CCTCTCCGAGGATATCGATCCCTACACAGCAATGCAATTCGTAGTTGTAAGCAAA 360
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Qy   324 CCTCTCCGAGGATATCGATCCCTACACAGCAATGCAATTCGTAGTTGTAAGCAAA 383

Db   361 GGAAAAGATATTTTCGCTTTCGCTCATCAAAAAGCAATGTGGATGCTCGATCATCAAT 420
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Qy   384 GGAAAAGATATTTTCGCTTTCGCTCATCAAAAAGCAATGTGGATGCTCGATCATCAAT 443

Db   421 CCGATACGTCGTGTGGCCATTTACATTCTAGTGCATCCATTATTTCCCTATTCATCATC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   444 CCGATACGTCGTGTGGCCATTTACATTCTAGTGCATCCATTATTTCCCTATTCATCATC 503

Db   481 ACCACAATTCTCGTCAACTGACATCCTGATGATAATGCCGACAACGGCCCACGTTGAGTCC 540
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Qy   504 ACCACAATTCTCGTCAACTGACATCCTGATGATAATGCCGACAACGGCCCACGTTGAGTCC 563
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Db  5503 GCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACACATGTACTACGACATC 5562
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Qy  5664 GCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACACATGTACTACGACATC 5723

Db  5563 TGGCAGCAATTCGATCCGAGGGCACCCAGTACATAGCTATGATCAGCTGTCCGAATTC 5622
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Qy  5724 TGGCAGCAATTCGATCCGAGGGCACCCAGTACATAGCTATGATCAGCTGTCCGAATTC 5783

Db  5623 CTGACGTACTGGAGCCCCGCTGCAGATCCACAAACCGAACAAGTACAAGATCATATCG 5682
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5784 CTGACGTACTGGAGCCCCGCTGCAGATCCACAAACCGAACAAGTACAAGATCATATCG 5843

Db  5683 ATGGACATACCCATCTGCGGTGACCTGTACTGCGTCGACCATCCTCGACGCCCTT 5742
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Qy  5844 ATGGACATACCCATCTGCGGTGACCTGTACTGCGTCGACCATCCTCGACGCCCTT 5903

Db  5743 ACGAAAGACTTCTTTGCCGCCCGCCCCGATAGAGGAGGCAATCCGATAGAGGAGACGGT 5802
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5904 ACGAAAGACTTCTTTGCCGCCCGCCCCGATAGAGGAGGCAATCCGATAGAGGAGACGGT 5963

Db  5803 ATAGGCGGCCCCGCCCCGATACGGAGGGCTACGAGCCGTCTCATCAACCGTGTGCGCTCAG 5862
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Qy  5964 ATAGGCGGCCCCGCCCCGATACGGAGGGCTACGAGCCGTCTCATCAACCGTGTGCGCTCAG 6023

Db  5863 CGTGAGGAGTACTGCGCCCCGGCTAATCCAGCACGCGCTGGCGAAAGCACAAGGCCGCGGC 5922
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Qy  6024 CGTGAGGAGTACTGCGCCCCGGCTAATCCAGCACGCGCTGGCGAAAGCACAAGGCCGCGGC 6083

Db  5923 GAGGGAGGTGGGTCCTTTGAGCCGGATACGGATCATGGCCGATGCCGATGGTGATCCGATGCC 5982
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6084 GAGGGAGGTGGGTCCTTTGAGCCGGATACGGATCATGGCCGATGCCGATGGTGATCCGATGCC 6143

Db  5983 GGGGACCCGGCCCGATGAAGCAACGAACGGCGGATGCGCCCGCTGGTGGAGATGGTAGT 6042
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6144 GGGGACCCGGCCCGATGAAGCAACGAACGGCGGATGCGCCCGCTGGTGGAGATGGTAGT 6203

Db  6043 GTTAACGTACTGCAGAAGGAGCTGCCGATGCCGATGAGAGTAATGTAAATAGTCCGGGT 6102
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6204 GTTAACGTACTGCAGAAGGAGCTGCCGATGCCGATGAGAGTAATGTAAATAGTCCGGGT 6263

Db  6103 GAGGATGCAGCGGCGGCGGCAGCAGCAGCGGCGGCGGCGGCCGCGGCGACGACG 6162
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Qy  6264 GAGGATGCAGCGGCGGCGGCAGCAGCAGCGGCGGCGGCGGCCGCGGCGACGACG 6323

Db  6163 GCGGGAAGTCCCGAGCCGGGTAGCCGGCGGCCGCCGCCGTTCGTGGAGAGCGAC 6222
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Qy  6324 GCGGGAAGTCCCGAGCCGGGTAGCCGGCGGCCGCCGCCGTTCGTGGAGAGCGAC 6383

Db  6223 GGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCCGAGATCGCCGAGCATCACG 6282
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Qy  6384 GGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCCGAGATCGCCGAGCATCACG 6443

Db  6283 TCGCGCACGGCGGCGATGTCTGAGCCGGCCTGAGCCTGCAGGCCTCCGGGAATGGCCTCCACT 6342
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Qy  6444 TCGCGCACGGCGGCGATGTCTGAGCCGGCCTGAGCCTGCAGGCCTCCGGGAATGGCCTCCACT 6503

Db  6343 TAGC 6346
         ||||
Qy  6504 TAGC 6507
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RESULT 3
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ID    US-07-998-289B-7 STANDARD; DNA; UNC; 5461 BP.
AC    xxxxxx
DT
DE    Sequence 7, Application US/07998289B
CC    Sequence 7, Application US/07998289B
CC    GENERAL INFORMATION:
CC       APPLICANT: Black, Bruce C
CC       APPLICANT: Taylor, Martin
CC       APPLICANT: Heckel, David G
CC    TITLE OF INVENTION: Method for Monitoring Pesticide
CC    TITLE OF INVENTION: Resistance
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Wed Jul  8 10:17:00 1998

US-08-554-424-7.rnp

Left column:

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Db   541 ACTGAGGTGTGATATCACCGGAATCTACACATTTGAATCAGCTGTGTAAAGTGATGGCACGA   600
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Qy   564 ACTGAGGTGTGATATCACCGGAATCTACACATTTGAATCAGCTGTGTAAAGTGATGGCACGA   623

Db   601 GGTTCATTTATGCCCGTTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTA   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   624 GGTTCATTTATGCCCGTTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTA   683

Db   661 GTAATAGCTTTAGCTTATGTGACCATGGTATAGATTTAGGTAATCTAGCAGCCCTGCGA   720
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Qy   684 GTAATAGCTTTAGCTTATGTGACCATGGTATAGATTTAGGTAATCTAGCAGCCCTGCCA   743

Db   721 ACGTTAGGGTGCTGCGGAGCGCTTAAAACCGTAGCCATTGTGCCAGGCTTGAAGACCATC   780
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Qy   744 ACGTTAGGGTGCTGCGACGCGCTTAAAACCGTAGCCATTGTGCCAGGCTTGAAGACCATC   803

Db   781 GTCGGCGCCCTCATCGAATCGGTGAAGAATCTGCGCGATGTGATTATCCTGACCATGTTC   840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   804 GTCCGGCGCCCGTCATCGAATCGGTGAAGAATCTGCGCGATGTGATTATCCTGACCATGTTC   863

Db   841 TCCCTGTCGGTGTTCGCGTTGATGGGCCTACAGATCTATATGGGCGTGCTCACCGAGAAG   900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   864 TCCCTGTCGGTGTTCGCGTTGATGGGCCTACAGATCTATATGGGCGTGCTCACCGAGAAG   923

Db   901 TGCATCAAGAAGTTCCCGTCGGACGGTTCCTGGGCAATCTGACCGACGAGAACTGGGAC   960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   924 TGCATCAAGAAGTTCCCGTCGGACGGTTCCTGGGCAATCTGACCGACGAGAACTGGGAC   983

Db   961 TATCACAATCGAATAGCTCCAATTGGTATTCCGGAGGACGAGGGCATCTCATTCCGTTA  1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   984 TATCACAATCGAATAGCTCCAATTGGTATTCCGGAGGACGAGGGCATCTCATTCCGTTA  1043

Db  1021 TGGCGCAATATATCCGGTGCGGGCAATGCGACGATTACGTTCGCCTGCGAGGGTTT  1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1044 TGGCGCAATATATCCGGTGCGGGCAATGCGACGATTACGTTCGCCTGCGAGGGTTT  1103

Db  1081 GGTCCGAATCCGAATTATGGCTACACCAGCTTCGATCGTTCGGATGGGCTTCCTGTCC  1140
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Qy  1104 GGTCCGAATCCGAATTATGGCTACACCAGCTTCGATCGTTCGGATGGGCTTCCTGTCC  1163

Db  1141 GCCTTCCGGCTGATGACAGGACTCTGGGAGGATCGTACCAGCTGGTGTTGCGCGCC  1200
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Qy  1164 GCCTTCCGGCTGATGACAGGACTCTGGGAGGATCGTACCAGCTGGTGTTGCGCGCC  1223

Db  1201 GCCCGGACCATGGCACATGCGTCTCTTATAGTCAATCATCTTCCTAGGTTCATTCTATCTT  1260
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Qy  1224 GCCCGGACCATGGCACATGCGTGTTCTTATAGTCAATCATCTTCCTAGGTTCATTCTATCTT  1283

Db  1261 GTGAATTGATTTGGCCATTGTTGCCATGTCGTATGACGAAATTGCAAAGGAAGGCCGAA  1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1284 GTGAATTGATTTGGCCATTGTTGCCATGTCGTATGACGAAATTGCAAAGGAAGGCCGAA  1343

Db  1321 GAAGAGAGGCTGCCGAAGAGGAGCGCACTGCGATCGCGCAGAGCTCCCGCCGCCAA  1380
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Qy  1344 GAAGAGAGGCTGCCGAAGAGGAGCGCGATACGGCGCAGAGCTCCCGCCGCCAA  1403

Db  1381 GCGGCCAAGCTGGAGGAGGCGGGGCCAATGCGCAGGCTCAGGCAGCCGGATGGCGGCTCC  1440
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Qy  1404 GCGGCCAAGCTGGAGGAGGCGGGGCCCAATGCCCAGGCTCAGGCAGCCGGATGCCGGCTGCC  1463

Db  1441 GCCGAAGAGGCTGCCACTGCGATCGCGATCCGGAAATGCCAAGAGTCCGACGTATTCTTGCATCAGC  1500
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Qy  1464 GCCGAAGAGGCGGCTGCCACTGCGATCCGGAAATGCCAAGAGTCCGACGTATTCTTGCATCAGC  1523

Db  1501 TATGAGCTATTTGTTGGGCGGCGAGAGGGCAACGATGACAACAAAGAAGATGTCC  1550
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Qy  1524 TATGAGCTATTTGTTGGGCGGCGAGAGGGCAACGATGACAACAAAGAAGATGTCC  1583

Db  1561 ATTCCGGAGGCTCGAGGTGGAGTCCGGAGTCGGAGGCCGGTTATACAAAGACAACCAGCACCT  1620
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Qy  1584 ATTCCGGAGGCTCGAGGTGGAGTCCGGAGTCGGAGCCGGTTATACAAAGACAACCAGCACCT  1643
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Right column:

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Db  1621 ACCACAGCACACCAAGCTACCAAAGTTCGTAAAGTGAGCACG----------------  1662
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Qy  1644 ACCACAGCACACCAAGCTACCAAAGTTCGTAAAGTGAGCACGACATCCTTATCCTTACCT  1703

Db  1663 ------------------------------------TACACGATACGGAAC  1677
                                             ||||||||||||||
Qy  1704 GGTTCACCGTTAACATACGCAGGGGATCACGTAGTTCTCACAAGTACGATACGGAAC  1763

Db  1678 GGACGTGGCCGCTTGGTATACCCGTAGCGATCGTAAGCCATTGGTATTGTCAACATAT  1737
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Qy  1764 GGACGTGGCCGCTTGGTATACCCGTAGCGATCGTAAGCCATTGGTATTGTCAACATAT  1823

Db  1738 CAGGATGCCCAGCAGCACTTGCCCTATGCCGACGACTCGAATGCCGTCACCCCGATGTCC  1797
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Qy  1824 CAGGATGCCCAGCAGCACTTGCCCTATGCCGACGACTCGAATGCCGTCACCCCGATGTCC  1883

Db  1798 GAAGAGAATGGGCCATCATAGTGCCCGTTGACTATGATCCTGACTATGGGCAACATCAGGTTC  1857
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1884 GAAGAGAATGGGCCATCATAGTCCCCGTTGACTATGATCCTGACTATGGGCAACATCAGGTTC  1943

Db  1858 TCGTATACCTCGCATCAGTCCGAATATCGTATACCTCACATGGCGATCTCACTCGCGGCGGC  1917
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1944 TCGTATACCTCGCATCAGTCCGAATATCGTATACCTCACATGGCGATCTCACTCGCGGCGGC  2003

Db  1918 ATGGCCCGTCATGGGCGTCAGCACAATGACCAAGGAGAGCAAATTGCGCAACCGCAACACA  1977
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Qy  2004 ATGGCCCGTCATGGGCGTCAGCACAATGACCAAGGAGAGCAAATTGCGCAACCGCAACACA  2063

Db  1978 CGCAATCAATCACAGTGGCGCGCCACCAATGGCGCGCCACCACCTGTCTGCTGGACACCAATCACAAG  2037
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Qy  2064 CGCAATCAATCACAGTGGCGCGCCACCAATGGCGCGCCACCACCTGTCTGCTGGACACCAATCACAAG  2123

Db  2038 CTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCACGGACGAAGCTGGCAAGGAGGACGTTAA  2097
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Qy  2124 CTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCACGGACGAAGCTGGCAAGGAGGACGTTAA  2183

Db  2098 CATCATGACAATCTCTTTATCGAGCCCGTCCAGACACAAACGGTGGTTGATATGAAAGAT  2157
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2184 CATCATGACACATCCTTTATCGAGCCCGTCCAGACACAAACGGTGGTTGATATGAAAGAT  2243

Db  2158 GTGATGGTCCTGAATGACATCATGAACACGGCTGGTCGGCACAGTCGGGCACCAGCAAGCGAT  2217
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2244 GTGATGGTCCTGAATGACATCATGAACACGGCTGGTCGGCACCAGTCGGGCACCAGCAAGCGAT  2303

Db  2218 CGCGGTGTCTCCGTTACTATTCCCAACAGAGGACGATGAGGAGATGGACGTTC  2277
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Qy  2304 CGCGGTGTCTCCGTTACTATTCCCAACAGAGGACGATGAGGAGATGGACGTTC  2363

Db  2278 AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTGTTTGTGTGTGGACTGT  2337
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Qy  2364 AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTGTTTGTGTGTGGACTGT  2423

Db  2338 TGCTCGGGTTTGGTTGGTTGAAATTTCAGGAGGTGGGTATCGCTCATCGTCTTCGTC  2397
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Qy  2424 TGCTGGGGTTTGGTTGGTTGAAATTTCAGGAGTGGGTATCGCTCATCGTCTTCGTC  2483

Db  2398 GAGCTCTTCATCGCTGTCGTTGGTCAACACGATGTTCATGCGCAATGGATCACCAC  2457
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Qy  2484 GAGCTCTTCATCGCTGTCGTTGGTCAACACGATGTTCATGCGCAATGGATCACCAC  2543

Db  2458 GATATGAACAAGGAGAATGGCCGGTGCTCAAGAGTGGCAACTATTTCTTCACCGCCACC  2517
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Qy  2544 GATATGAACAAGGAGAGTGGACGCGGTGGCAACTATTTCTTCACCGCCACC  2603

Db  2518 TTTGCCATCGAGGCCACCATGGAAGCTAATGGCCATGAGCCCCAAGTACTATTTCCAGGAG  2577
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Qy  2604 TTTGCCATCGAGGCCACCATGGAAGCTAATGGCCATGAGCCCCAAGTACTATTTCCAGGAG  2663

Db  2578 GGCTCGAAACATCTTCGACTTCATTATCGTGCCCTATCGTATTGGAACTTCGAG  2637
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2664 GGCTCGAAACATCTTCGACTTCATTATCGTGCCCTATCGTATTGGAACTTCGAG  2723

Db  2638 GGTGTCCAGGTCGTCTGTCCGTATTGCGTTCCTTCGATTGCTGCGTGTATTCAAACTGGCC  2697
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Qy     3804 ATCATTATTCATGCACACGACGAGGATATACTCGATGAATATCCGATGATTGCTGCCCC 3863
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Db     3664 GATTCGTACTATAAGAAATTCCGATCTTAGCCGTGACGATGACTCGCCGTTCTCGGCAA 3723

Qy     3864 GATTCGTACTATAAGAAATTCCGATCTTAGCCGTGACGATGACTCGCCGTTCTCGGCAA 3923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3724 GGATGGGGCAATTACGACTCATCTTCGGGTGGATGGGAATGCAA 3783

Qy     3924 GGATGGGGCAATTACGACTCATCTTCGGGTGGATGGGAATGCAA 3983
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Db     3784 GCTGTTATCACTATGATTTAATGAGTAGCTTGGCATTAGAGATGTACATCTG 3843

Qy     3984 GCTGTTATCACTATGATTTAATGAGTAGCTTGGCATTAGAGATGTACATCTG 4043
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Db     3844 CCACAAAGACCCATACTGCAGGATATTTATACTATATGGACAGAGAATATTTACGGTTATA 3903

Qy     4044 CCACAAAGACCCATACTGCAGGATATTTATACTATATGGACAGAGAATATTTACGGTTATA 4103
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Db     3904 TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTTCAAAGTGTACTTGACCAAC 3963

Qy     4104 TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTTCAAAGTGTACTTGACCAAC 4163
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Db     3964 GCGTGGTGTGGCTGCGATTCGTGATTGTCATGGTATGCGTTATCAACTTCGTTGCTTCA 4023

Qy     4164 GCGTGGTGTGGCTGCGATTCGTGATTGTCATGGTATGCGTTATCAACTTCGTTGCTTCA 4223
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Db     4024 CTTGTTGGAGCTGCTGGTGGTATTCAAGCCTTCAAGACTATGCGAACGTTAAGAGCACTGAGA 4083

Qy     4224 CTTGTTGGAGCTGCTGGTGGTATTCAAGCCTTCAAGACTATGCGAACGTTAAGAGCACTGAGA 4283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4084 CCACTACGTGCCATGTCCCGTATGCAGGCATGAGGTCGTCGTAATGCGCGTCGGTACAA 4143

Qy     4284 CCACTACGTGCCATGTCCCGTATGCAGGCATGAGGTCGTCGTAATGCGCGTCGGTACAA 4343
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Db     4144 GCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTCTAATATTTTGGCTAATTTTTGCC 4203

Qy     4344 GCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTCTAATATTTTGGCTAATTTTTGCC 4403
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4204 ATAATGGGTGTACAGCTTTTGCTGGAAAATATTTAAGTGCGGAGGACGAATGGCACG 4263

Qy     4404 ATAATGGGTGTACAGCTTTTGCTGGAAAATATTTAAGTGCGGAGGACGAATGGCACG 4463
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4264 AAGCTCAGCCACGACGCATGTGACAACGAACTACACGTGG 4323

Qy     4464 AAGCTCAGCCACGACGCATGTGACAACGAACTACACGTGG 4523
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Db     4324 GTGAATTCAGCAGGTCAGTGAATTCATGACAGAAGATCAGAAAAGTAC 4383

Qy     4524 GTGAATTCAGCAGGTCAGTGAATTCATGACAGAAGATCAGAAAAGTAC 4583
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     4384 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTCACGGAGGTGGAC 4443

Qy     4584 GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTCACGGAGGTGGAC 4643
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4444 AAGCAACCAATTCGTGAAACGAACATCTACACGTGATTTATATTTCGTATGTTAATGAG 4503

Qy     4644 AAGCAACCAATTCGTGAAACGAACATCTACACGTGATTTATATTTCGTATGTTAATGAG 4703
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Db     4504 TTTGGATCATTTTCACACTCGTTGTTATCATTGGTTATCATTGATAATTTTAATGAG 4563

Qy     4704 TTTGGATCATTTTCACACTCGTTGTTATCATTGGTTATCATTGATAATTTTAATGAG 4763
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Db     4564 CAAAAGAAAAAAGCAGGTGGATCATTAGAAAGTTCATGACAGAAGATCAGAAAAGTAC 4623

Qy     4764 CAAAAGAAAAAAGCAGGTGGATCATTAGAAAGTTCATGACAGAAGATCAGAAAAGTAC 4823
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Db     4624 TATAGTGCTATGAAAAAGAATGGGCTCTAAAAAGCCATTCAAGACCAAGG 4683

Qy     4824 TATAGTGCTATGAAAAAGAATGGGCTCTAAAAAGCCATTCAAGACCAAGG 4883
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Db     4684 TGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATATAATCATT 4743

Qy     4884 TGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATATAATCATT 4943
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Qy     2724 GGTCCCAGGGTCTGTCCGTATTGCGTTCCTTTCGATTGCTGCCGTGTATTCAAACTGGCC 2783
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Db     2698 AAGTCTTGGCCCACACTTAATTTACTTCGATTATTCGATTATGGACGCACCATGGCGCTTTG 2757

Qy     2784 AAGTCTTGGCCCACACTTAATTTACTTCGATTATTCGATTATGGACGCACCATGGCGCTTTG 2843
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2758 GGTAATCTGACATTTGTACTTTGTCATTATCATCTTCATCTTCATTCTTTCGCGGTGATGGGAATGCAA 2817

Qy     2844 GGTAATCTGACATTTGTACTTTGTCATTATCATCTTCATCTTCATTCTTTCGCGGTGATGGGAATGCAA 2903
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2818 CTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGGCGACCTGCCCGCGC 2877

Qy     2904 CTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGGCGACCTGCCCGCGC 2963
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Db     2878 TGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTGTTCCGGTGCTCTCGCGGAGAA 2937

Qy     2964 TGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTGTTCCGGTGCTCTCGCGGAGAA 3023
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2938 TGGATCGAGTCCATGTGGGACTGCGATGTCTCGTGCATGTCTCGTGCATTCCCTTCTTC 2997

Qy     3024 TGGATCGAGTCCATGTGGGACTGCGATGTCTCGTGCATGTCTCGTGCATTCCCTTCTTC 3083
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Db     2998 TTGGCCACCGTTGTCATCGGCCAATCTTGTGTCGTACTTAACCTTTTCTTAGCCTTTGCTTTTG 3057

Qy     3084 TTGGCCACCGTTGTCATCGGCCAATCTTGTGTCGTACTTAACCTTTTCTTAGCCTTTGCTTTTG 3143
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Db     3058 TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAATAAAATA 3117

Qy     3144 TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAATAAAATA 3203
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Db     3118 GCCGAGGCCCTTCAATCGAATTGGGCCGATTAAAAGTTGGGTAAGCGTAATATTGCTGAT 3177

Qy     3204 GCCGAGGCCCTTCAATCGAATTGGGCCGATTAAAAGTTGGGTAAGCGTAATATTGCTGAT 3263
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3178 TGTTTCAAGTTAATACGTAACAAAATTGACATGTCGACAAGCTGGAGCTG----- 3232

Qy     3264 TGTTTCAAGTTAATACGTAACAAAATTGACATGTCGACAAGCTGGAGCTG 3323
                                                  ||||||||||||||||||||
Db     3233 -----------------------------------AGCATGGTGACAACGAACTGGAGCTG 3258

Qy     3324 AGGACCAACCAGATCAGTTGGATTTGGAGCGAAGAGCATGGTGACAACGAACTGGAGCTG 3383
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3259 GGCCACGACGAGATCCTCGCCGACGGCCTCATCGAAGAGGGATCAAGAGCAGAGCAA 3318

Qy     3384 GGCCACGACGAGATCCTCGCCGACGGCCTCATCGAAGAGGGATCAAGAGCAGAGCAA 3443
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Db     3319 CTGGAGGTGGCCATCGGGGATGCCATCGGGGATGCCATCGGGGATGCCATCGGGGATGCGGCCAGCAAGGAGGATTA 3378

Qy     3444 CTGGAGGTGGCCATCGGGGATGCCATCGGGGATGCCATCGGGGATGCGGCCAGCAAGGAGGATTA 3503
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Db     3379 AAGCCGAAGAAATCCAAATATCTAAATAACGCAACG--------------- 3414

Qy     3504 AAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCAACTCAATTAACCAC 3563
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Db     3415 -------------------------------------GACGACGAC 3423

Qy     3564 CAAGACAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCCCTTACAGGACGACGAC 3623
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Db     3424 ACTGCCAGCATTAACTCATATGGTAGCCCATAGAGTGTAGCTCATAGAGTGTAGCCCAC 3483

Qy     3624 ACTGCCAGCATTAACTCATATGGTAGCCCATAGAGTGTAGCTCATAGAGTGTAGCCCAC 3683
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Db     3484 AAGGGCCAGCCGCCGAGAACTGGCCGAGGGGCCGAATGCAGCCGCCGAGCAGGAGGATTA 3543

Qy     3684 AAGGGCCAGCCGCCGAGAACTGGCCGAGGGGCCGAATGCAGCCGCCGAGCAGGAGGATTA 3743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3544 GGTCTCGACGAGGAACTGGCCGAGGGGCCGAATGCAGCCGCCGAGCGGCCGCTCGACGGTGAT 3603

Qy     3744 GGTCTCGACGAGGAACTGGCCGAGGGGCCGAATGCAGCCGCCGAGCGGCCGCTCGACGGTGAT 3803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3604 ATCATTATTCATGCACACGACGAGGATATACTCGATGAATATCCGATGATTGCTGCCCCC
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CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/998,289
CC   FILING DATE: 30-DEC-1992
CC   CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Harrington, James J.
CC   REGISTRATION NUMBER: P-38,711
CC   REFERENCE/DOCKET NUMBER: 31,732
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 201-831-3246
CC   TELEFAX: 201-831-3305
CC   INFORMATION FOR SEQ ID NO: 7:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 5461 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
SQ   SEQUENCE 5461 BP; 1425 A; 1259 C; 1374 G; 1403 T; 0 OTHER.

Query Match              67.2%;   Score 4374;   DB 11;   Length 5461;
Best Local Similarity   96.7%;   Pred. No. 0.00e+00;
Matches   5445;   Conservative   0;   Mismatches   9;   Indels 177;   Gaps 3;
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Db    1  ATGACAGAAGATTCCGACTCGATATCGAGGAAGAACGCAGTTGTTCCGTCCCTTACC   60
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Qy   24  ATGACAGAAGATTCCGACTCGATATCGAGGAAGAACGCAGTTGTTCCGTCCCTTACC   83

Db   61  CGGAATCATTGGTGCAAATGCAACAACGCATTGCGCGCGATATGGTCGCCGATATGGTGCAAGAAGGAG  120
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Qy   84  CGGGATCATTGGTGCAAATGCGAACAACGCATTGCGCGCGATATGGTCGCCGATATGGTCAACAGGAGGAG  143

Db  121  CTGGAAAGAAAGAGAGCCGAGGGAGGAGTGCGCCGCGATATGGTCGTCCAAGAAGAAAAAACAAAAA  180
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Qy  144  CTGGAAAGAAAGAGAGCCGAGGGAGGAGTGCGCCGCGATATGGTCGTCCAAGAAGAAAAAAACAAAAA  203

Db  181  GAAATCCGATATGATGAGGACGAGGAGGATGAAGTCCACAACCGGATCCTACACTTGAA  240
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Qy  204  GAAATCCGATATGATGAGGACGAGGAGGATGAAGTCCACAACCGGATCCTACACTTGAA  263

Db  241  CAGGGTGTGCCAATACCTGTTCAGGGAGCGGCAGCTTCCCGCGGAATGGCCTCCCACT  300
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Qy  264  CAGGGTGTGCCAATACCTGTTCAGGGAGCGGCAGCTTCCCGCGGAATGGCCCCCACT  323

Db  301  CCTCTCGAGGATATCGATCCCTACTACAGCAATGCAATGCTGACAATGTGGATGCTGACTACTCGTAGTTCGTAAGCAA  360
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Qy  324  CCTCTCGAGGATATCGATCCCTACTACAGCAATGCAATGCTGACAATGTGGATGCTGACTACTCGTAGTTCGTAAGCAA  383

Db  361  GGAAAAGATATTTTCGCTTTTCGCTTTTCGCATTACATTGGATGCTCGATCAAAAGCAATGTCCATTCATTCAAT  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  384  GGAAAAGATATTTTCGCTTTTCGCTTTTCGCATTACATTGGATGCTCGATCAAAAGCAATGTCCATTCATTCAAT  443

Db  421  CCGATACGTCGTGTGGCCATTACATTCTAGTGCATCATCATATTTCCCTATTCATCATC  480
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Qy  444  CCGATACGTCGTGTGGCCATTACATTCTAGTGCATCATCATATTTCCCTATTCATCATC  503

Db  481  ACCACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCACGGTTGAGTCC  540
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Qy  504  ACCACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCACGGTTGAGTCC  563

Db  541  ACTGAGGTGATATTCACCGAATCTACACATTGAATCAGCTGTTAAAGTGATGGCCACGA  600
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Qy  564  ACTGAGGTGATATTCACCGAATCTACACATTGAATCAGCTGTTAAAGTGATGGCCACGA  623

Db  601  GGTTTCATTTATGCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTA  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  624  GGTTTCATTTATGCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTA  683

Db  661  GTAATAGCTTAGCTTATGTGACCATGGGTATAGATTTAGGTAATCAGCCCCTGCGA  720
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Qy  684  GTAATAGCTTAGCTTATGTGACCATGGGTATAGATTTAGGTAATCAGCCCCTGCGA  743
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Db  4744  ATGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATCGCTTACGATGCGTCGGAC  4803
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Qy  4944  ATGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATCGCTTACGATGCGTCGGAC  5003

Db  4804  ACGTATAACGCGGGTCCTAGACTATCTCAATGCGATATTCGTAGTATTTCAGTTCCGAA  4863
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Qy  5004  ACGTATAACGCGGGTCCTAGACTATCTCAATGCGATATTCGTAGTATTTCAGTTCCGAA  5063

Db  4864  TGTCTATTAAAAATATTCGCTTTACGATATCACTATTTTATTGAGCCATGGAATTTATTT  4923
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Qy  5064  TGTCTATTAAAAATATTCCCTTTACGATATCACTATTTTATTGAGCCATGGAATTTATTT  5123

Db  4924  GATGTAGTAGTGTCATTTTATCCATCTTAGGTCTTGTGTACTTAGCGATATTCGAGAAG  4983
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5124  GATGTAGTAGTGTCATTTTATCCATCTTAGGTCTTGTGTACTTAGCGATATTCGAGAAG  5183

Db  4984  TACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTGGCGAAAGTGGGCCGTGTCCTT  5043
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Qy  5184  TACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTGGCGAAAGTGGGCCGTGTCCTT  5243

Db  5044  CGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCCGCGTTGGCCATGTCGCTG  5103
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Qy  5244  CGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCCGCGTTGGCCATGTCGCTG  5303

Db  5104  CCGGCCCGTTCAACACTGCCTGCTGTCGTGTTCCTGGTCATGTTCATCTTGCCATTTTC  5163
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5304  CCGGCCCGTTCAACACTGCCTGCTGTCGTGTTCCTGGTCATGTTCATCTTGCCATTTTC  5363

Db  5164  GGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCGGCATTAACGACGTCTACAACTTC  5223
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5364  GGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCGGCATTAACGACGTCTACAACTTC  5423

Db  5224  AAGACCTTTGGCCAGAGCATGATCCTGTCTCTTCAGATGTCGACGTCAGCCGGTTGGGAT  5283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5424  AAGACCTTTGGCCAGAGCATGATCCTGTCTCTTCAGATGTCGACGTCAGCCGGTTGGGAT  5483

Db  5284  GGTGTACTTGGACGGCCATTATCAATGAGGAAGCATGCGATCCACCCCGACAACGACAAAGGC  5343
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5484  GGTGTACTTGGACGGCCATTATCAATGAGGAAGCATGCGATCCACCCCGACAACGACAAAGGC  5543

Db  5344  TATCCGGGCAATTGTGGTTCAGCGACCGTTGGAATAAACGTTTCTCCTCTCATACCTAGTT  5403
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5544  TATCCGGGCAATTGTGGTTCAGCGACCGTTGGAATAAACGTTTCTCCTCTCATACCTAGTT  5603

Db  5404  ATAAGCTTTTTGTGATAGTTATTAATATGTACATTGCTGTGTCATTCTGTCATTCTCGAGAAC  5454
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5604  ATAAGCTTTTTGATAGTTTATTAATATGTACATTGCTGTGTCATTCTGTCATTCTCGAGAAC  5654
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RESULT 4
ID   US-07-998-289-7 STANDARD;  DNA;  UNC;  5461 BP.
AC   xxxxxx
DT
DE   Sequence 7, Application US/07998289
DE   Sequence 7, Application US/07998289
CC   GENERAL INFORMATION:
CC   APPLICANT: Black, Bruce C.
CC   APPLICANT: Taylor, Martin
CC   APPLICANT: Heckel, David G.
CC   TITLE OF INVENTION: Method for Monitoring Pesticide
CC   TITLE OF INVENTION: Resistance
CC   NUMBER OF SEQUENCES: 10
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: American Cyanamid Company
CC   STREET: One Cyanamid Plaza
CC   CITY: Wayne
CC   STATE: New Jersey
CC   COUNTRY: U.S.A.
CC   ZIP: 07470
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
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Db 1738 CAGGATGCCCAGCAGCACTTGCCCATGCCGACGACTCGAATGCGTCACCCGATGTCC 1797
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Qy 1824 CAGGATGCCCAGCAGCACTTGCCCATGCCGACGACTCGAATGCGTCACCCGATGTCC 1883

Db 1798 GAAGAAATGGGCCATCATAGTGCCCGTGTACTATGCCAATCTAGGCTCCGACACTCA 1857
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Qy 1884 GAAGAAATGGGCCATCATAGTGCCCGTGTACTATGCCAATCTAGGCTCCGACACTCA 1943

Db 1858 TCGTATACCTCCGATCAGTCCCGAATATCGTATACCTCACATGGCCGATCTCGGCGGC 1917
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1944 TCGTATACCTCCGATCAGTCCCGAATATCGTATACCTCACATGGCCGATCTCGGCGGC 2003

Db 1918 ATGGCCGTCATGGGCGTCAGCACAATGACCAAGGAGCAAATTGCGCAACCGCAACACA 1977
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Qy 2004 ATGGCCGTCATGGGCGTCAGCACAATGACCAAGGAGCAAATTGCGCAACCGCAACACA 2063

Db 1978 CGCAATCAATCAGTGGGCGCCACCAATGGCGGCCACCACTGTCTGCTACACCATCACAAG 2037
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Qy 2064 CGCAATCAATCAGTGGGCGCCACCAATGGCGGCCACCACTGTCTGCTACACCATCACAAG 2123

Db 2038 CTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCACGGACGAAGCTGGCAAGATTAAA 2097
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Qy 2124 CTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCACGGACGAAGCTGGCAAGATTAAA 2183

Db 2098 CATCATGACAAATCCTTTATCGAGCCGTCAGACACAAACGTGGTTGATATGAAAGAT 2157
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Qy 2184 CATCATGACAAATCCTTTATCGAGCCGTCAGACACAAACGTGGTTGATATGAAAGAT 2243

Db 2158 GTGATGGTCCTGAATGACATCATCGAACAGGCCGTCGGCACAGTCGGGCAAGCGGAT 2217
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Qy 2244 GTGATGGTCCTGAATGACATCATCGAACAGGCCGTCGGCACAGTCGGGCAAGCGGAT 2303

Db 2218 CGCGGTGTCTCCGTTACTATTTCCCAACAGAGGACGATGACGAGGATGGGCCGACGTTC 2277
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Qy 2304 CGCGGTGTCTCCGTTACTATTTCCCAACAGAGGACGATGACGAGGATGGGCCGACGTTC 2363

Db 2278 AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCCATGATGATGCGTTCGCTCGTCCCTTCGTC 2337
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Qy 2364 AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCCATGATGATGCGTTCGCTCGTCCCTTCGTC 2423

Db 2338 TGCTCGGTTTGGTTGAAATTCAGGAGTGGTATCGCTCATCCGTATCCCTTCGTC 2397
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2424 TGCTCGGTTTGGTTGAAATTCAGGAGTGGTATCGCTCATCCGTATCCCTTCGTC 2483

Db 2398 GAGCTCTTCATCACGCTGTTGCATTGTGTCAACACGATGTTCATGGCAATGGATCACCAC 2457
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2484 GAGCTCTTCATCACGCTGTTGCATTGTGTCAACACGATGTTCATGGCAATGGATCACCAC 2543

Db 2458 GATATGAACAAGGAGGATGGAACGCGTGCTGCAACTATTCTTCACCGCCACC 2517
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Qy 2544 GATATGAACAAGGAGGATGGAACGCGTGCTGCAACTATTCTTCACCGCCACC 2603

Db 2518 TTTGCCATCGAGGCCACCATGCCAGTAATGCCATGAGCCCAAGTACTATTTCCAGAGAG 2577
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Qy 2604 TTTGCCATCGAGGCCACCATGCCAGTAATGCCATGAGCCCAAGTACTATTTCCAGAGAG 2663

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Qy 2664 GGCTGGAACATCTTCGACTTCGATTATCGTGCCCTATCCGCTATTGGAACTGGACTCGAG 2723

Db 2638 GGTGTCCCAGGGTCTGTCCGTATTACAATTACTTAATTTGATTTCGATTATCATCTTCAAACTGGCC 2697
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Qy 2724 GGTGTCCCAGGGTCTGTCCGTATTACAATTACTTAATTTGATTTCGATTATCATCTTCAAACTGGCC 2783

Db 2698 AAGTCTTGGCCCACACTTAATTTACTTGCATTTGACTTTGCATTATGGGACCGCCACCATGCGGCTTTG 2757
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Qy 2784 AAGTCTTGGCCCACACTTAATTTACTTGCATTTGACTTTGCATTATGGGACCGCCACCATGCGGCTTTG 2843

Db 2758 GGTAAATCGACATTTGACTTTGTCATTATCATCTTTGCCGGTGATGGGAATGCAA 2817
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Qy 2844 GGTAAATCGACATTTGACTTTGTCATTATCATCTTTGCCGGTGATGGGAATGCAA 2903

Db 2818 CTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGCGGACCTGCGCGGC 2877
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Qy
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Db 721  ACGTTTAGGGTGCTGCGAGCGGCTTAAAACCGTAGCCAATTGTGCCAGGCTTGAAGACCATC 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 744  ACGTTTAGGGTGCTGCGAGCGGCTTAAAACCGTAGCCAATTGTGCCAGGCTTGAAGACCATC 803

Db 781  GTCGGCGCCGTCATCGAATCGGTGAAGAATCTGCGCGATGTGATTATCCTGACCATGTTC 840
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Qy 804  GTCGGCGCCGTCATCGAATCGGTGAAGAATCTGCGCGATGTGATTATCCTGACCATGTTC 863

Db 841  TCCCTGTCGGTGTTGATGGGCCTACAGATCTATATGGGCGTGCTCACCGAGAAG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 864  TCCCTGTCGGTGTTGATGGGCCTACAGATCTATATGGGCGTGCTCACCGAGAAG 923

Db 901  TGCATCAAGAAGTTCCCGCTGGACGGTTCCTGGGCAATCTGACCGACGAGAACTGGGAC 960
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Qy 924  TGCATCAAGAAGTTCCCGCTGGACGGTTCCTGGGCAATCTGACCGACGAGAACTGGGAC 983

Db 961  TATCACAATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGGGCATCTCATTTCCGTTA 1020
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Qy 984  TATCACAATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGGGCATCTCATTTCCGTTA 1043

Db 1021 TGCGGCAATATATCCGGTGCGGGGCAATGCGACGACGATTACGTGTGCCCTCGAGGGGTTT 1080
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Qy 1044 TGCGGCAATATATCCGGTGCGGGGCAATGCGACGACGATTACGTGTGCCCTCGAGGGGTTT 1103

Db 1081 GGTCCGAATCCGAATTATGGCTACACCAGCTTCGATTCGTTCGGTGGCTTTCCTGTCC 1140
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Qy 1104 GGTCCGAATCCGAATTATGGCTACACCAGCTTCGATTCGTTCGGTGGCTTTCCTGTCC 1163

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        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1224 GCCGGACCATGGCACATGCTGTTCTTTATAGTCATCATCTTCCTAGGTTCATTCTATCTT 1283

Db 1261 GTGAATTTGATTTGGCCATGTGTGCTATGACGAATTGCAAAGGAAGGCCGAA 1320
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1284 GTGAATTTGATTTGGCCATGTGTGCTATGACGAATTGCAAAGGAAGGCCGAA 1343

Db 1321 GAAGAGAGGGCTGCCGAAGAGGAGGCGATACGTGAAGCGGAAGCTGCCGCGCCCAAA 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1344 GAAGAGAGGGCTGCCGAAGAGGAGGCGATACGTGAAGCGGAAGCTGCCGCGCCCAAA 1403

Db 1381 GCGGGCCAAGCTGGAGGAGGCGGGGCCAATGCGGGCGTCAGGCAGCAGCTCAGGCGGCTGCC 1440
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1404 GCGGGCCAAGCTGGAGGAGGCGGGGCCAATGCGGGCGTCAGGCAGCAGCTCAGGCGGCTGCC 1463

Db 1441 GCCGAAGAGGCTGCACTGCTGCGATCGTTCGGTAAGTGGACGTTCCGACGTATTCTTGCATCAGC 1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1464 GCCGAAGAGGCTGCACTGCTGCGATCGTTCGGTAAGTGGACGTTCCGACGTATTCTTGCATCAGC 1523

Db 1501 TATGAGCTATTTGTTGGGCGGCGAGAAGGGCAACGATGACAACAACACAACAGAGAGATGTCC 1560
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1524 TATGAGCTATTTGTTGGGCGGCGAGAAGGGCAACGATGACAACAACACAACAGAGAGATGTCC 1583

Db 1561 ATTCGGAGCGTCGAGTCGGTCGGTGAGTTCGTAAAGTGAGCACG--------------- 1620
        ||||||||||||||||||||||||||||||||||||||||||||
Qy 1584 ATTCGGAGCGTCGAGTCGGTCGGTGAGTTCGTAAAGTGAGCACGTACACCGATACGGACG 1643

Db 1621 ACCAGCAGCACCAAGCTACCAAGTTCGTAAAGTGAGCACGCCGTATCCGACGAGCAA 1662
        ||||||||||||||||||||||||||||||||||||||||||||||
Qy 1644 ACCAGCAGCACCAAGCTACCAAGTTCGTAAAGTGAGCACGCCGTATCCGACGAGCAA 1703

Db 1663 --------------------------------TACACCGATACGGAAC 1677
                                        |||||||||||||||||||
Qy 1704 GGTTCACCCGTTTAACATACGCAGGGGGGGATCGCTTTGGTATCCCGGTAGCGGATCTACACCGATACGGAAC 1763

Db 1678 GGACGCTGGGCGCTTTGGTATACCCGGTAGCGGATCGGTAGCGTGATCGGTATTGGTCTGTCAACATAT 1737
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1764 GGACGCTGGGCGCTTTGGTATACCCGGTAGCGGATCGGTAGCGTGATCGGTATTGGTCTGTCAACATAT 1823

Db 1764
Qy
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**Left column**

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Qy          |||||||||||||||||||||||||||||||||||||||||||||||||||||
   2904     CTGTTCGGAAGAGTAATCATGATGACCATTCAGGACGACTTCCGGATGGGCGACCTGCCGCGCC   2963

Db   2878   TGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTTGGCGCTCTGCGGAGAA   2937
Qy   2964   TGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTGTGCGGCGTGCTGCGGAGAA   3023

Db   2938   TGGGATCGAGTCCATGTGGGACTACGTGGGCGATGTCTCGTGCATTCCCTTCTTC   2997
Qy   2998   TGGGATCGAGTCGGGACTGGGACTACGTGGGCCGATGTCTCGTGCATTCCCTTCTTC   3083

Db   2998   TTGGCCACCGTGTCATCGGCAATCTGTGGTACTTAACCTTTCTTAGCCTTGCTTTG   3057
Qy   3084   TTGGCCACCGTGTCATCCGGCAATCTGTGGTACTTAACCTTTCTTAGCCTTGCTTTG   3143

Db   3058   TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAATAAAATA   3117
Qy   3144   TCCAATTTTGGCTCATCTAGCTTATCAGCGCCGATTAAAAGTTGGGTTAAGCGTAATATTGCTGAT   3203

Db   3118   GCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTTGGGTTAAGCGTAATATTGCTGAT   3177
Qy   3204   GCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTTGGGTTAAGCGTAATATTGCTGAT   3263

Db   3178   TGTTTCAAGTTAATACGTAACAAATTGACAAATCAAATCAAATGATCAACCATCAG-----   3232
Qy   3264   TGTTTCAAGTTAATACGTAACAAATTGACAAATCAACCATCCAGGTGAG   3323

Db   3233   ----------AGCATGGTGACAACGAACTGGAGCTG   3258
Qy   3324   AGGACCAACCAGATCAGTTGGATTTGGAGCGAAGAGCATGGTGACAACGAACTGGAGCTG   3383

Db   3259   GGCCACGACGAGATCCTCGCCCGACGGGCCTCATCAAGAGGGGATCAAGAGCGACACGCAA   3318
Qy   3384   GGCCACGACGAGATCCTCGCCCGACGGGCCTCATCAAGAGGGGATCAAGAGCGACAACGCAA   3443

Db   3319   CTGGAGGTGGCCATCGGGGATGGCCATGGAATTCACGGAATTCACGGGCGACATGAAGAACAAC   3378
Qy   3444   CTGGAGGTGGCCATCGGGGATCGGGATGGCCATGGAATTCACGGGCGACATGAAGAACAAC   3503

Db   3379   AAGCCGAAGAAATCCAAATATCTAAATAACGCACG---------   3414
Qy   3504   AAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCAACTCAATTAACCAC   3563

Db   3415   -------GACGGACGAC   3423
Qy   3564   CAAGACACAATAGACTGGAACACGACGAGCTAAACCATAGAGGTTTGTCCTTACCAGGACGGACGAC   3623

Db   3424   ACTGCCAGCATTAACTCATATGGTAGCCATAACTCTTCGATGAATCGGACCCAC   3483
Qy   3624   ACTGCCAGCATTAACTCATATGGTAGCCATAACTCTTCGATGAATCGGACGGAGCCAC   3683

Db   3484   AAGGGCCAGCCGCCGAGACGATTGGAGGGCGAGGAGAGGCGCCGACGCCAGCAGGAGGATTTA   3543
Qy   3684   AAGGGCCAGCCGCCGAGACGATTGGAGGGCGAGGAGAGGCGCCGACGCCAGCAGGAGGATTTA   3743

Db   3544   GGTCTCGACGGACGGAATGCGCAATCGACGGAGGAGGCCGAGGGCCCGCGACGGGTGAT   3603
Qy   3744   GGTCTCGACGGACGGAATGCGCAATCGACGGAGGAGGCCGAGGGCCCGCGACGGGTGAT   3803

Db   3604   ATCATTATTCATGCACACGAGATATTCCGATCTTAGCCGTCGATGAATCGGACGGCCCC   3663
Qy   3804   ATCATTATTCATGCACACGAGATATTCCGATCTTAGCCGTCGATGAATCGGACGGCCCC   3863

Db   3664   GATTCGTACTATAAGAAATTTCGATGAAAACTTTCGATTAATTGAGGATAAATATTTGAAACA   3723
Qy   3864   GATTCGTACTATAAGAAATTTCGATGAAAACTTTCGATTAATTGAGGATAAATATTTGAAACA   3923

Db   3724   GGATGGGGCAATTGAGACTGACTACGACGACTTTTCGATGAAAACTTTCAATTAATTGAGGATAAATATTTGAAACA   3783
Qy   3924   GGATGGGGCAATTGAGACTGACTACGACGACTTTTCGATGAAAACTTTCAATTAATTGAGGATAAATATTTGAAACA   3983

Db   3784   GCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTG   3843
Qy          |||||||||||||||||||||||||||||||||||||||||||||||||||||
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**Right column**

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Qy   3984   GCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTAGAAGATGTACATCTG   4043

Db   3844   CCACAAAGACCCATCCATACTGCGCAGGAGATATTTTATACTATATGGTTATA   3903
Qy   4044   CCACAAAGACCCATCCATACTGCGCAGGAGATATTTTATACTATATGGTTATA   4103

Db   3904   TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGTCGGCTTCAAGTGTACTTGACCAAC   3963
Qy   4104   TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGTCGGCTTCAAGTGTACTTCACCAAC   4163

Db   3964   GCGTGGTGTTGGCTCGATTGCGTCATGATGATCGCCTATCAACTTCGTTCGTTCTTCA   4023
Qy   4164   GCGTGGTGTTGGCTCGATTGCGTCATGATGTCGTATCGCCTATCAACTTCGTTGCTTCA   4223

Db   4024   CTTGGTGGAGCTGGTGGTATTCAAGCCTTCAAGACATGCGAAGGGTCGTCGTTAATGCGGCT   4083
Qy   4224   CTTGGTGGAGCTGGTGGTATTCAAGCCTTCAAGACATGCGAAGGGTCGTCGTTAATGCGGCT   4283

Db   4084   CCACTACGTGCCATCTTCAATGTGCCCGTATCGCAGGGCATGAGGGTCGTCTAATATTTTGCC   4143
Qy   4284   CCACTACGTGCCATCTTCAATGTGCCCGTATCGCAGGGCATGAGGGTCGTCTAATATTTTGCC   4343

Db   4144   GCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTGTCTAATATTTGGCTAATTTGCC   4203
Qy   4344   GCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTGTCTAATATTTGGCTAATTTGCC   4403

Db   4204   ATAATGGGTGTACAGCTTTTGCTGGAAAATATTTTAAGTGCGAGGACATGAATGGCACG   4263
Qy   4404   ATAATGGGTGTACAGCTTTTGCTGGAAAATATTTTAAGTGCGAGGACATGAATGGCACG   4463

Db   4264   AAGCTCAGCCACGACGAGATCATACCAAATCGGCAATGCCTGCCGGAGAGCGAGAACTACACGTGG   4323
Qy   4464   AAGCTCAGCCACGACGAGATCATACCAAATCGGCAATGCCTGCCGGAGAGCGAGAACTACACGTGG   4523

Db   4324   GTGAATTCAGCAATGAATTCGATCATGTGAGGTAGGTAACGGTATCGTGCCTTTCCAAGTG   4383
Qy   4524   GTGAATTCAGCAATGAATTCGATCATGTGAGGTAGGTAACGGTATCGTGCCTTTCCAAGTG   4583

Db   4384   GCCACCTTCAAAGGCTGGATACAAATCATGACGATGCTATCGATTCACGGAGGTGGAC   4443
Qy   4584   GCCACCTTCAAAGGCTGGATACAAATCATGACGATGCTATCGATTCACGGAGGTGGAC   4643

Db   4444   AAGCAACCAATTCGTGAAACGAACATCTACATGTGATTTATATTTCGTATTCTTCATCATA   4503
Qy   4644   AAGCAACCAATTCGTGAAACGAACATCTACATGTGATTTATATTTCGTATTCTTCATCATA   4703

Db   4504   TTTGGATCATTTTCACACTCAATCTGTTCATTCATTGATAATTTAATGAG   4563
Qy   4704   TTTGGATCCTTTTCACACTCAATCTGTTCATTCATTGATAATTTAATGAG   4763

Db   4564   CAAAGAAAAAGCAGGTGAGATCATTAGAAATGTTCATGACAGAGATCAGAAAAAAGTAC   4623
Qy   4764   CAAAGAAAAAGCAGGTGAGATCATTAGAAATGTTCATGACAGAGATCAGAAAAAAGTAC   4823

Db   4624   TATAGTGCTATGAAAAAGATGGCTCTAAAAAGCCATTCAAGACCAAGG   4683
Qy   4824   TATAATGCTATGAAAAAGATGGGCTCTAAAAAACCATTCAAGACCAAGG   4883

Db   4684   TGGCCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATT   4743
Qy   4884   TGGCCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATT   4943

Db   4744   ATGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGAC   4803
Qy   4944   ATGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGAC   5003

Db   4804   ACGTATTAACGGCGGTCCTAGAACTATCTCAATGCATCGCTAGTATTTCGTAGTATTTCCGAA   4863
Qy   5004   ACGTATTAACGGCGGTCCTAGAACTATCTCAATGCATCGCTAGTATTTCGTAGTATTTCCGAA   5063

Db   4864   TGTCTATTAAAAATATTCGCTTTACGATATCACTATTTTATTCACTATTTATTGAGCCATGGAATTTATTT   4923
Qy   5064   TGTCTATTAAAAATATTCGCTTTACGATATCACTATTCACTATTTATTGAGCCATGGAATTTATTT   5123
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Db   4924  GATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTTAGCGATATTATCGAGAAG  4983
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5124  GATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTTAGCGATATTATCGAGAAG  5183

Db   4984  TACTTCGTCGTCGCCGACCCTGCTCCGAGTGGTGCCGTGTGGCGAAAGTGGGCCGTGTCCTT  5043
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5184  TACTTCGTCGTCGCCGACCCTGCTCCGAGTGGTGCCGTGTGGCGAAAGTGGGCCGTGTCCTT  5243

Db   5044  CGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCCTG  5103
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5244  CGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCCTG  5303

Db   5104  CCGGCCCTGTTCAACATCTGCCTGCTGCGTGTTCCTGGTCATGTTCATCTTGCCATTTTC  5163
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5304  CCGGCCCTGTTCAACATCTGCCTGCTGCGTGTTCCTGGTCATGTTCATCTTGCCATTTTC  5363

Db   5164  GGCATGTCGTTCTTCATGCACGTGAAGGAGAAGGACGGCATTAACGACGTCTCACAACTTC  5223
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5364  GGCATGTCGTTCTTCATGCACGTGAAGGAGAAGGACGGCATTAACGACGTCTCACAACTTC  5423

Db   5224  AAGACCTTTGGCCAGAGCATGATCCTGCTCTTCAGATGTCGACGTCAGCCGGTTGGGAT  5283
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5424  AAGACCTTTGGCCAGAGCATGATCCTGCTCTTCAGATGTCGACGTCAGCCGGTTGGGAT  5483

Db   5284  GGTGTACTGGACGCCATTATCAATGAGGAAGCATGCGATCCACCCGACAACGACAAAGGC  5343
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5484  GGTGTACTGGACGCCATTATCAATGAGGAAGCATGCGATCCACCCGACAACGACAAAGGC  5543

Db   5344  TATCCCGGCAATGTGTTCAGCGACCGTTGGAATAACGTTTCTCCTCTCCATACCTAGTT  5403
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5544  TATCCCGGCAATGTGTTCAGCGACCGTTGGAATAACGTTTCTCCTCTCCATACCTAGTT  5603

Db   5404  ATAAGCTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTGCGAGAAC  5454
                 |||||||||||||||||||||||||||||||||||||||
Qy   5604  ATAAGCTTTTGATAGTTATTAATATGTGCTGCTGTCATTCTGCGAGAAC  5654
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RESULT   5
ID    PCT-US97-24256-1 STANDARD; DNA; UNC; 6318 BP.
AC    xxxxxx
DT
DE    Sequence 1, Application PC/TUS9724256
CC    Sequence 1, Application PC/TUS9724256
CC    GENERAL INFORMATION:
CC       APPLICANT:  Cornell Research Foundation, Inc.
CC       TITLE OF INVENTION:  INSECT SODIUM CHANNELS FROM
CC       TITLE OF INVENTION:  INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
CC       TITLE OF INVENTION:  FLIES
CC       NUMBER OF SEQUENCES:  19
CC       CORRESPONDENCE ADDRESS:
CC          ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
CC          STREET:  Clinton Square, P.O. Box 1051
CC          CITY:  Rochester
CC          STATE:  New York
CC          COUNTRY:  USA
CC          ZIP:  14603
CC       COMPUTER READABLE FORM:
CC          MEDIUM TYPE:  Floppy disk
CC          COMPUTER:  IBM PC compatible
CC          OPERATING SYSTEM:  PC-DOS/MS-DOS
CC          SOFTWARE:  Patentin Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER:  PCT/US97/24256
CC          FILING DATE:
CC       CLASSIFICATION:
CC       PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER:  US 08/772,512
CC          FILING DATE:  24-DEC-1996
CC       ATTORNEY/AGENT INFORMATION:
CC          NAME:  Goldman, Michael L.
CC          REGISTRATION NUMBER:  30,727
CC          REFERENCE/DOCKET NUMBER:  19603/602

CC
CC
CC
CC
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CC
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CC

TELECOMMUNICATION INFORMATION:
   TELEPHONE:  716-263-1304
   TELEFAX:  716-263-1600
INFORMATION FOR SEQ ID NO:  1:
SEQUENCE CHARACTERISTICS:
   LENGTH:  6318 base pairs
   TYPE:  nucleic acid
   STRANDEDNESS:  single
   TOPOLOGY:  linear
MOLECULE TYPE:  cDNA
SEQUENCE 6318 BP;  1713 A;  1341 C;  1597 G;  1667 T;  0 OTHER.

Query Match    56.4%;    Score 3676;    DB 1;    Length 6318;
Best Local Similarity 84.9%;    Pred. No. 0.00e+00;
Matches 4986;  Conservative 0;  Mismatches 806;  Indels 84;  Gaps 21;

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Db   151  ATACGATAGATGACGAGGACGAAGAGATGAAGGTCCACAGCCGATCCCACACTTGACACAG  210
               |  |||||||||||||||||| ||||||||||||||||||||
Qy   207  ATCCGATAATGATGACGAGGACGAGGACGATGAAGGTCCACAACCGATCCTACACTTGACACAG  266

Db   211  GGTGTGCCTATACCTGTTCGAATGCAGGGCAGCTTCCGCCGCGGAATTGGCCTTCCACTCCT  270
               |||||||||| ||||||||  |||||||||||||||||||||||||||||||||
Qy   267  GGTGTGCCAATACCTGTTCGATTGCAGGGCAGCTTCCGCCGCGGAATTGGCCTCCCACTCCT  326

Db   271  CTCGAGGATATCGATCCCTTCTACAGTAGTAATGTACTGACATTGTAGTAATAAGTAAAGGA  330
               ||||||||||||||| ||||  |||||||||| |||| ||||||  ||||||| ||||||
Qy   327  CTCGAGGATATCGATCCCTACTACAGCACAATGTACTGACACTGTGAGTTGTAAGCAAAGGA  386

Db   331  AAGGATATATTTTCGTTTTCTGCCTCAAAAGCAATGTGCTGCGATCCATTCAATCCG  390
               ||  ||||||||  |||||||  |||||||||||| |||||||||  ||||||||||
Qy   387  AAAGATATTTTTCGCTTTTCTGCATCAAAAGCAATGTGATGCTCGATCCATTCAATCCG  446

Db   391  ATACGTCGTGTAGCCATTTATATTTAGTGCATCCCTTGTGTTTCGTTATTCATTATCACC  450
               ||||||||||||||||||||||||||| |||| ||||| | |||||||||||||||||||
Qy   447  ATACGTCGTGTGGCCATTTACATCTAGTGCATCCATCATTATTTTCCTATTCATCATCACC  506

Db   451  ACTATTCTAACTAATTGTATTTTAATGATAATAATGCCGACAACGCCACGGTTGAGTCCACT  510
               |||  |||||||||||||||||| | |||||||||||||||||||||||||||
Qy   507  ACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCACGGTTGAGTCCACT  566

Db   511  GAGGTGATATTCACCGGACTCACACATTGAATCACTACACACATTTGAATCAGCTGTTAAGTGATGGCACGAGGT  570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   567  GAGGTGATATTCACCGGACTCACAATCACACACATTGAATCAGCTGTTAAAGTGATGGCACGAGGT  626

Db   571  TTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGCATGGAATTGGCTGGACTTCGTAGTA  630
               |||||||||||||||||  ||||||||| |||||||||||||||||||||||||||||||||||
Qy   627  TTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGAGATGGCATGGAATTGGCTGGACTTCGTAGTA  686

Db   631  ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGGTAATCTCGAGCTTTGAGAACA  690
               |||||||||||| |||||||||||||||||||  |||||||||||||||||||||||| ||
Qy   687  ATAGCTTTTAGCTTATGTGACCATGGTATAGATTTAGGTAATCTCAGCAGCCCTCGCGAACG  746

Db   691  TTTAGGTACTGCGAGCTCGAAAACCTAGCCATTGTGCCAGTCTAAAAAAACCATTGTC  750
               |||||||||||| || |||||||| | ||||||||  ||||||| ||  |||||||| |||
Qy   747  TTTAGGTGCTGCGAGCGCTAAAACCGTAGCCATTGTGCCAGGTTGCGAGACCATCGTC  806

Db   751  GGTGCTGTCATTGAATCGTGAAAAATCTACGCGATTGATAATTTGACAATGTTTTCC  810
               |||||| ||||||  ||||||| || |||||| |||| | |||||  ||||||||||
Qy   807  GGCGCCCGTCATCGAATCGGTGAGAATCGCCGCACAAATCTATATGGGTGTTCTAACACAAAAGTGC  866

Db   811  CTGTCCGTGTTCGCCGGTTACGTGACCTGCTCCACAAATCTATATGGGCGTGCTCACGAGAAGTGC  870
               ||||||||||||||||||||||  ||||  |||||  | ||||||
Qy   867  CTGTCCGTGTTCGCGTTACGTGACCCTACAGATCTATATGGGCCTCACCGGAGCAGTAGTGC  926

Db   871  ATTAAACGATTCCCCCTGGACGGCAGTTGGGGCAATCTGACCCAGATGAAAAACTCGTTTCTA  930
               ||  || ||||||||||  |||||  ||||||||||||||||| ||| ||||||
Qy   927  ATCAAGAAGTTCCCGGACGGTTCCTGGGGCAATCTGACCACGAGGAACTGGGACTAT  986

Db   931  CACAATAGCAACAGTTCCAATTGGTTTACGGAGAACGATGGCGAGTCATATCCGGTGTGC  990
               |||| ||||||  ||||| ||||||  ||||||||||||||||||| ||||||||||
Qy   987  CACAATCGCCAATAGCTCCAATTGGTATTCCGAGGACGACGGGGGATTATCGTCTGCCCTGCCGC  1046

Db   991  GGGAATGGTATCCGGTGCGGGACAATGCGGGGCGAGGGAATTACGTCTGCCCTGCCGCAGGGCTTCGGC  1050
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Qy    2115 AATCACAAGCTC--GATCATCGGCGACTACGACAATCCTTTTATCGAGCCGCTCGAGTGTCACGGACGAAGCT 2171
           ||  |||  |||||||||||  ||||||||||||||  |||||| ||  ||||||  ||  |||||||| ||||
Db    2128 GGCAAATAAAACACCACGACAATCCTTTTATCGAGCCGCTTCCGTCCAGACACAAACGGTGGTT 2187

Qy    2172 GGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCGCCCGTCCAGACACAAACGGTGGTT 2231

Db    2188 GACATGAAAGATGTTATGTGTCTTAAATGATATCATCATTGAACAAGCCGCTGGTCGGCATAGT 2247

Qy    2232 GATATGAAAGATGTGATGGTCCTGAATGACATCATCATTCAGGAGTGGGTATCGCTCATCGTCTTC 2291

Db    2248 CGTGCTAGTGAACGAGGTG-------------------------AGGACGATGACGAAGAT 2283

Qy    2292 CGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTCCCAACAGAGGACGATGACGAGGAT 2351

Db    2284 GGTCCCACATTCAAGGACATCGCCCTCGAATACATCCTAAAAGGCCGAGAATCTTTTGT 2343

Qy    2352 GGGCCGACGTTCAAAGACACTCGAAGTGATCCTCAAAGGCCATCAAAGCCATGATGTGTTTTGT 2411

Db    2344 GTATGGGACTGTGTTGGTGTGTTAAAATTCAGGAATGGGTGTCCTTTATTGTGTTC 2403

Qy    2412 GTGTGGGACTGTGTCGTGGGGTTTGGTTGAAATTTCAGGAGTGGGTATCGCTCATCGTCTTC 2471

Db    2404 GATCCATTCGTCGGAGCTCTTCATTACCCTGTATTGTGGTCAATACGATGTTTATGGCC 2463

Qy    2472 GATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGATGTTCATGGCA 2531

Db    2464 ATGGATCATCACGACGATCCGGAATTAGAGAAGTGTCTGAAAAGTGGTAACTATTTC 2523

Qy    2532 ATGGATCACCACGATATGAACAAGGAGATGGAACCGGTCTCAAGAGTGGCAACTATTTC 2591

Db    2524 TTCACGGCCACTTTTGCAATTGAAGCCAGCAGAAACTGATGGGCCATGAGCCCGAAGTAC 2583

Qy    2592 TTCACCGGCCACCTTTGCCCAAGCTCTTGCCCACACTTAATTTACTTACTCATTGATTATGGGACCACC 2651

Db    2584 TACTTCCAGGAAGGCTGGAACATTTGATTCATTATTGTGGCCTTGTCTCTGGAA 2643

Qy    2652 TATTTCCAGGAGGGCTGGAACATCTTGACTTCATTGTGACTTTGCATTATCATCTTTGCGGTG 2711

Db    2644 TTGGGCCTGGAGGGTGTCCAGGGCCTGTGTGTTGAGAGTTTTGTTGCTTGTGTA 2703

Qy    2712 CTGGGACTCGAGGGTGTCCAGGGTGTCCTATTGCGTTCCGTATTGCGTATGGGGCGTGTA 2771

Db    2704 TTCAAATTGGCAAAATCATGGCCCACACTCAATTTCATTGCATTGGGCCGGACA 2763

Qy    2772 TTCAAACTGGCCAAGCTCTTGCCCCACACTTAATTTACTTACTCATTGATTATGGGACCACC 2831

Db    2764 ATGGGTGCATTGGTAATCTGACATTTGACATCTGTACTTTGCATCTTTGTCATCTTTGCCGTG 2823

Qy    2832 ATGGGCGCTTTGGGTAATCTGACATTTGACTTTGCATTTGCATTCATCTTTCATCTTTGCGGTG 2891

Db    2824 ATGGGAATGCAACTTTCGGAAAGAACTATATTGACCAAGGATCGCTTCAAGGACCAT 2883

Qy    2892 ATGGGAAATGCAACTGTTCGGAAAGAAGAATTATCATGAGATCACAAGGACCGCTTTCCGGATGGC 2951

Db    2884 GAATTACCGCGCTGCAAATCATGGCCCACAGCTTCATGGCTTCATGATTGTCCGAGTG 2943

Qy    2952 GACCTGCCGCCGCTGCAATCTTGCCCCACAGCTTCATGATCGGTCTTCATGATCGTGTTCCGGGTG 3011

Db    3004 ATACCCTTCTTCTTGCCCGTCGTCGTGATAGGCAATCTTGTGGTTCTTAATCTTTTCTTA 3063

Qy    3072 ATTCCCTTCTTCTTGCCCGTCGTCATCGGCAATCTTGTGGTACTTAACCTTTTCTTA 3131

Db    3064 GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTTATCAGCCCGACAATGAT 3123

Qy    3132 GCCTTGCTTTTGTCCAATTTTGGCTCATCGGTTATCAGCCGCCGCCGATAACGAT 3191

Db    3124 ACCAATAAAAATAGCAGAGGCCTTCAATCGTATTGCTTCGTTTAAGAACTGGGTGAAACGT 3183

Qy    3192 ACGAATAAAAATAGCCCAGGCCTTCAATCGAATTGCGGATTTAAAAAGTTGGGTTAAGCGT 3251
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Qy    1047 ||  ||| ||||||||||||||| ||| ||||||| |||||||| || ||
           GGCAATAATATCCGGTGCGGGCGGCAATGCGACGACGATTACGTGTGCCTGCCTTGCCTGGGGGTTTGT 1105

Db    1051 CCAATCCCAACTACGACTCACCAGTTTCGATTCATTCGGCTTCCTTGTCGGCG 1110

Qy    1107 CCGAATCCGAATTATGGCCACCAGCTTCGATTCGTTCGGATGGGCTTCCTTCCTGTCCGC 1166

Db    1111 TTTCGTCTCATGACCCAAGATTTCTCGGAGGATCTGTATCAGCCACGTGCTGCTCGAAGCAGCT 1170

Qy    1167 TTCCGGCTGATGACACAGGAGACTTCTGGGAGGATCGTACCAGCTGGTGTTGCGGCCCGCC 1226

Db    1171 GGACCCTGGCACATGTTGTTCTTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTG 1230

Qy    1227 GGACCATGGCACATGCTGCTCTTCTTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTG 1286

Db    1231 AATTTGATTTTGCCATTGTTGCCATGTCTTTATGACGAATTGCAAAGAGAGGCCGAAGAA 1290

Qy    1287 AATTTGATTTTGCCATTGTTGCCATGTCTATGTGTATGCAGAATTGCAAAGGAGGCCGAAGAGA 1346

Db    1291 GAAGAGGCTGCCCAGGAGGAGGGCGATACGAGAGCTGAGAAGAAGCGGCCAGCCAAGGCG 1350

Qy    1347 GAAGAGGCTGCCGAAGAGGAGGGCGATACGTGAAGCTGAAGAACTGCCGCCCGCCCAAAGCG 1406

Db    1351 GCCAAACTGGAGGAGCGGCGGCCAATGCGCTCAAGCCGGCTCAGGATGCGGATGCC 1410

Qy    1407 GCCAAGCTGGAGGAGCGGCCAATGCGCCAGGCCAGCAGCGGATGCGGGCTGCCCGCC 1466

Db    1411 GCTGCGGGCAGCTGCATCCGAGATGGCAAAGAGTCCACGTACTCTTGCATTAGCTAT 1470

Qy    1467 GAGAGGGCGCACTGCATCCGGAAATGGCCAAGGTCCATCGCACGTATTCTTTGCATCAGCTAT 1526

Db    1471 GAACTGTTTGTTGGTGGCGGCAGGAGGAGGCAACGACGATGACAACAAGAGAAGATGTCCATA 1530

Qy    1527 GAGCTATTTGTTTAACTGCAGGGCGGATGACGTCAGTCTCTCACGAGAGAAGAGATGTCCATT 1586

Db    1531 CGCAGCGTCGAAGTGGAATCGGAGTCGGTGAGCGTTATACAAAGACAACCAGCACCTACC 1590

Qy    1587 CGGAGCGTCGAAGTGGAGTCGGTGAGCGTTATACAAAGACAACCAGCACCTACC 1646

Db    1591 ACAGCAC-CC--GCTACTAAAGTCCGTAAAGTTAGCACGACTTCCTTATCCTTACCTGT 1647

Qy    1647 ACAGCACCACCAAGCTACCAAAGTTCGTAAAGTGAGCACGACATCCTTATCCTTACCTGT 1706

Db    1648 TCACCATTTAACCTACGCCGGGATCACTAGTCATGGCATGGTTACAAGTACACAATACGAAATGGG 1707

Qy    1707 TCAAACTGGTTAACTAACATACGCCGGGGATCAGTTCTCACGAAGTACACGATACGGAACCGGA 1766

Db    1708 CGTGGACGTTTTGGTATACGGAGGTAGCGATCGCAAGCCATTGGTACTGGACAAACATATCAG 1767

Qy    1767 CGTTGGACGTTTTTGGTATACCCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG 1826

Db    1768 GATGCCCAGCAGCATTTGCCCTATGCCGATGAGCTCGGAATGCGTAACACCAATGTCCGAA 1827

Qy    1827 GATGCCCAGCAGCACTTGCCCTATGCCGACGACTCGGTAATGCGTCACCCCGATGTCCGGAA 1886

Db    1828 GAGAATGGTGCCATTATAGTTACGGCCTACTATTGTGAATTTAGGTTCAGACATTCTTCA 1887

Qy    1887 GAGAATGGGGCCATCATTATTGCCAAATTGCGGCAACTTTGCCCAACTTCAACTCATCG 1946

Db    1888 TATACCTCGGATCAATCAAGAATCTCGTATACAATCCACATGGTGATTTATTGGGTGGCATG 1947

Qy    1947 TATACCTCGCATCAGTCCGGAATATCGTATACCTCACAGTGGCGATCGGCGGCATG 2006

Db    1948 GCGGCCATGGGTGCCATTATAGTTACGGCCAGTCGCCAGTCGCCAACACGC 2007

Qy    2007 GCCGGTCATGGGCGGTCAGCACGAGTCGCAAATTGCCCGCAACACACGC 2066

Db    2008 AATCAATCAATCGGTGCTCGCAACCAATGGTGGCAGTAGTACGGCTGGTGGTGGCTATCCC 2067

Qy    2067 AATCAATCAGT-GG-GC-GCCACCCAATGGGCGCACCA---C--CTG-TC-TGGACA--CC 2114

Db    2068 GATGCCAATCACAGAGGAACAAAGGGATTATGAAATGGGTCAGGATTATACAGACGACGAAGCT 2127
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Db  4225 AATGCGCTGGTTCAAGCTATACCGTCCATCTTCAATGTGCTATTCGTGTGTCTCTGATATTT 4284
         |||||||||||||| |||||||||||||||||||||| ||||||| |||||||||||||||
Qy  4329 AATGCGCTGGTTCAAGCTATACCGTCCATCTTCAATGTGCTATTCGTGTGTCTAATATTT 4388

Db  4285 TGGCTTATTTTGCCATTATGGAGTACAGCTTTTTGCTGGAAAATATTTTAAGTGTAAA 4344
         ||||| ||||||||||||||||||| |||| |||||||||||||||||| ||||||||
Qy  4389 TGGCTAATTTTGCCATTATGGAGTACAGCTGTTTTGCTGGAAAATATTTTAAGTGCGAG 4448

Db  4345 GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGATTCGTAATGCCTGCAAAAGT 4404
         ||    | ||  ||| || |||| ||||||||| ||||  |||||||||| |||||||
Qy  4449 GACATGAATGGCACGAAGCTCAGCCCACGAGATCATACCAATCGCAATGCCTGCGAGAGC 4508

Db  4405 GAAAACTACACCTGGGAAAATTCGGCAATGAACTTCGATCATGTAGGCTAATGCCGTATCTC 4464
         || |||||||| ||||||||| || || |||||| |||| ||  ||||  |||||||||
Qy  4509 GAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATACCATCGATGTAACCGTATCTG 4568

Db  4465 TGTCTATTTCAAGTGGCCACCTTTAAGGGCTCGATCCAGATTGATGATGCCATTGAT 4524
         || ||||| ||| ||||||| ||| ||||||||  | ||||| |||||||||||||
Qy  4569 TGCCTTTTCCAAGTGGCCACCTTCAAAGCTGGATACAAATCATGACGATGCTATCGAT 4628

Db  4525 TCACGAGAGGTGGACAAGCAGCCGATCCGAGAAACCAATATCTACATGTATTTATATTTC 4584
         ||||||||||||||||||||||| |||||  |||||||||| ||| ||| ||| ||||
Qy  4629 TCACGAGAGGTGGACAAGCAACAATTCGTGAAACGAACATCTACATGTATTTATATTTC 4688

Db  4585 GTATTCTTCATTATATTTGGATCATTTTCACACTCAATCTGTTCATTGGTGTTATCATT 4644
         |||||||||||||||  |||||||| ||||||| ||||||||||||| ||||||||||
Qy  4689 GTATTCTTCATCATATTTGGATCATTTTCACACTCGTTCATCTGTTCATTGGTGTTATCATT 4748

Db  4645 GATAATTTTAATGAACAAAGAGAGAAAGCTGGTGGATCATTGAAAATGTTCATGACAGAA 4704
         ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Qy  4749 GATAATTTTAATGAGCAAAGAAAAGCAGGTGGATCATTAGAAAATGTTCATGACAGAA 4808

Db  4705 GATCAGAAAAGTACTATATTGCTATGAAAAGATGGGCTCTAAAAACCATTAAAACCC 4764
         ||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Qy  4809 GATCAGAAAAAGTACTATATTGCTATGAAAAGATGGGCTCTAAAAACCATTAAAACCC 4868

Db  4765 ATTCCAAGACCGAGGTGGCGACCACCAAGCAATAGTATTCGAAATAGTTACAGATAAAAAA 4824
         |||||||||||||||||||| |||||| ||| ||||||||| || |||| |||||||||
Qy  4869 ATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTGAAATAGTTGAAATAAGAAA 4928

Db  4825 TTCGATAATCATTGATGTTGTCATTGAAAACATGTTTACCGACCCTCGATCGG 4884
         |||||||| ||  |||||||||| |||| |||| ||||||||||||||||||||
Qy  4929 TTCGATAATCATTATGTTTATTCATTGGTCTGAACATGTTCATTGGTGTGATCGT 4988

Db  4885 TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAAACTCAATGCGATATTCGTAGTT 4944
         |||||| ||| |||| |||||||| |||||| ||| | | |||||||||||||| ||||
Qy  4989 TACGATGCGTCCGACACGTACAACCGGTCCTCAATGCGGATTCGGATATTCGTAGTT 5048

Db  4945 ATTTTCAGTGGCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATTCAAAGAG 5004
         ||||||||||||| ||||||||| ||||||||||||||||| ||||||||||||| |||
Qy  5049 ATTTTCAGTTGCGAATGTCTATTAAAAAATATTCGCTTTACGATATCACTATTTATTGAG 5108

Db  5005 CCATGGAATTTATTTGATGTAGTGTCATTTGTGTACCATCTTAGGTCTTGTACTCAGC 5064
         |||||||||||||||| |||| ||||  ||||||||||| || ||  |||||||||||
Qy  5109 CCATGGAATTTATTTGATGTAGTGTTGTCATTTGTCATCTTCCGGTCTTAGTACTTAGC 5168

Db  5065 GACATCATTGAGAAGTATTTCGTATCGCGGACACTGCTCCTTCAAGGGTATCCGACGTTGCGTTCGCG 5124
         || |||||| |||| ||| ||||| |  |||||||||||  ||||| ||||||||||||||| |||
Qy  5169 GATATATCGAAGTACTTCGTGTGTCCCGACCCCTGCTCCTCCGAGTGCGTGGTGGCGAAA 5228

Db  5125 GTGGGTCGTGTCCTCGCGTTAGTCAAGGGTATCCGACGGTTGCGTTGCTCCGG 5184
         ||||||| ||  | |||||||| |||||||||| |||| || |||||| |||||
Qy  5229 GTGGGGCCGTGTCCTCGACGTGGAAGGGAGCCAAGGGCATTCGGACACTGCTCTCGCG 5288

Db  5185 TTAGCCATGTCTGCCGCCTTATTGTCGCCTTATTCAACATTGTCTTGTCGTGTCGTTC 5244
         |||| ||||||| ||||| |   | | ||||||||||  |||| ||||||||||||||
Qy  5289 TTGGCCATGTCGCCTGCGCCCTGTCCAACATCGATTGATCAATGCATGTTC 5348

Db  5245 ATCTTTGCTATCTTTGGCATGTCCTCTTCATTGACGTGTCAAAGAGAGCGGCATAAAT 5304
         |||||||||||| ||  |||| ||||||||| ||||  |||||||||||  ||||||
Qy  5349 ATCTTTGCCATTTCGTCGTCTTCATGCACGTGACACGTGAAGGAGAGAGCGGCATTAAAC 5408

Db  5305 GCTGTGTATAATTTTAAGACATTTGGCCAAAGTATGATATAATTGCTTGTTCAGATGTACC 5364
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APPLICATION NUMBER: US 60/034,361
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,649
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE 6318 BP; 1713 A; 1341 C; 1597 G; 1667 T; 0 OTHER.

Query Match 56.4%; Score 3676; DB 21; Length 6318;
Best Local Similarity 84.9%; Pred. No. 0.00e+00;
Matches 4986; Conservative 0; Mismatches 806; Indels 84; Gaps 21;

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Db     151  ATACGATATGATGACGAGGACGAAGAGAAGGTCCACAGCCGGATCCACACTTGAACAG  210
            | |||||||| |||||| ||||| || ||||||||||| |||||||| |||||||||||
Qy     207  ATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGAACAG  266

Db     211  GGTGTGCCTATACCTGTTCGAATGCAGGGCAGTTCCCGCGGAATTGGCCTCCACTCCT  270
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     267  GGTGTGCCAATACCTGTTCGATTGCAGGGCAGTTCCCGCGGAATTGGCCTCCACTCCT  326

Db     271  CTCGAGGATGATCGATCCCTTCTACAGTAATGTACTGACATTTGTAGTAATAAGTAAAGGA  330
            |||||||||||| |||| ||||||||||||||||||||||||||||||  |||||  |||||
Qy     327  CTCGAGGATCGATCCCTACTACAGCAATCGTGACACTCGTAGTGTGTAAGCAAAGGA  386

Db     331  AAGGATATTTCGTTTTCTCGCCTCAAAAGCAATGTGCGTCGCTCGATCCATTCAATCCG  390
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Qy     387  AAAGATATTTTCGCATCACAAAGCAATGTGGATCGTCGATCCATTCAATCCG  446

Db     391  ATACGTCGTGTAGCCATTTATATTTTAGTGCATCCCTGTTTCGTTATTCATTATCACC  450
            |||||||||||||||| ||||| ||||| |||||| ||||||| |||| ||||||||||||
Qy     447  ATACGTCGTGTGGCCATTACATTCTAGTGCATCCTATTTTCCTATTCATCATCACC  506

Db     451  ACTATTCTAACTAATTGTATTTAATGATAATGCCGACACGCCCACGGTCGAATCCACA  510
            || ||||| || || | |||||| ||||||||| |||||||||||||| || |||||||||
Qy     507  ACAATTCTCCAACTGCATCCTGATGATAATGCCGACAACGCCCACGGTTGAGTCCACT  566

Db     511  GAGGTGAATTCACCGGAATCTACACATTGAATCACATTTGAATCAGCTGTTAAAGTGACGAGGT  570
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     567  GAGGTGATATTCACCGGAATCTACACATTGAATCACATTTGAATCAGCTGTTAAAGTGACGAGGT  626

Db     571  TTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTAGTA  630
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     627  TTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTAGTA  686

Db     631  ATAGCTTTAGCTTATGTGACCATGGCATAGATTTAGGTAATCTCGCAGCTTTGAGAACA  690
            ||||||||||||||||||||||||| | |||| | ||||||||||||||||||| || |||
Qy     687  ATAGCTTTAGCTTATGTGACCATGGTATAGATTTAGGTAATCTCGCAGCTTTGAGAACG  746

Db     691  TTTAGGTGACTGCGAGCTCTGAAAACCGTAGCCATTGTGCCAGTCTCAAAAACCATTGTC  750
            ||||||||||||||||||||| | |||| ||||| | ||||| |||| ||| |||||||
Qy     747  TTTAGGTGGTCGCAGCGCTTAAAACCGCTTAAAACCGGTTGCCATTGTGCCAGCCATCGTC  806

Db     751  GGTGCTGTCATTGAATCTGTAAAAAATCTACGGCGATGTGATAATTTGACAATGTTTCC  810
            ||||||||||||||||||||||||| |||| | | || | ||||||||| ||||||||||
Qy     807  GGGCGCCGTCATCGAATCGGTGAAGAATCTCGCGCGATGTGATTATCCTGACCATGTTCTCC  866

Db     811  CGTCGGTGTCGCGCTGATGGGCTACAAACTCTATATGGTGTTCTAACACAAAAGTGC  870
            |||||||||| |||||||||||| || || | || ||||| |
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Qy    5409  GAGGTCTACAACTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTCAGATGTCGACG  5468
            | || |||| |||||| ||||||||||||||||||| ||||||| || |||||||||| ||
Db    5365  TCAGCCGGTTGGGATGGTGTGTTAGATGCCATTATCAATGAGGAAGATTGCGATCCACCC  5424

Qy    5469  TCAGCCGGTTGGGATGGTGTACTGGACGTACTGGGCCATTATCAATGAGGAAGCAGCCACCC  5528
            ||||||||||||||| ||| |||| |||||||| |||| |||||||||||||||| |||||
Db    5425  GACAACGACAAGGGCTATCCGGGCAATTGTGGTTCAGCGACGTCTGGAATTACGTTTCTC  5484

Qy    5529  GACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTGAATAACGTTTCTC  5588
            |||| |||||| ||||||||||||||||||||||||||| ||| || ||| ||||||||||
Db    5485  CTTTCATATCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTC  5544

Qy    5589  CTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTC  5648
            || ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    5545  GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGTCTCACCGACGACGATTACGAT  5604

Qy    5649  GAGAACTATAGTCAGGACCGACCGGGACGGTCAACGACGGCAAGAGGGCTCAACGACGACGACGTACGAC  5708
            ||||||||||  ||| ||| |||||||| | | || ||| ||| ||  || |||||||| ||
Db    5605  ATGTACTACGAGATTTGGCAACAATTCGATCCCGGAGGGCCACCCAGTACATACGGCTACGAC  5664

Qy    5709  ATGTACTATGAGATCTGGCAGCAATTCGATCCCGGAGGGCACCCCAGTACATACGCTATGAT  5768
            |||||||| |||| || | |||| |||||||||| ||||||| ||| ||||||||| |||  |
Db    5665  CAGTGTCCGAGTTTCTGACGTGTTCTGGAGCCCGCCGCTGCAGATCCGAACAAG  5724

Qy    5769  CAGTGTCCGAATTCCTGACGTGTTACTGGAGCCTGCAGATCCGAGATCCCACCAAACCGAACAAG  5828
            ||||||||||| |||||||||||||  |||||| ||| |||||||||||  |||||||||||||
Db    5725  TACAAAATCATCGATGGACATGCCGATATGTCGGGCGGCCGACATGATGTACTGTGTGAT  5784

Qy    5829  TACAAGATCATATGATGACATACCCATCTGTCGCGGTGACCTCATGATGTACTGCGTCGAC  5888
            |||| ||||| | |||||  | | |||||||||  ||| ||  ||||||||||||  ||| |
Db    5785  ATATTGGATGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGGTAATCCAAGGGGAGACG  5844

Qy    5889  ATCCTGACGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAGAGGAGACG  5948
            ||| |||| ||||| || || |||||||||||||||||| ||||| ||||| |||||||||
Db    5845  GGTGAAATTGGTGAGATAGCGGCGGCGACCAGAGGCTATGATCCGGTGTCGTCA  5904

Qy    5949  GGTGAGATTGGTGAGATAGCGGCCGGCGATACGGACGGGCTACGAGCCCGTCTCATCA  6008
            |||||||||||||||||||||| ||| ||| ||||||| |||||||  |||| |||||
Db    5905  ACACTGTGGCGCCAGCGTGAGGAGTACTGCGCCAAGCTGATACAGAATGCGTGGCG  5960

Qy    6009  ACGCTGTGCGCGCTCACGGTGGGAGTACTCGCCCCGTAATCCAGCACGCCTGCGCG  6064
            || ||||||| ||| | || || |||||| |  |||| || |||||| ||||| ||
Db    6009  ACGCTGTGCGCGCTCACGGTGGGAGTACTCGCCCCGTAATCCAGCACGCCTGCGCG  6064
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RESULT 6
ID      US-08-808-793-1 STANDARD; DNA; UNC; 6318 BP.
AC      xxxxxx
DT
DE      Sequence 1, Application US/08808793
DE      Sequence 1, Application US/08808793
CC      GENERAL INFORMATION:
CC      APPLICANT: Soderlund, David M.
CC      APPLICANT: Ingles, Patricia J.
CC      TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
CC      TITLE OF INVENTION: AND USE THEREOF
CC      NUMBER OF SEQUENCES: 32
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC      STREET: Clinton Square, P.O. Box 1051
CC      CITY: Rochester
CC      STATE: New York
CC      COUNTRY: USA
CC      ZIP: 14603
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/808,793
CC      FILING DATE:
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:

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Qy   867  CTGTCGGTCGGTTCCGCGTTGATGGGCCTACAGATCTATAGGGCTGCTCACCGAGAAGTGC  926
          |||||| | |||| ||   ||||| | ||||||  |||||
Db   871  ATTAAACGATTCCCCTGACACGGCAGTTGGGCGAATCGACCGATGAAAAACTGGTTTTCTA  930

Qy   927  ATCAAGAAGTTCCCGCTGGACGCGTTCCTGGGCCAATCTGACGAGGAACTGGGACTAT    986
          ||||| |||||  |||  |||| |  || |||||||  ||||
Db   931  CACAATAGCAACAGTTCCAATTGGTTACGGAGAACGATGGCCAGTCATATCCGGTGTGC    990

Qy   987  CACAATCCGAATAGCTCCAATTGGTATTCCGAGGACGAGGCATTCATTCCGGTTATGC  1046
          ||||||  ||||   ||||||| | || |||| || ||  || |  || |||| |||
Db   991  GGGAATGTATCCGGTGCGGGACAAATGCGGCGAGGATTACGTCTGCCTGCCAGGGCTTCGGC  1050

Qy  1047  GGGAATGTATCCGGTGCGGGACAAATGCGGCGAGGATTACGTCTGCCTGCCAGGGCTTCGGC  1106
          |||  |||  | || |  ||||||||  || |  | |||  || |  ||  | ||||  ||
Db  1051  CCCAATCCCAACTACGACTCACACAGTTCGATGGCTTCATTCGGTTGGGCTTCCTGTCGGCG  1110

Qy  1107  CCGAATCCGAATATGGCTACACCAGCTTCGATTCGGATCGTTCGATTGGGCTTCCTGTCCGCC  1166
          ||||||||||||  |  || |||| ||  | || || |  || ||| |  ||||||| |||
Db  1111  TTTCGTCTCATGACCCAAGATTTCGTTCTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTG  1170

Qy  1167  TTTCCGGCTGATGACACAGAGACTTCTGGGAGGATCGGATGGATCGGGCCAATGTGTTGCGGGGTTTGT  1226
          ||||| |||||  || |||||  ||||  ||||
Db  1171  GGACCCTGGCACATGTGTTCTTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTG  1230

Qy  1227  TTCCGGACTGATGACACAGAGACTGTGTTCTTTGTCTTTATTGTCATCATCTTCCTAGGTTCATTCTATCTTGTG  1286
          ||||| |||||  || || ||  ||  |||| || ||| |||||||||||
Db  1231  GGACCGCGAGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTTGTTTTGT  1290

Qy  1287  AATTTGATTTTGGCCATTGTTGGCGGCGAGGAGGCGCAATCGGATGACGATGAAGGCCGAAGAA  1346
          ||||||||||||||||  |||||||||  |||| ||||  ||||||| || |  || |||||
Db  1291  GAAGAGGCTGCCGAGGAGGAGGCGCGATACGAGAAGCCGAGAAGAAGCGGCCGCAGCCAAGCGG  1350

Qy  1347  GAAGAGGCTGCCGAGGAGGAGGCCGGATACGTGAAGCGGCAAGAGAAGCGGCCGCAGCCAAGCGG  1406
          ||||||||||||||||||||||| ||||  ||||||||  |||||||||||||||||  || |
Db  1351  GCCAAACTGGAGGAGGCGGGCCAATGAGCTCAGCGCTCCAGGATGCAGCCGATGCC  1410

Qy  1407  GCCAAGCTGGAGGAGGCGGGCCAATGAGCTCAGCGCTCCAGGATGCAGCCGATGCC  1466
          ||||| || ||||||||||||||||  | |||||  ||||   ||| | | |||||||
Db  1411  GCTGCGCCAGCTCTGCATCCCGAGATGCGCAAATGCCCCACGTCCCACGCTACTCTTGCATTAGCTAT  1470

Qy  1467  GAAGAGGCTGCACTGTCTGCATCGCATCCGGAAATGCCGTATTCTTGCATTCAGCTAT  1526
          |||||||  | ||| ||  |||| || |  ||| ||||||||  ||| |||||||||
Db  1471  GAACTGTTTGTTGGGCGGCGGCGAGAGGCCAACGATGACACAAACAAAGAGAAGTGGAAATGGG  1530

Qy  1527  GAGCTATTTGTTGGGCGGCGGCGAGAGGCAACGATGACAACAAAGAGAAGAGAAGTGGTCCATT  1586
          | ||||| |||||||||||||||||||| |||||| |  ||||||||||| ||||  | | ||
Db  1531  CGCAGGCTCGAAGTGAATCGGAGTCCGTAAAGTAGCACGCAAGAACCAGCCAGCCACCTACC  1590

Qy  1587  CGCAGGCTCGAAGTGAATCGGAGTCCGTATACAGCGTATACAAAGAACAACCAGCCACCTACC  1646
          | |||||  ||    |  ||||| |   |  ||| ||   ||||
Db  1591  ACAGCAC-CC--GCTACTAAAGTCCGTAAAGTCCGTATCCTTCCTATCCTTGGT  1647

Qy  1647  ACAGCACCACCAAGTTCGTAAAGTGAGCACGAATCGGCACATTCCTTCCTATCCTTGGT  1706
          |||||||| || |||||||||||||  || || || |||| |||| ||||| ||||||||
Db  1648  TCACCATTTAAGTTGCCATTAGTTCACAAGTCACAACAGTACAATACGAACGGA  1707

Qy  1707  TCACCGTTTAACGTCACTAGTTCACAAGTCACAACAGTACAATACGGAACGGA  1766
          |||| |||||  ||||  ||||||||||||||||||||||  |||||| ||||
Db  1708  CGTGGACGTTTTGGTATACCAGTAGGCGATCGGAGTCGTGAGCGTTAACACCAGTGTCAAAACATAGCAG  1767

Qy  1767  CGTGGCCCAGGACGTTTTGGTATACCCCTAGGCGATCGGAGTCGTGAGCGTTATTGGTCGTAACCCGATCTTAACCAATTGTCAACAATATCAG  1826
          |||||||  |||||  |||||||||||| |||||  |  ||| ||| |||||
Db  1768  GATGCCCAGCGAGCATCCTGCCCTATGCCGAGATCGGCCGATGACTGGAAAGCGGTAACACCAATGTCCGAA  1827

Qy  1827  GATGCCCAGCAGCACTTGCCCTATGCCGAGACTCGGAAGTGCCGTATCCGACGTCACCCCGATGTCCGAA  1886
          |||| |||  |  ||||||| || |||| | ||||||||||||  ||||
Db  1828  GAGAATGGTGCCATTAGTACCAGCTACATTGTAATTAGGTTCTAGACATTCTTCA  1887

Qy  1887  GAGAATGGGGCCGCATCATAGTGCCCGGTGTATCATAGTGCCCGGTACTCAGGCTACACTCG  1946
          |||||||||  ||  |   ||| |  |  ||| | |    |  || ||||  ||||||||  |
Db  1888  TATACCTCGCCATCAATCAAGAATCTCGTATACAACTCAGTGGTTGATTTGATTTATTGGGTGGCATG  1947

Qy  1947  TATACCTCGCCAATGATCCCGAATATCGTATAACCTCACATGGGCGAATCTACTCGGCCGGCATG  2006
          |||||||||| ||| ||||| |||||||||||||  ||||  |||||  | ||||||||||||
Db  1948  GCGGCCATGGGTGCCAGCACAATGACCAAAGAGAGCAAATTGCGCAGTCGCAGTCCCAACACGC  2007

Qy  2007  GCGGCCATGGGTGCCAGCACAATGACCAAAGAGAGCAAATTGCGCAGTCGCAGTCCCAACACGC  2066
          |||  |||||  |  | |||   | ||||     | |  | |  ||  |  |||   |||||
Db  2008  GCCGTCATGGGCCGTCAGCGAATCAATGCAGAGGAGCAAATTGCGCAACCGCAGCAAATTGC  2067

Qy  2067  AATCAATCAAT----C--GG-GC--GCCACCAATGGTGCGCGGCCACCA---C--CTG-TC-TGGACA--CC  2114
          |  |||||||| |  || || |  |  |||||     ||| |  |  | |  |   |   ||| |   |
Db  2068  AATCAATCAGTCAAGGCCAGTTGGGCAATCTGACGAGGAACTGGGACTAT  2127

Qy  2115  AATCAACAAGCTC---GATCATCGCGACTACGAAATTGGCCTGGACTGCACCGGACGAAGCT  2171
          |||||  ||| |     |||| | |  |||||| |||| || ||||  | |  || |||
Db  2128  GGCAAAATAAAACACCACGACAATCCTTTATCGAGCCCGTCAAACTCAAACAGTGGTA  2187

Qy  2172  GGCAAGATTAAACATCATGACAATCCTTTATCGAGTGAGCCCGTCCAGACAACACAACGGTGGTT  2231
          ||||| ||||| |  || |||||||| |  || ||  | || |||| |   |   ||| ||||
Db  2188  GACATGAAAGATGTTATGGTCTTAAATGATATATCATTGACACATCAGTGAATGACACATCAGTG  2247

Qy  2232  GGCAAGATTAAACATGACAATCCTTTATCGAGTGAGCCCGTCGTGTCGGCGGCACAGT  2291
          |                                      ------------AGGACGATGACGAAGAT
Db  2248  CGTGCTAGTGAACGAGTG                                   2283

Qy  2292  GGGCCAAGCGACTCGCGGGGTGTCCGTCTCCGTTGCTCCGTTACTATTTCCCAACACATCCAACATCTTTGT  2351
          |  || | | | |  | ||  |   |  |  |||  | |||   ||| |||||| | || || |||
Db  2284  GGTCCCACATTCAAGGACACGGCCCTCGAATACATCCGAATACATCCTCAAAGGCATCTTTTGT  2343

Qy  2352  GGGCCGAGCGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTTGTTTTGT  2411
          |  ||||||| || |||||||||| | |||||| ||| |  || |  |||||||||||||| |
Db  2344  GTATGGGACTGTTGTTGGGCGTGTGTTAAAATTCAGGATGGGTGTCTTTATTGTGTTC  2403

Qy  2412  GTGTGGGACTGTTGCTGGGGTTTGGTTGGTTGTGAAATTTCAGGATGTGGTGTATCGTCCTCTC  2471
          | ||||||||||| ||||| |||| |||| |  |||||||||||| | ||| ||| |||| | |
Db  2404  GATCCATTCGTGGAGCTCTTCATTACCCTGTGTATTACGATGTTTAATGCC  2463

Qy  2472  GATCCCTTCGTCGCGACTCTCATCACGCGTGCGTGCATTGCGTGTTCACGATGTTCATCGGCA  2531
          |||||  ||| | | |||| ||| || | ||| | | || |||| | ||||||| || |  ||
Db  2464  ATGGATCATCACGACACATGAATCCGGAATTGAGAGAAGTTGCTGAAAAGGTGGTAACTATTTC  2523

Qy  2532  ATGGATCACCACGACACATGAATCAACAAGGAGATGGAACGCGCGTCTCAAGAGTTGGCAACTATTTC  2591
          |||||||| || |||||| |||   ||||| |||  || |||  | |||| |||| ||||| ||||
Db  2524  TTCACGGCCCACTTTGCAATTGAAGCCAGCCCGAAACTGAAAGCTGAGCCCCAAGTAC  2583

Qy  2592  TTCAAACCGCCAAGTTCTTGGCCCCATCGAGCGGCCAATGAAGGCCATGAGCCCCAAGTAC  2651
          ||||  ||| ||| ||||||||||||  |  ||  ||||  ||||||||| |||||| |||
Db  2584  TACTTCCAGAAGGCTGGAACATTTCGATTTCATTATTGTGGGCTTGTCTCTGGAA  2643

Qy  2652  TATTTCCAGGAGGGCTTTGGGTAATCTGCACTTCATTATTGTACTTTGCTTGCGTTATTGGAA  2711
          || ||||||||| || |||||||  ||| |  | |||||| |  |||||  | |||| |||||
Db  2644  TTGGGCCTGGAGGGGTCCAGGGGTGTCCAGGGGTCTGTTGAGAAGTTTTCGTTTCGTTGTGTA  2703

Qy  2712  CTGGGACTCCAGGGGTGTCCAGGGGTCTGTCGTATTGCGTTTCCTTCGATTGCTGCGTGTA  2771
          ||||| ||||||||||| ||||||| | ||  | | ||||| | | ||||| | | |||||
Db  2704  TTCAAATTGGCAAAATCATGGCCCCACCACTCAATTTACTCATTTACTCATTATGGGGACGCACC  2763

Qy  2772  TTCAAACTGGCCAAGTCTTGGCCCCAAGTTAATTTACTTATCATTATGGGACGACGGA  2831
          ||||| |||||||||  ||||||||| |||||||||| | || |||||||| | ||||
Db  2764  TACTTCCAGGAAGGCTGGAACATTTCGATTTATCATTCTTGCATTTCTCATCTTTGCCGTG  2823

Qy  2832  ATGGGTGCATTGGGTAATCTGCTTATCTGACTTGTGACTTGTACTTTGTCATTATCATCTTGCGTG  2891
          |||||||| ||||||||  ||||  |  || ||| |||  ||| ||| | ||||| ||| ||
Db  2824  ATGGGTGCTTTTGGGTAATCTGCTTATCTGACTTTGTGACTTTGTACTTTGTCATTATCATCTTTGCCGTG  2883

Qy  2892  ATGGGGATGCAACTTTTCGGAAAGAACTATATTGGACCACAAGGATCGCTTCAAGGACCAT  2951
          |||||||| |  | ||||| |||| ||| | || ||  |||||| || || ||||| ||
Db  2884  GAATTACCGCGGCCGCGGAACTTCACCGACTTCATGATTCCGAGTG  2943

Qy  2952  GATGCCCAGCCGCGGTCCTGCGGAACTTCACCGACTTCATGATCATGATCGTGTCCCGGGTG  3011
          |   |   || || |   |||| ||||||||||||||||||||  |   |  | ||  | ||
Db  2944  CTGTGCCGAGAATGGATCGAGTGCATGCATGGGACTGACTCGATGTATGGCGGATGTCTCAGCTGT  3003

Qy  3012  CTCTGCCGGAGAATGGATCGAGTGCATGCATGGGACTGACTCGATGTATGGCGGATGTCTCGTGTGC  3071
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Db    3004 ATACCCTTCTTCTTGGCCACGGTCGTGATAGGCAATCTTGTGGTTCTTAATCTTTTCTTA 3063
           || ||||||||||||||||| || || || |||||||||||||| ||||| |||||||||
Qy    3072 ATTCCCTTCTTCTTGGCCACCGTTGTCATCGGCAATCTTGTGGTACTTAACCTTTTCTTA 3131

Db    3064 GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTTATCAGCCCCGACTGCCGACAATGAT 3123
           || |||||||||||||| || || |||||||| |||||||| ||||||||||| || |||
Qy    3132 GCCTTGCTTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGAT 3191

Db    3124 ACCAATAAAATAGCAGAGGCCTTCAATCGTATTGCTCGTTTTAAGAACTGGGTGAAACGT 3183
           || ||||||||||| |||||||||||||| ||||  || ||||| |  ||||| || |||
Qy    3192 ACGAATAAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTTGGGTTAAGCGT 3251

Db    3184 AATATTGCCGATTGTTTTAAGTTAATTCGAAATAAATTGACAAATCAAATAAGTGACCAA 3243
           |||||||| |||||||| |||||||| || || ||||||||||||||||||||||| |||
Qy    3252 AATATTGCTGATTGTTTCAAGTTAATACGTAACAAATTGACAAATCAAATAAGTGATCAA 3311

Db    3244 CCATCAG---------------A-A-CA--------TGG--CGAT-A--ATG-------- 3265
           |||||||               | | ||        |||  |||  |  |||
Qy    3312 CCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTTGGAGCGAAGAGCATGGTGACAAC 3371

Db    3266 -AACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTTGATCAAAAAGGGTATGAAG 3324
            |||||||| |||| || ||||| ||| | | ||| ||| | ||||| ||||| || |||
Qy    3372 GAACTGGAGCTGGGCCACGACGAGATCCTCGCCGACGGCCTCATCAAGAAGGGGATCAAG 3431

Db    3325 GGCGAGACCCAGCTGGAGGTGGCCATTGGCGATGGCATGGAGTTCACGATACATGGCGAT 3384
           |   |||| || |||||||||||||| || ||| | ||||| ||||||||||| |||||
Qy    3432 GAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGATACACGGCGAC 3491

Db    3385 ATGAAAAACAACAAGCCGAAGAAATCAAAATTCATGAACAACACAACGATGATTGGAAAC 3444
           ||||| |||||||||||||||||||| ||||   | || ||| ||||||||||||| |||
Qy    3492 ATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCAAC 3551

Db    3445 TCAATAAACCACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGGTTTGTCCATA 3504
           ||||| |||||||||||||||||||||||||| |||||||||||||||||||||||| ||
Qy    3552 TCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCCTTA 3611

Db    3505 CAGGACGATGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG 3564
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3612 CAGGACGACGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG 3671

Db    3565 GACGAGAGCCACAAGGGCAGCGCCGAGACCATCGAGGGCGAGGAGAAACGCGACGTCAGC 3624
           ||||||||||||||||||||||||||||| || |||||||||||||| ||||||| ||||
Qy    3672 GACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGCGCGACGCCAGC 3731

Db    3625 AAAGAGGACCTCGGCCTCGACGAGGAACTGGACGAGGAGGCCGAGGGCGATGAGGGCCAG 3684
           || |||||  | || ||||||||||||||||||||||||| |||  |||| ||||||| |
Qy    3732 AAGGAGGATTTAGGTCTCGACGAGGAACTGGACGAGGAGGGCGAATGCGAGGAGGGCCCG 3791

Db    3685 CTGGATGGTGACATTATCATTCATGCGCAAAACGACGACGAGATAATCGACGACTATCCG 3744
           || || ||||| || || |||||||| ||   |||||| || ||| |||| || |||||
Qy    3792 CTCGACGGTGATATCATTATTCATGCACA---CGACGAGGATATACTCGATGAATATCCA 3848

Db    3745 GCCGACTGTTTCCCCGACTCGTACTACAAGAAGTTTCCGATCTTGGCCGGCGACGAGGAC 3804
           || || || | |||||| |||||||| ||||| ||||||||||| ||||| ||||| |||
Qy    3849 GCTGATTGCTGCCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGAC 3908

Db    3805 TCGCCGTTCTGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCAATTAATTGAAAAT 3864
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3909 TCGCCGTTCTGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCAATTAATTGAAAAT 3968

Db    3865 AAATATTTTGAAACCGCAGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCCTTA 3924
           |||||||||||||| || |||||||||||||||||||||||||||||||||||||| |||
Qy    3969 AAATATTTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTA 4028

Db    3925 GAAGATGTTCATTTACCCGATCGACCTGTCATGCAGGATATACTGTACTACATGGACAGG 3984
           |||||||| ||| | ||  |  ||||  |  ||||||||||  | ||||| ||||||||
Qy    4029 GAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTTATACTATATGGACAGA 4088

Db    3985 ATATTTACGGTGATATTCTTTTTGGAGATGTTGATCAAATGGTTGGCCCTGGGCTTTAAG 4044
           ||||||||||| |||||||| ||||| ||||| ||||| |||||||| || ||||| ||
Qy    4089 ATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAA 4148

Db    4045 GTTTACTTCACCAATGCCTGGTGTTGGCTGGATTTCGTGATTGTCATGCTATCGCTTATA 4104
           || ||||||||||| || ||||||||||| |||||||||||||||||| ||||||||||
Qy    4149 GTGTACTTCACCAACGCGTGGTGTTGGCTCGATTTCGTGATTGTCATGGTATCGCTTATC 4208

Db    4105 AATTTGGTTGCCGTTTGGTCGGGCTTAAATGATATAGCCGTGTTTAGATCAATGCGCACA 4164
           || || |||||          ||      || |||    |  || |   | ||||| ||
Qy    4209 AACTTCGTTGCTTCACTTGTTGGAGCTGGTGGTATTCAAGCCTTCAAGACTATGCGAACG 4268

Db    4165 CTGCGCGCCCTAAGGCCATTGCGTGCTGTCTCTAGATGGGAGGGTATGAAAGTTGTCGTG 4224
            |  | || || || ||| | |||||  | ||  |   | |||| ||||  || |||||
Qy    4269 TTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGGTCGTCGTT 4328

Db    4225 AATGCGCTGGTTCAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTCTGATATTT 4284
           ||||||||||| ||||||||||||||||||||||||||||||||||||||||| ||||||
Qy    4329 AATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTCTAATATTT 4388

Db    4285 TGGCTTATTTTTGCCATTATGGGAGTACAGCTTTTTGCTGGAAAATATTTTAAGTGTAAA 4344
           ||||| ||||||||||| ||||| ||||||||||||||||||||||||||||||||  |
Qy    4389 TGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTAAGTGCGAG 4448

Db    4345 GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT 4404
           ||    |||| |||   ||| ||||| || |||||||| ||||| ||||||||| | ||
Qy    4449 GACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATCGCAATGCCTGCGAGAGC 4508

Db    4405 GAAAACTACACCTGGGAAAATTCGGCAATGAACTTCGATCATGTAGGTAATGCGTATCTC 4464
           || |||||||| ||||  ||||| |||||||| ||||||||||||||||| ||||||||
Qy    4509 GAGAACTACACGTGGGTGAATTCAGCAATGAATTTCGATCATGTAGGTAACGCGTATCTG 4568

Db    4465 TGTCTATTTCAAGTGGCCACCTTTAAGGGCTGGATCCAGATTATGAACGATGCCATTGAT 4524
           || || || |||||||||||||| || |||||||| || || ||||||||||| || |||
Qy    4569 TGCCTTTTCCAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGAT 4628

Db    4525 TCACGAGAGGTGGACAAGCAGCCGATCCGAGAAACCAATATCTACATGTATTTATATTTC 4584
           |||||||||||||||||||| || || || ||||| || |||||||||||||||||||||
Qy    4629 TCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATTTATATTTC 4688

Db    4585 GTATTCTTCATTATATTTGGATCATTTTTCACACTCAATCTGTTCATTGGTGTTATCATT 4644
           ||||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    4689 GTATTCTTCATCATATTTGGATCCTTTTTCACACTCAATCTGTTCATTGGTGTTATCATT 4748

Db    4645 GATAATTTTAATGAACAAAAGAAGAAAGCTGGTGGATCATTAGAAATGTTCATGACAGAA 4704
           |||||||||||||| |||||||| ||||| ||||||||||||||||||||||||||||||
Qy    4749 GATAATTTTAATGAGCAAAAGAAAAAAGCAGGTGGATCATTAGAAATGTTCATGACAGAA 4808

Db    4705 GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCATTAAAAGCC 4764
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4809 GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCATTAAAAGCC 4868

Db    4765 ATTCCAAGACCGAGGTGGCGACCACAAGCAATAGTATTCGAAATAGTTACAGATAAAAAA 4824
           ||||||||||| ||||||||||||||||||||||| || |||||||| || ||||| |||
Qy    4869 ATTCCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAA 4928

Db    4825 TTCGATATAATCATTATGTTGTTCATTGGCTTAAACATGTTTACCATGACCCTCGATCGG 4884
           |||||||||||||||||||| ||||||||  | |||||||| |||||||||||||||||
Qy    4929 TTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATCGT 4988

Db    4885 TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAAACTCAATGGGATATTCGTAGTT 4944
           ||||| || || ||  |||| |||   ||||| ||| | ||||||| |||||||||||||
Qy    4989 TACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGATATTCGTAGTT 5048

Db    4945 ATTTTCAGTGGCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATTTCAAAGAG 5004
           |||||||||  |||||||||||||||||||||||||||||||||||||||||| |  |||
Qy    5049 ATTTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATTTTATTGAG 5108

Db    5005 CCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTCAGC 5064
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Qy    5109 CCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTTAGC 5168

Db    5065 GACATCATTGAGAAGTATTTCGTATCGCCGACACTGCTCCGTGTGGTGAGAGTGGCCAAA 5124
           || || || |||||||| ||||| |||||||| |||||||| |||||| | ||||| |||
Qy    5169 GATATTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTGTGGCGAAA 5228

Db    5125 GTGGGTCGTGTCCTGCGTTTAGTCAAGGGTGCCAAGGGTATCCGGACGTTGCTGTTCGCG 5184
           ||||| |||||||| ||  | || ||||| |||||||| || |||||  |||| ||||||
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CC     ZIP: 14603
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, Version #1.30
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: PCT/US97/24256
CC       FILING DATE:
CC       CLASSIFICATION:
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 08/772,512
CC       FILING DATE: 24-DEC-1996
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Goldman, Michael L.
CC       REGISTRATION NUMBER: 30,727
CC       REFERENCE/DOCKET NUMBER: 19603/602
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: 716-263-1304
CC       TELEFAX: 716-263-1600
CC   INFORMATION FOR SEQ ID NO: 2:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 6315 base pairs
CC       TYPE: nucleic acid
CC       STRANDEDNESS: single
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA
SQ   SEQUENCE 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 OTHER.

Query Match               56.3%;   Score 3664;  DB 1;   Length 6315;
Best Local Similarity     84.8%;   Pred. No. 0.00e+00;
Matches 4980;  Conservative  0;  Mismatches 812;  Indels 84;  Gaps 21;

Db   151 ATACGATATGATGACGAGGACGAAGATGAAGGTCCAGCCGGATCCACACTTGAACAG 210
         |  |||||||||||||||||||||| ||||||||||||||| |||  || |||| ||||||
Qy   207 ATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTGAACAG 266

Db   211 GGTGTGCCTATACCGTGTCGAATGCAGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT 270
         |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   267 GGTGTGCCAATACCGTGTCGAATGCAGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT 326

Db   271 CTCGAGGATATCGATCCCTTCTACAGTAATGACTAATGGTAGTAATAAGTAAGGA 330
         |||||||| |||||||| |||||| ||||||||||||||||| ||||  ||||||
Qy   327 CTCGAGGATATCGATCCCTACTACAGCAATGTACGACTAGTTGTAAGCAAAGGA 386

Db   331 AAGGATATATTTTCGTTTTTCTGCCTCAAAAGCAATGTGCTCGATCCATTCAATCCG 390
         ||||||||||||||||||||||||||||||||| |||| |||||||||||||| ||||
Qy   387 AAAGATATTTTTCGCGTTTTCTGCCATCAAAAGCAATGTGGATGCTCGATCCATTCAATCCG 446

Db   391 ATACGTCGTGTAGCCATTATATTTAGTGCATCCCTTGTTTTCGTTATTCATTATCACC 450
         ||||||||||||||||||||||||| ||||||||||||||| |||||||||||||||||
Qy   447 ATACGTCGTGTGGCCATTACATTCAGTGCATCCCATTATTTTCCCTATTCATCATCACC 506

Db   451 ACATTCTAACTAATTGTATTTAATGATAATGCCGACAACGCCACCGTCGAATCCACA 510
         |  ||||   | |  ||   |||| ||||| |||||||||||||||||||| || |||||
Qy   507 ACAATTCTCGTCAACTGACATCCTGATGATAATGCCGACAACGCCACCGTTGAGTCCACT 566

Db   511 GAGGTGATATTCACCGGAATCACACATTGAATCAGCTGTTAAAGTGATGGACGAGGT 570
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   567 GAGGTGATATTCACCGGAATCACACATTGAATCAGCTGTTAAAGTGATGGACGAGGT 626

Db   571 TTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGCATAGATTTAGGTAATCTCGCAGCTTTGAGAACA 630
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   627 TTCATTTTATGCCCGTTACGTATCTTAGAGATGCATGGCATAGATTTAGGTAATCTCGCAGCTTTGAGAACA 686

Db   631 ATAGCTTAGCTTATGTGACCATGGCATAGATTTAGGTAATCTAGCAGCTTTGAGAACA 690
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   687 ATAGCTTAGCTTATGTGACCATGGTATAGATTTAGGTAATCTAGCAGCTTTGAGAACA 746

Db   691 TTTAGGGTACTGCGAGCTCTGAAAACCGTAGCCATTGTCCAGGTCTAAAAACCATTGTC 750
         |||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||
Qy   747 TTTAGGGTGCTGCGAGCCGTTAAAACCGTAGCCATTGTGCCAGGTCTTGAAGACCATCGTC 806
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Qy  5229 GTGGGCCCGTGTCCTTCGACTGGTGAAGGGAGCCAAGGCATTCGGACACTGCTCTTCGCG 5288
         |  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5185 TTAGCCATGTCGTTGCCTGCCTTATTCAACATTTGTCTGTTCTTGTTCCTGTTGATGATGTTC 5244
         ||  ||||||  || |  ||   ||||||||||||| |||| ||| |||||||||||
Qy  5289 TTGGCCATGTCGCTGCCGCCCTGTTCAACATCTGCTTGCTCGTGTTCCTGTTCATGTTC 5348
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5245 ATCTTTGCTATCTTTTGGCATGTCCTTCTTCATGCATGTCAAAGAGAAGAGCCGCATAAAT 5304
         |||||| ||  || || |  |||||||||  || |  |||||| |||||  ||
Qy  5349 ATCTTTGCCATTTTCGGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCCGCATTAAC 5408
         |||||| |  | || |||||||||| |||||||||| ||||||||||||||||||||||
Db  5305 GCTGTGTATAATTTTAAGACATTTGGCCAAAGTATGATATTGCTGTTTCAGATGTCTACC 5364
         |||||| || ||||   ||| ||||||||||||| || ||||||||||||| ||||
Qy  5409 GACGTCTACAACTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTCAGATGTCGACG 5468
         |  |||||| |  | |||||||  ||||||||| || || ||||||||||| |||||||
Db  5365 TCAGCCCGGTTGGGATGGCGTGTTAGATGCCCATTATCAATGAGGAAGATTGCGATCCACCC 5424
         || |  || |  ||||||||| |  || ||||| |||||||||||||||||||||
Qy  5469 TCAGCCCGGTTGGGATGGCGTACTGGACGCCCATTATCAATGAGGAAGCATGCCGATCCACCC 5528
         ||||||||||||||||||||||  || ||||| |||||||||||||||||||||||
Db  5425 GACAACGACAAGGGCTATCCGGGCAATTGTGGTTCAGCGACTGTTGAATTACGTTTCTC 5484
         ||| ||||  ||||||||||  ||||| ||||||||||||| || |  |||||||||||
Qy  5529 GACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCACCGTTGGAATAACGTTTCTC 5588
         ||| || ||| |||||||| ||||| ||  ||||||||||||||||||||||||
Db  5485 CTTTCATATCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTCGTCATTCTC 5544
         |    | || ||  ||||| |||| |||||||||||||||||||||||||||||||||
Qy  5589 CTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTGTCATTCTC 5648
         ||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  5545 GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGGTCTCACCGACGATTACGAT 5604
         |||||||| ||  |||| |  |  || || ||||||| |||||||||||||||||||
Qy  5649 GAGAACTAGTAGTCAGGCGACGTGCAAGAGGGTCTAACCGACGACGACTACGAC 5708
         |||||||||||||||||||||||||||||||||||||||||| |  ||||||
Db  5605 ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGGCACCCAGTACATAACGCCTACGAC 5664
         ||||| ||||| |||| ||||| ||||||||||||||||||||||||||||||||  |
Qy  5709 ATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATACGCCTATGAT 5768
         |||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db  5665 CAGCTGTCCGAGTTTCTGGACGTGCTGGAGCCGCCGCTGCAGATCCAAAGCCGGAACAAG 5724
         |||||||||||||||||||||||||||||| |  ||||| |||| |||||||||||
Qy  5769 CAGCTGTCCGAATTCCTGGACGTACTGGAGCCCGCGCTGCAGATTCCACAAACCGGAACAAG 5828
         ||  ||||||||||||||||||||| ||||||||| |||||| || |||||||||||
Db  5725 TACAAAATCATATCGATGGACAATGCCCATCGTGTCGCGTGATGTACTGTGTGGAT 5784
         ||| || |||||| ||||| || |||| |  ||  |||||||||| || ||||
Qy  5829 TACAAGATCATATCGATGGACATACCCATCGTGTCGCGTGATGTACTGCGTCGAC 5888
         |||||| | || |||||||||| ||  ||||||||| |||||||||||||||||
Db  5785 ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAATCCGATCAGGAGGACG 5844
         ||  ||||||||| ||  || |||| |||||||||||| |  || |||||||||||
Qy  5889 ATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGCAAGGGCAATCCGATAGAGGAGACG 5948
         |  ||  ||||||||||||||| |||||||||||||||||| || |||||||||||||||
Db  5845 GGTGAAATTGGTGAGATAGGCGCGCGGACCAACGCGAGGGCTATGATCCGGTCGTCGTCA 5904
         ||||||||||||||||  ||   || || |   ||||||| || |||||||||||||
Qy  5949 GGTGAGATTGGTGAGATAGCCGGCCGCGGGACGCCGATACGGAGGGCTACGAGCCCGTCATCA 6008
         |||||||||| ||||||||||||| ||||||||  ||  ||||||||||||||||
Db  5905 ACACTGTGGCGCCAGCGTGAGGAGTACTGCGCCAACTGATACAGAATGCGTGGCG 5960
         ||||||||| ||||||||||||||||  ||   ||| |  |  ||||||||||
Qy  6009 ACGCTGTGGGCGTCAGCGTGGCCGTCTGAGGAGTACTGCGGCTAATCCAGCCACGCCCTGGCG 6064
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RESULT 7
ID   PCT-US97-24256-2 STANDARD; DNA; UNC; 6315 BP.
AC   xxxxxx
DT
DE   Sequence 2, Application PCT/US9724256
CC   Sequence 2, Application PCT/US9724256
CC   GENERAL INFORMATION:
CC     APPLICANT: Cornell Research Foundation, Inc.
CC     TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC     TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
CC     TITLE OF INVENTION: FLIES
CC     NUMBER OF SEQUENCES: 19
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
CC       STREET: Clinton Square, P.O. Box 1051
CC       CITY: Rochester
CC       STATE: New York
CC       COUNTRY: USA

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Db   751 GGTGCTGTCATTGGTGAATCTGTAAAAAATCACGGCGATGTGATAATTTTGACAATGTTTTCC  810
         ||  ||  ||  ||||||| || || ||||||||||  ||  ||   ||||||| || ||||
Qy   807 GGGCCGTCATCGAATCGGTGAGAGAATCGCGCGCATGTGATTATCCGATTATCCTGACCATCTTCTCC  866

Db   811 CTGTCGGTGTTCGCGTTGATGGGCCTACAAATCTATATGGTGTTCTAACACAAAAGTGC  870
         ||||||||| |||  ||  |||| ||  |  || ||||  ||
Qy   867 CTGTCGGTGTTCGCGTTGATGGGCCTACAGATCTATATGGCGTGCTCACCGAGAAGTGC  926

Db   871 ATTAAACGATTCCCCTGGACGGCAGTTGGGGCAATCTCGACGGATGAAAACTGGTTTCTA  930
         ||  ||||   |||||||| | |||  ||| ||||  |   ||||  ||| || ||||
Qy   927 ATCAAGAAGTTCCCGCTGGACGGTTCCTGGGCAATCTGACCGAGAGAACTGGGACTAT  986

Db   931 CACAATAGCAACAGTTCCAATTGGTTACGGACGAACGATGGCGAGTCATATCCGGTGTGC  990
         ||||  |  ||||| |||||||||   |   ||  ||  ||   || ||   |
Qy   987 CACAATCGCAATAGCTCCAATTGGTATTCCGGAGGACGAGGCCATCTCATTCCCGGTATGC  1046

Db   991 GGGAATGTATCCGGTGCGGGACAATCGGCGCGAAGAGATTACGTCTGCCTGCCAGGGCTTCGGC  1050
         ||||||||| |||||| |||  ||||| | |||||  ||   |||| | || ||| |||||
Qy  1047 GGCAATATATCCGGTGCGGGCGAATCGGCGCAGAAGATTCCGGACTGTGTTCGGGGTTTGGT  1106

Db  1051 CCCAATCCCAACTACGACTACACCAGTTGCTTCGACTCATTCGGTTGGGCTTTCCTGTCGGCG  1110
         ||  |||||||||| || ||  ||||| |  || |  |||||  || |||  |||
Qy  1107 CCGAATCCGAATTATGGCTACACCAGCTTCGGATGGGCTTTCCTGTCCCGCC  1166

Db  1111 TTTCGTCTCATGACCCAAGATTCTGTTCTTATAGTCATCATCTTCCTAGGTTCAATCTATCTTGTG  1170
         ||   | | ||| ||||  |||  |||| |  ||||||||||||||| |||| ||||||
Qy  1167 TTCCGGCTGATGACAAGCGCTTCTGGGAGGATCTGTATCAGCACGTGCTGCAAGCAGCT  1226

Db  1171 GGACCCTGGCACAGTGTTCTTTATAGTCATCATCTTCCTAGGTTCAATCTATCTTGTG  1230
         |||||||||||  ||||  ||||  ||||||||||||||||||||||||||||||||||
Qy  1227 GGACCATGGCACATGCGTCCATGTCTTTATAGTCATCATCTTCCTAGGTGTTCGGGGTTTGGT  1286

Db  1231 AATTTGATTTGGCCATTGTTGCCATGTCTTATGACGAATTGCAAAGAGAGGCCGAAGAA  1290
         ||||||||||  |||  ||||  ||  || ||  ||  ||| |||||| |  ||| |||||
Qy  1287 AATTTGATTTTGGCCATTGTTGCCATGTCTATGACGAATTGCAAAGGAAGGCCGAAGAA  1346

Db  1291 GAAGAGGCTGCCGAGGAGGCCGATCCCGAGAAGCTGGGAGAAGGCGCAGCCAGGCCAGGCG  1350
         ||||||||| ||||||||||| |   ||| |  ||||| || |||||||  ||||||  || |
Qy  1347 GAAGAGGCTGCCGAGGAGGCCGATCCCGAGAAGCTGGGAGAAGGCGCAGCCAGGCCAGGCG  1406

Db  1351 GCCAAACTGGAGGAGGCGGAATCGGAGGCGGGCCAATGGCCAGGCCTCAAGCCGGCTCCAGCC  1410
         |||||  |||||||||||  |   ||| ||   ||||  | || | ||  ||||| |
Qy  1407 GCCAAGCTGGAGGAGGCGGAATCGGAGGCGGGCCAATGGCAGCAGCCGGATGCAGCAGCCAACC  1466

Db  1411 GCTGCGGCAGCTCTGCATCCCGAGAGTGTTCCCACGTACTCTTGTCATTAGCTAT  1470
         ||| ||||||| ||||||||  ||||  ||||||| |||  ||  ||||  ||  |||
Qy  1467 GCTGCGGCAGCTCTGCATCCCGAGAGTGTTCCCACGTACTCTTGTCATTCTTGCATCAGCTAT  1526

Db  1471 GAACTGTTTTGTTGCCGAGGAGGCCAACGATGACAACAAGGAGAAGATGTCGATA  1530
         |||||| ||||||||||||||||||||  | |||||||||| |  || || || |
Qy  1527 GAAGTGTTGTTGTTGCCGAGGAGGCCAACGATGACAACAACAAAGAGAAGATGTCCATT  1586

Db  1531 CGGCACGGTCGAAGTGGAATCGAGTGTCGGTGAGCCGTTATACGACAACCAGCACCTACC  1590
         || ||||||  ||||| |  || || | ||||||| | |   ||| || |
Qy  1587 CGGCACGGTCGAAGTGGAGTCGGTGAGCCGTTATACGACAACCAGCACCTACC  1646

Db  1591 GCTGCGGCAGCTCTGCATCCCGAGAGTACTCTTGTCATTAGCTAT  1647
         |  || ||  || ||||||||  ||||||| ||| |||||||||||
Qy  1647 GCTGCGGCAGCTCTGCATCCCGAGAGTACTCTTGTCATTCTTGCATCAGCTAT  1706

Db  1648 TCACCATTTAACCTACGCCGGGGATCACGTAGTTCACACAGTACCAATACGAAATGGG  1707
         ||||| |  ||||| || || ||| | ||||| | ||||||||||  ||||| |||
Qy  1707 TCAAACTGGCCAAGTCTTGGCCATCACGTAGTTCACACAGTACCAAGTACGACGGGA  1766

Db  1708 CGTGGACGTTTGTATACGCGGGATCCAGCAGGTAGCGATCGCAAGCCGTACTGGTACTCCTTACCTGGT  1767
         || ||||||| |  | ||| | || | ||| || |||||| ||||||| |||||||||| ||||||||
Qy  1767 CGTGGCCGCTTTGGTAATCGCAGGGTGTCCAGGGTCTGCGTATTCGTCCGATGTCGCGTGCGGGTG  1826

Db  1768 GATGCCAGCAGCATTGCCCTATGCCGATGACTGGGGATCCTGAATGCCGTAACACCAATGTCCGAA  1827
         ||||  |||||| | ||||| | |  || |  |  |||||  ||||| |
Qy  1827 GATGCCCAGCAGCACTTGCCCATCCCGACGACTCGAAGTGCCGATGTCACCCCGATGTCCGAA  1886

Db  1828 GAGAATGGTGCCATTATAGTACCAGCCTACTATTGTAATTAGGTTCTAGACATTCTTCA  1887
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Db   ... ||||||| ||||| |||||| ||  || |  ||||||||||||||||  ||||| |||  1946
         GAGAATGGGGCCCATCAATCAGTGCCGTGTACTATGCGATCTAGGCTCCGGACCACTCATCG
Qy  1887

Db  1888 TATACCTCGGATCAATCAAGAAATCTCGTATACATCCAATCACCATGGTGGCATG  1947
         ||||||||||||  ||||||||   ||  ||||| || ||||| || || ||||
Qy  1947 TATACCTCGGATCAATCAGTCCCGAATATCGTATACCTCACAGTGGTGGCGGCATG  2006

Db  1948 GCGGCCATGGTGCCAGCACAATGACCAAAGAGGCAAATTGCCGCAGTCGCCAACACAGC  2007
         ||  ||||| | || | ||  |  |||||||| ||  |||  | ||| ||||||||||
Qy  2007 GCCGTCATGGGCGTCAGCAATGACCAACGAGCAAATTGCCCAACCGCAACACACGC  2066

Db  2008 AATCAATCAATCGGTCGCTGCAACCAATGTGGCAGTAGTACGGCCGGTGGCTATCCC  2067
         |||||||||||||  |  | ||  ||  || ||| |   |  ||  ||  ||||
Qy  2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGGCCACCAC--CTGTC--TGGA--C-A--CC  2114

Db  2068 GATGCCAATCACAACAAGGATTATGAAATGGTCAGGATTATACAGACGAAGCT  2127
         |||||  ||| | |  | ||||||  |||    |||  |||||  ||||  |||
Qy  2115 AATCACCAAGCTC---GATCATCGCGACTACAGTCTTTTATGCGAAAACTCTTTGT  2171

Db  2128 GGCAAAATAAAACACCACGACAATCCTTTATGCGAGCCCCTGGTTAAAATCTTTGT  2187
         || ||  || |  || || || |||  |||||||||| ||||||| ||| |||||||
Qy  2172 GGCAAGATTAAACATCGACAATCCTTTATCGAGCCCGTTCCAGACACAACCGGTGGTT  2231

Db  2188 GACATGAAAGATGTTATGGTCTAAATGATATCATTGAACAGCCCGGTCGGCATAGT  2247
         ||| |||||||||  |  | ||    |||| | |||| || ||| || || |||
Qy  2232 GATATGAAAGATGTGATGGTCCTGAATGCACATCGAACAGCCCGGTCGGCCACAGT  2291

Db  2248 CGTGCTAGTGAACGAGGTG------AGGACGATGACGAAGAT  2283
         |  | || ||  | ||||          ||   || || |||
Qy  2292 CGGGCAAGCGATCGCGGTGTCTCCGGTTGTCTCCGGTTACTATTTCCATGTTCATGGCC  2351

Db  2284 GGTCCCACATTCAAGGACATCGCCCTCGAATATATCCGAATAATCCGGAAATCTTTGT  2343
         ||| |  || ||||  | || |  | | || |  || |||||  ||  | ||||||||
Qy  2352 GGGCCGACGTTCAAGAGACACTCGAGGTGATCCTCAAAGGATCGCAAGTGTTTTGT  2411

Db  2344 GTATGGGACTGTGTTGTTGGGTGGTAAAATTCAGGAATGGTGTCCTTTATTGTGTTC  2403
         |  ||||||| ||| |  || || |   |||||||  | |  | || || | ||||||
Qy  2412 GTGTGGGACTGTGTTGCTGGGTTTGGTTGAAATTTCAGGAGTGGTATCCGATCCATCGGTCTTC  2471

Db  2404 GATCCATTCGTGGAGCTCTGTCATTACCCTGTGTATTGTGGTCAATCAATGTTCATGGCC  2463
         ||| |  |  | || || || || |  || || ||||| || || |  |||||||||||
Qy  2472 GATCCCTTCGTCGAGCTCTTCATCACGCTGTGCAATCGTGGTGGTCAACGCGATGTTCATGGCA  2531

Db  2464 ATGGATCATCACGACATGAATCCGGAATTCGAAATTCGGAGGAAGTTGTCGAAAATCTTTGT  2523
         ||||| || ||||  | |  |   || || ||||||| | |||||| |||   ||||||||
Qy  2532 ATGGATCACCACGATATGAACCAGAAGTGGAACAAGGAGATGGAACCGTGCTGCAACTATTTC  2591

Db  2524 TTCACGCCCACTTTGTCAATTGGCAAATCATGTCAATTTGCATGGCCAGCAGAAACTGATG  2583
         |||  |||  || || || |   |||||||| || ||||||||||||||||  |  | |||
Qy  2592 TTCAAACTGCCACCTTTGCCATCTGCCATCATTGAAGTGGCCATGATGGCCATGGGAAGTAC  2651

Db  2584 TACTTCCAGAAGGCTGGAACATTTTCGATTTCATTATTGTGGCCTTGTCTGCTGGAA  2643
         ||||||||||| || || |  || ||||||| |||| ||||||| | | |  || |
Qy  2652 TATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATTGTCGTGGCCCTATCGTTATTGGAA  2711

Db  2644 TTGGGCCTGGAGGGTGTCCAGGGGCCGTCAGGGTGCTGAAAGTGTTGTAACTATTC  2703
         || |  |||||||| ||||||| |||| | |||||| || |  || |||| ||| |
Qy  2712 CTGGGACTCGAGGGTGTCCAGGGTGTCCGTATTGTCCGATTGCGTATTGCTGCAACTATTC  2771

Db  2704 TTCAAATTGGCAAAATCATGTGCCAACTGGTGAATTTCGATTTCATTCGGTTATGGGCCCGGACA  2763
         |||  |||||| || || || || || || |  |||| |||| ||||||| |  ||| ||| |
Qy  2772 TTCAAACTGGCCAAGTCTTGCCCACCTTTGCCATCATTGATTTCATTCATTATGGGACCGACC  2831

Db  2764 ATGGGTGCATTGGTAATCGTTGACTTTGTACTTGCATTATCATCTTCGCATCTTTGCGTGT  2823
         ||||| || || ||||  |  || || | |  || || |  |||||||| ||||| ||||
Qy  2832 ATGGGCGCTTTTGGGTAATCGTTGTACTTGTACTTTGCATTATCATCTTCATCTTTGCGGGT  2891

Db  2824 ATGGGAATGCAACTTTTCGGAAAGAACTATATTGGTAATAGATGATCCTTCAAGGACCAT  2883
         ||||| |||||| || || ||||| || |  ||| ||| ||||  |  ||||| ||||
Qy  2892 ATGGGAATGCAACTGTTCGGAAAGAATTATCATGATCCACAAGGACCACCGGCGGC  2951

Db  2884 GAATTACCGCCGCTGGAATTTCACCGACTTCATGCAGCTTCATGATTGTGTTCCGAGTG  2943
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Qy  2952  GACCTGCCGCGCTGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTGTTCCGGGTG  3011
                |||||| | ||||||||||||| ||||||  |||||| ||||| |||
Db  2944  CTGTGCGGAGAGTGGATCGAGTCCAGTGGGACGCCATGTATGTGGGACGCTCAGCTGT    3003

Qy  3012  CTCTGCGGAGAAATGGATCGAGTCCAGTGGGACGCTGGGACATGTACGGTGGGCCGATGTCTCGTGC  3071
          |||||||||||  |||||  ||||||| ||| |  ||||||||||| ||||||  ||||| |||||
Db  3004  ATACCCTTCTTCTTCTTGGCCACCGTCGTGCTGTGTCTGTCATCTGGCCAATCTGTGGTACTCTTCCTTA  3063

Qy  3072  ACCAATAAAATAGCAGAGGCCTTCAATCGTATTGCCTATTGGTCTCGTTTAATCGTGCAAATGATTC  3131
                  ||||||||||||| |||||||||| ||||  | |||||||||||||||| ||
Db  3064  ATTCCCTTCTTCTTGGCCACCGTCGTGCTGTGTCTGTCGGTACTTCGTGGTACTTTTCCTTA       3123

Qy  3132  GCCTTGCTGTTTGTCCAATTTGGCTTCATCTAGCTTATCAGCCGACTGCCGATAACGAT     3191
          ||||||||||||||||||| |||||||||||||| | |||| | |||||||| ||| ||
Db  3124  ACCAATAAAATAGCAGAGGCCTTCAATCGTATTGCTATTGGTCTCGTTTAAGTCGGGTGAAACGT  3183

Qy  3192  ACGAGTTAAGCTATAGCCGAGGCCTTCAATCGAATTGCCCGATTTAAAAGTTGGGTTAAGCGT   3251
          |||||||| | | ||||||||||||| |||||||| |||| ||||||||||||||||| ||||
Db  3184  AATATTGCCGATTGTTTAAGTAATTGCGAAATAAATGACAAATCAAATAAGTGACCAA       3243

Qy  3252  AATATTGCTGATTGTTTCAAGTTAATACGGTATAAGTGACAAATCAAATAAGTGATCAA    3311

Db  3244  CCATCAG--------A-A-CA------TGG--CGAT-A--ATG--------              3265
          |||||| |        | | ||         |||  |    |||
Qy  3312  CCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTTGGAGCGAACAGCATGGTGACAAC   3371

Db  3266  -AACTGGAGTTGGGTCATGACGAAATCATGGGGCGATGGCCATTGGGATTTGAGCGAAATCGTGAAG   3324
           |||||||||||||||| || |||||||| ||||| |||||||| ||||||||||| |
Qy  3372  GAACTGGAGCTGGGACGACGACGAGATCCTCGCCGACGTTCACGATTACGATACGGCGAT    3431

Db  3325  GGCGAGACCCAGCTGGAGGTGGCCATTGGCCGATGGCCATGGAGTTCACGATACGGCGAT  3384
          ||||||||||||||||||||| ||||||| |  |||||||||||| |||  |||| ||||
Qy  3432  GAGCAGACGCAACTGGAGGTGGCCAGCATTCACGATACACGGCGATCTG               3491

Db  3385  ATGAAAAACAACAAGCCAAGAAATCAAAATTCAAAATCCATTCATCATGGTGACAAC     3444
          |||||||||||||||| |||| |||| |  || |||| | |||| ||||| ||||
Qy  3492  ATGAAGAACAACAAGCCGAGAAATGGCGAGGAAGCGGCAGCGATGATTGGCAAC         3551

Db  3445  TCAATAAACCACCACCAAGAACAATAGACTGAACATGGGTTGTCCATA               3504
          |||||||||||||| |||||| |||||||||| || ||||| |||| |
Qy  3552  TCAATTAACCACCACCAAGAACAATAGACTGAACACGGGTTGTGTGTCCTTA          3611

Db  3505  CAGGACGATGACACTGCCCAGCATTCATATGGTAGCCATAAGAATCGACCATTCAAG      3564
          |||||||||||||||| ||||||||||||||||  ||||||||||||||||| |||||
Qy  3612  CAGGACGACGACACTGCCCAGCATTCATATGGTAGCCATAAGAATCGACCATTCAAG      3671

Db  3565  GACGAGACCCACAAGGACCGCCGCAAGGGCGGGCCACAGCGCCGACGTCAGC           3624
          |||||||||||||||||||||||||||| | |||||||| |||||||||||| ||||
Qy  3672  GACGAGACCCACAAGGGCCCGAGACGCGGGCGGAGAAGCGGCGGCCAGC              3731

Db  3625  AAGAGGACCTCGGCCTTAGGTTAGTTCTCGAGGAACTGGAGGGGCCAG               3684
          |||||||||||| || |  ||||||||| ||||||| ||||||||| |
Qy  3732  AAGGAGGATTTAGGTTCTCGAGGAACTGGAGGGGCCGAGGGCGGCGGCCCG            3791

Db  3685  CTGGATGGTGACATCATCATTCATGCCGAGGATGGGGCAATTAATGAATTCCG          3744
          |||||||||| ||||||| |  ||||| ||||||||||||| ||||| ||||
Qy  3792  CTCGACGGTGGATATCATTCATTATTCATGGCCGATGAATATCCA                 3848

Db  3745  TCGGCGGACTGTTCCCGGACTCTACGAAGAGTTCCGATCTTGGCCGCCGCGACGAGGAC   3804
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Qy  3849  GCCGCCGGACTGTTCCCGGACTCTACGAAGAGTTTCCGATCTTGGCCGCCGATGAATGAC  3908

Db  3805  TCGGCGGTTCCGGCGGATATCATTCAATTGACTATGAGTAGCTTGGCCTTA           3864
          | |  |||||||||||||  |||||||| |||| ||||||||||| ||||||
Qy  3909  TCGCGGTTCCGGCGGATATCATTCATTTCAATTAATGAGTAGCTTTAGGT             3968

Db  3865  AAATATTTGAAACAGTATCACTATGAGTAGCTTTAGCTTGGCCTTA                3924
          ||||||||||| ||| ||||||||| |||||| ||||||||||| |
Qy  3969  AAATATTTGAAACGCTTATCACTATGATTTAGTAGCTTTATTGGCCATTA            4028

Db  3925  GAAGATGTTCATTACCCGACCTGTCATGCAGCCATTACCCGATATTTTATACTATAATGGACAGG  3984
          |||||||||||| || |||||||||||||  |||||||||||||||| |||  |||||||||||
Qy  4029  GAAGATGTACATCTGCCACAAGACCCATACTGCAGGATATTTATACTATAATGGACAGA       4088
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Db  3985  ATATTTACGGTGATATTCTTTTTTGGAGAGTGTGATCAAATGGTTGGCCCTGGGCTTTAAG  4044
          |||||||||||| ||| |||||| ||||| |||||||||||| |||||||| |||||||||
Qy  4089  ATATTTACGGTTATATTCTTCTTGAAATGTTAATCAAGTTAATCAAGTGGTTGGCGCTCGGCTTCAAA  4148

Db  4045  GTCTACTTCACCAATGCCGTGGTGTTGGCTGGTGTTCGTGATGTCATGCTATCGTATA     4104
          || |||||||||||| ||  ||||||| || ||||| || ||||||| |  ||| ||
Qy  4149  GTGTACTTCACCAATGCCGTGGTGTTGGCTGGTGTTCGTGATGTCATGCTATCGTTATC    4208

Db  4105  AATTGGTTGCCGTTTGTGTCGGGCTAAATGATATAGCCGTGTTTAGATCAATGCGGCACA  4164
          || || ||||| ||| ||||||||||||| | ||| |  ||||||| | |  | ||||||
Qy  4209  AACTTCGTTGCTTCACTGTTGGAGCTGGTGCGGTATTCAAGACCTTCAAGACATGCGAACG  4268

Db  4165  CTGCGCGGGCCCTAAGGCCATTGCCAGTGTCCTCCGTATGGCATGCAGGGCATCAGAGGG  4224
          | |||||||||  |  || | | |||||||||||| | || | |||||||  ||||||||
Qy  4269  TTAAGACACTGAGACACCACTACGTGTATGCCATGTCCCGTATGTCCCGTATGCCTGCGTT  4328

Db  4225  AATCGCGTCGTTCAAGCTATACCGTCCATCTCATCTCAATGTGCTATTGGTGTGTCATATTCTC  4284
          ||||||||||||||||| ||| ||||||||||||||||||| ||||||||||||||| ||||
Qy  4329  AATCGCGTCGTTCAAGCTATACCGTCCATCTCATCTCAATGTGCTATTGGTGTGTCAATATTT  4388

Db  4285  TGGCTTATTTTTGCCATTATGATGGAGTACAGCTTTTTTGCTGGAAAATATTTAAGTGTAAA  4344
          |||  ||||||| |||| |||| ||| ||||| ||||| ||| | |  ||||||||| |||
Qy  4389  TGGCTAATTTTTGCCATAATGGGGTACAGCTTTTTTGCTGGAAAAATATTTAAGTGCGGAG    4448

Db  4345  GATGGTAATGACACTGCTGCTGAGCGTATAATCGGAATCGTAATGCCTGCAAAAGT       4404
          |||||||| || |||||||||||||||| || | | |  |||||| |||| ||||
Qy  4449  GACATGATGGCACGAAGCTCAGCCACGAGCTCAGCCACGATCACCAAATGCCTGCGAGAGC   4508

Db  4405  GAAAACTACACCTGGGAAAATTCCGCAATGAACTTCGATCATGGTAATGCGTATCTC      4464
          |||  ||||||||||||||||| ||| |||||  ||||||||||| |||||| ||||
Qy  4509  GAGAACTACACCTGGGTGGTATTCAGCAATGAATTCGATCATGGTAGTGGTCTATCTG    4568

Db  4465  TGTCTTATTTCAAGTGGCCACCTTTAAGGCTTTCAAGCTTCAAACCTTCCAGATTGAT   4524
          |||  ||||| |||||||||||| |||||   ||||| ||| ||  || ||||||||||
Qy  4569  TGCCTTTTCCAAGTGGCCACCTTTAAGGCTCAAAGGCTCAAAGGTCGATACGAGATCGAT  4628

Db  4525  TCACGAGGTGGACAAGCCGATCCGGAAAATCAATATCTCACACTCGTTCAATCGT       4584
          ||||||||||||||||||| ||||||||||||  |||||||| ||||||||  |
Qy  4629  TCACGAGGTGGACAAGCCGATCCGTGAAACGAACATCGTAATCTACTACATGTTATATTTC  4688

Db  4585  GTATTCTTCATTATATTGGTAGCCATATGGTTCATTGGTGTTATCATT             4644
          |||||||||| |||||| ||  |||||||||||||||  |||| ||||
Qy  4689  GTATTCTTCATTATATTTGGTAGCCATATGGTTCATTGGTGTTATTCATT            4748

Db  4645  GATAATTTAATGAACAAGAAGAAGAAAGCAGGTGATCATGGATCATTACGACGAA       4704
          ||||||||||||| |||||||||||||||||| ||||||||||||| ||  ||||
Qy  4749  GATAATTTAATGAGCAAAGAAGAAAGCAGGTGATCATGGATCATTATTTTATTGAG      4808

Db  4705  GATCAGAAAGTACTATAATGTCTATGAAAAGATGGGCTCTAAAAAACCATTAAAAGCC    4764
          |||||||| ||||| | ||||| ||||||||||  ||||||||||| ||||||| ||||
Qy  4809  GATCAGAAAAGAGTACTATAATGCTATGAAAAGAGTGGCTCTAAAAAACCATTAAAAGCC  4868

Db  4765  ATTCCAAGACCGAGGTGGCCACCAGAACAATAGTCGATATTCAGATAAAAAAA         4824
          || | ||||||||||||||||||| ||||| ||| ||||||||| |||||||
Qy  4869  ATTCCAAGACCGAGGTGGCCACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAA  4928

Db  4825  TTCGATATAATCATTATGTGTTCATTGGCTTAAACGTTACCATGGATATTCGATAGCGG  4884
          |||||||| || || ||||| ||||||| |||||  || ||  |||  ||||||| |||
Qy  4929  TTCGATATAATCATTATGTGTTCATTGGCTTCCAATATTACGATATCCAATGGATAATCCA  4988

Db  4885  TACGACGCCTCGAGGCGAATGCTTTATTCGCTTACAACTTCAAACTCAATGGATTCGTAGTT  5004
          |||||||| |||||| |||||| || |||| ||| ||||||| || || | | ||||||
Qy  4989  TACGATGCGTCGGACAACGGCGGTCGGATATTTTACGATCGCAATATCACTATTTTATTGAG  5048

Db  4905  AATTTCAGTTTGAAATAATGAGTAGCTTTTGGCCCTTA                        5004
          |||||||||||||||||| |||||||||||| ||| ||
Qy  5049  ATTTCAGTTTCGAATATTCAATGTCTATTAGTGAATATTATGGTCTTATTTATTGAG     5108

Db  5005  CCATGGAATTATTGATGTAGTAGTGTCTTCATTTTATCCTGTCTTCACCAG           5064
          |||||| |||||||||||||||||||||||||||  |||||||||| |||| |
Qy  5109  CCATGGAATTTATTGATGTAGTAGTGTCTTATTTTATCCTGTCTTTAGTGTCTTACTTAGC  5168
```

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CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC     STREET: Clinton Square, P.O. Box 1051
CC     CITY: Rochester
CC     STATE: New York
CC     COUNTRY: USA
CC     ZIP: 14603
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/808,793
CC     FILING DATE:
CC     CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: US 60/034,361
CC     FILING DATE: 24-DEC-1996
CC     CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: US 60/012,649
CC     FILING DATE: 01-MAR-1996
CC     CLASSIFICATION: 435
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Braman, Susan J.
CC     REGISTRATION NUMBER: 34,103
CC     REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: 716-263-1636
CC     TELEFAX: 716-263-1600
CC   INFORMATION FOR SEQ ID NO: 2:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 6315 base pairs
CC       TYPE: nucleic acid
CC       STRANDEDNESS: single
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA
SQ   SEQUENCE 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 OTHER.

Query Match        56.3%;  Score 3664;  DB 21;   Length 6315;
Best Local Similarity 84.8%;  Pred. No. 0.00e+00;
Matches 4980;  Conservative  0;  Mismatches 812;  Indels  84;  Gaps  21;

Db   151 ATACGACATATGATGACGAGGACGAGAGATGAAGGCCCACAGCCGGATCCCAACACTTGAACAG 210
          |||| ||||||||||||||||||| ||||||| |||||| ||||||||||||||||||||||
Qy   207 ATCCGATATGATGACGAGGACGAGGATGAAGGTCCACACTTGAACAG 266

Db   211 GGTGTGCCTATACCTGTTCGAATCAGGCACGATGCAGGATGCAGCTCCCGCGGAATTGGCCTCCACTCCT 270
          ||||||||  || ||||||||| ||||| ||| |||||||||||||||||||||||||||||||
Qy   267 GGTGTGCCAATACCCTGTTCGTTCGATTGGCCGGGGAGGGCAATCCGGGAATTGGCCTCCACTCCT 326

Db   271 CTCGAGGAATATCGATCCCTTCTACAGTAGCTCGTAACAGTTGTGACATTGTAGTAATAAGTAAGAGGA 330
          |||||||||||||||||||||||||||||||||||||||| || ||||||||||| || |||||||
Qy   327 CTCGAGGAATATCGATCCCTACTACAGCAATCAACAGTACTGACAATTCGTAGTTGTAAGCAAAGGA 386

Db   331 AAGGATATATTTTCGTTTTCGCTCGTCGATCCCTCAAAAGCAATGTGGCTCTCGATCCATTCAATCCG 390
          || |||||||||  |||||| ||||||||||||| ||||||||||| |||||||||||||||| |||
Qy   387 AAAGATATATTTTCGCTTTTCGTCGATCAAAAGCAATCAAAAACCGAACAAGCTGAGTCGATCCATCAATCCG 446

Db   391 ATACGTCGTGTAGCCATTATATATTTAGTGCATCCCTGTGTTTTCGTTATTCATTATCACC 450
          |||||||||| |||||| || |||| ||||||||||| ||||||| ||||||| |||||||
Qy   447 ATACGTCGTGTGGCCATTTACATTACATTCGTAGTCGTCATCATTATTTTCCCTATTCATCATCACC 506

Db   451 ACTATTCTAACTAATTGTATTTTAATGATAATTCCGACAACGCCCACGGTCGAATCCACA 510
          || |||||  |||| |||||| ||||||||||| ||||||||||||||||| || |||||
Qy   507 ACAATTCTCGTCAACTGCATCGATGATAATGCCGACAACGCCCACGGTTGAGTCCACT 566

Db   511 GAGGTGATATTCACCGGAATCTACCACATTTGAATCAGCTGTTAAAGTGATTGGCACGAGGT 570
          ||||||||||||||||||||| ||| ||||||||||||||||||||||||||| ||||||||
Qy   567 GAGGTGATATTCACCGGAATCACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT 626

Db   571 TTCATTTATGCCCGTTACGTATCTTAGATGATGCATGGAATTGGCTGGACTTCGTAGTA 630
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Db  5065 GACATCATGAGAGTATTCGTATCGCCGACACTGCTCCGTGTGGTGAGAGTGGCCAAA 5124
          || || ||||||||| ||||| |||  |||  |||| ||| ||| ||||||||||
Qy  5169 GATATTATCGAGAGTACTTCGTCGTCCGGTTAGTCAAGGTGCCAAGGTGTCGTTCCGG 5228

Db  5125 GTGGGTGCGTCGTTCTCGACTGGTCAAGGTGTCCGGTATCCGAAGGTATCGCTTGCTTGCCGG 5184
          ||||| |||||| ||||||||||| ||||  |||||| || |  ||||  |||| |||||||
Qy  5229 GTGGGCCGTGTCCTTCGACTGGTGAAGGGCATTCGGACACTGCTCTTCCGCG 5288

Db  5185 TTAGCCATGTCGTTGCCTCCTTATTCAACATTTGTCTGTTCTTGGTCGATGTTC 5244
          ||||||||||||| | ||| |||||| |||||||| ||| ||||||| ||||||
Qy  5289 TTGGCCATGTCGCTCGCCGGCCCTGTTCAACATCTGCCTGCTCGTTCCTGGTCATGTTC 5348

Db  5245 ATCTTTGCTATCTTTGGCATGTCCTTCTTCATGCATGTCAAAGAGAAGAGCGGCATAAAT 5304
          |||||||| |||| ||||||||| |||||||||||| ||| ||||||||||||||||| |
Qy  5349 ATCTTTGCCATTTCGGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCGGCATTAAC 5408

Db  5305 GCTGTGTATAATTTAAAGACATTGGCCAAAGTATGATATATTGCTGTTTCAGATGTCTACC 5364
          | |||||| |||| ||||| | |||||||| | ||||| | |||||| ||||||||| |||
Qy  5409 GACGTCTACAACTTCAAGACCTTTGGCCAGAGCATGATCATCCTGCTCTTTCAGATGTCGACG 5468

Db  5365 TCAGCCGGTTGGGATGGTGTAGATGCCATTATCAATGAGGAAGATTGCGATCCACCC 5424
          |||||||||||||||||||||  |  ||||||||||||||||| |||| ||||||||
Qy  5469 TCAGCCGGTTGGGATGGTGTACTGGACGGCCATTATCAATGAGGAAGCATGCGGATCCACCC 5528

Db  5425 GACAACGACAAGGGCTATCCGGGCAATTGTGGTTCAGCGACTGTTGGAATTACGTTTCTC 5484
          ||||  |||||| |||||||||||||||||||||||||||| ||||||||  |||||||||
Qy  5529 GACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTGGAATAACGTTTCTC 5588

Db  5485 CTTTCATATCTAGTTATAAGCTTTTTGATAGTTATTATAATGTACATTGCTGTCGTCATTCTC 5544
          || |||||  ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Qy  5589 CTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTCGTCATTCTC 5648

Db  5545 GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGGTCTCACCGACGACTATGAT 5604
          ||||||||||| |||||  ||||||| || || |||||||| |  ||||||||| |||
Qy  5649 GAGAACTATAGTCAGGCCACCGAGGACGGTCAAGAGGGTCAACCGACGACTACGAC 5708

Db  5605 ATGTACTACGAGATTGGCAACAATTCGATCCGGAGGTACCCAGTACATAAGATACGAC 5664
          ||||||||||||||| ||||||||||||||||||||  |||||||||| || || |||
Qy  5709 ATGTACTACGAGATCGGCAACAATTCGATCCGGAGGGCACCCAGTACATACGGCTATGAT 5768

Db  5665 CAGCTGTCCGAGTTCCTGAGCACGTGCTCGGAGCGCCGCCTGCAGATCCAGAAGCCGAACAAG 5724
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||||||||
Qy  5769 CAGCTGTCCGAATTCCTGAGCACGTGCTCGGAGCGCCGCCTGCAGATCCAGAAACCGAACAAG 5828

Db  5725 TACAAAATCATATCGATGGACATCGCGATATGTCGGGGCCACATGATGTACTGTGTGGAT 5784
          |||||||||||||||||||||||||||||| | || || ||||||||||||| || || |
Qy  5829 TACAAGATCATATCGATGGACATCGCGATACCCATCTGTCGCGTGACCTCATGTACTGCGTCGAC 5888

Db  5785 ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAATCCAGGAGGAGACG 5844
          || | ||| |||| |||| |||||||||||||||||||||| ||||| | ||||||||
Qy  5889 ATCCTCGACGCCCCTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAGAGGAGACG 5948

Db  5845 GGTGAAATTGGTGAGATTGGCGGCCGCGACACCGGACGGGCTATGATCGGTCGGTCGTCGTCG 5904
          ||||| |||||||||| | ||||||||| ||  ||| |||||||| |  ||  |||| | |||
Qy  5949 GGTGAGATTGGTGAGATAGCGGGCCGGGCCCGGATACGGAGGGGCTACGAGCCCGTCTCAATCA 6008

Db  5905 ACACTGTGGGCGCCAGCGTGGAGAGTACTGGCCCAAGCTGATACAGAATGCGTGGCG 5960
          || |||||| ||  ||||| ||||||||||||| |  |||| |  ||| ||||||||
Qy  6009 ACGCTGTGGCGTCGGCGTCAGCGTGGAGAGTACTGCGCGCCGGCTAATCCAGCACGCCCTGGCG 6064
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RESULT 8

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ID   US-08-808-793-2 STANDARD; DNA; UNC; 6315 BP.
AC   xxxxxx
DT
DE
CC   Sequence 2, Application US/08808793
CC   Sequence 2, Application US/08808793
CC   GENERAL INFORMATION:
CC     APPLICANT: Soderlund, David M.
CC     APPLICANT: Ingles, Patricia J.
CC     TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
CC     TITLE OF INVENTION: AND USE THEREOF
CC     NUMBER OF SEQUENCES: 32
```

US-08-554-424-7.rnp

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Qy  1707  TCACCGTTAACATACGCAGGGGATCACGTAGTTCCACAAGTACACGATACGGACGGA  1766
          ||||||||||||||  | | ||| |||||||| |||| | ||||||||| |||
Db  1708  CGTGGACGTTTGGTATCACCAGGTAGCATGGAATGGCTGCAAGCCATTGTACTGCAAACATATCAG  1767
          |||||||||||||||  |  ||| |||||  ||  |||||| ||||| ||| ||||||
Db  1767  CGTGGCCCGCTTTGGTATACCCGGTAGCGATCGTAAGCCATTGTATTGTCAACATATCAG  1826
Qy  1768  GATGCCCAGCAGCATTGCCCTATGCCGATCAGACTCGGAATGCCGTAACACCAATGTCCGAA  1827
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  1827  GATGCCCAGCAGCACTTGCCCTATGCCGCGATCGGAATGCCGTCACCCGATGTCCGAA  1886
Qy  1828  GAGAATGGTGCCATTAGTAGTACCAGCCTACTATTGTAATTTAGGTTCTAGACATTCTTCA  1887
          |||||||||||||||| ||||||| |||||||| | ||||||||| |||||| |||||
Db  1887  GAGAATGGGGCCATCATAGTGCCCGTGTACATATGCGTACTACTCGGCTCCGACCACTCATCG  1946
Qy  1888  TATACCTCGCATCAATCAAGAATCTCGTATACATCAACATCACATGGTGATTATTGGTGGCATG  1947
          ||||| |||| ||||||||||| |||||| ||  || ||| ||||||||
Db  1947  TATACCTCGCATCAATCAGTCCCGAATATCGTATATCGTATCCGTACTCGGCGGCATG  2006
Qy  1948  GCGGCCAATGGGTGCCAGCACAATTGACCCAGTCGCAGTCGCAGTGCGCAACACACGC  2007
          |||||||| ||| ||||| ||| || || ||| || ||||||||||| |||||
Db  2007  GCCCTCATGGCCGTCAGCACAATGACCAAGGAGCAAATGCGCAACCGCAACACACGC  2066
Qy  2008  AATCAATCAATCGTCGTCAACCAATGTGCCACCGAGTACGCGCGGTGGTGCTATCCC  2067
          ||||||||||| | |  ||||||| || | ||| ---|||| |  || | |  |||
Db  2067  AATCAATCAGT--GG-GC-GCCACCAATGGCGGCCAACAC--CTGTC--TGGA--C-A--CC  2114
Qy  2068  GATGCCAATCACAAGGAACAAAGGATTATGAAATGGTCAGGATTATACAGACGAAGCT  2127
          || ||||||||||||||| || ||||  ||||| |||| |||  |||| |||||||
Db  2115  AATCACAAGCTC---GATCATCCGCGACTACGAAATTGGCCTCGGATGCCACGGACGAAGCT  2171
Qy  2128  GGCAAAATAAAACACCACGACAATCCTTTATCGAGCCCGTCCAAACTCAAACAGTGGTA  2187
          || ||||| ||||| |||||| ||||||||||| |||||||| |||||| ||||| |||
Db  2172  GGCAAGATTAAAACATCATGACAATCCTTTTATCGAGCCCGTCCCAGACAGCAAACGGTGGTT  2231
Qy  2188  GACATGAAAGAATGTTATGGTCTTAAATGATGATCATTGACAAGCGCGCTGGTCGGCCATAGT  2247
          || ||||||||||||| |  |||||| |  || |||||| |||||||||||| ||||||| |||
Db  2232  GATATGAAAGATGTTGCCTGAATGACATCATGACAATCAGGCCGTCGCCGCCACAGT  2291
Qy  2248  CGTGCTAGTGACGAGGTG-------------------AGGACGATGACGACGAGAT  2283
          || ||||||||||||||                  | ||||||||||||||||
Db  2292  CGGGCAAGCGATCGCCGGTGCTCCGTTCATCATCATCCCCAACAGAGACGACGATGACGAGGAT  2351
Qy  2284  GGTCCCACATTCAAGGACGATCGCCCCTCCGATCGCGTGAATATATCCGATATATCTTTTGT  2343
          || ||||| ||||||| ||||| |||||||||  |||| | ||  ||| || |
Db  2352  GGGCCCACGTTCAAAGACACTCGAAGTGATCCTCAAAGGCATGCATGATCGATGGTGTTTTGT  2411
Qy  2344  GTATGGGACTGTTGTTGGGGTGTGGTTAAAATTCAGGAATGGGTCTCCTTTATTGTGTTC  2403
          || ||||||||||||||||| ||| || |||| ||||||||| ||||||| |||| ||||
Db  2412  GTGTGGGACTGTGCTGTTGCTGGGTTTTGGTTGAAATTCAGGAGTGGGTATCGCTCATCGTCTTC  2471
Qy  2404  GATCCATTCGTGGAGCTCTTCATTACCCTGTATTGTGGTCAATACAATGTTCATGGCC  2463
          |||| | |||||| ||| ||| ||||| |||| ||||  ||||| |||| |||||||
Db  2472  GATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTGTGGTCAACGATGTTCATGGCA  2531
Qy  2464  ATGGATCATCACGACGATGAATCCGGAATTGCGGAGAAGTGCTGAACTATATTTC  2523
          ||||||||||| |||| || ||||| |||| | ||| |||| | |||| || |
Db  2532  ATGGATCACCACGATGACAAGGATGGAACCGGTCTGCTCAAAGGCGTGCAACTATTTC  2591
Qy  2524  TTCACGGCCACTTTGCCATCTCGAGGCCAGCGAAACTGATGGCCAGGCCCGAAGTAC  2583
          ||||| || ||| |||||||||| || || |||||| ||||| || |||| |||||
Db  2592  TTCACCGGCCACCTTTGCCATCATCGAGGCCACCATGAGCCATGGGCCCCCAAGTAC  2651
Qy  2584  TACTTCCAGGAAGGCTGGAACATTTTCGATTTCATTATTGTGGCCTTGCTCTGCTGGAA  2643
          ||||  ||||||| ||  |||||  |||| |||| ||| ||||  || |||| ||||
Db  2652  TATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATCCTATTGGAA  2711
Qy  2644  TTGGGCCTGGAGGGTGTCGAGGTGTCCAGGGCTCTTCGTTTGCTTGCTAACTATTTC  2703
          |||| || ||||| ||  |||| |||| |||||||| |||| |||||  ||||||
Db  2712  CTGGGACTGGAGGGTGTCGAGGGGTCCCAGGGTCTGTCCTATTGCGTTCGATTGCTGCCGTGTA  2771
Qy  2704  TTCAAATTGGCAAATCATCATGGCCCACTGAATTTACTCATTTACTCATTGGT  2763
          ||||  ||||| || || |||  |||||  ||||| |||||||||||||||
Db  2772  TTCAAACTGGCCCAAGTGCTTGGCCCCACCAACTTACTCATTTACTCATTGGACCGCCACC  2831
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Qy   627  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631  ATAGCTTTAGTTATGTGACCATGGGCATAGATTTAGGTAATCTCGCGAGCTTTGAGACAA  690
Qy   687  ATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGGTAATCTTAGCTAGCAGCCCTGCGAACG  746
Db   691  TTTAGGTACTGCGAGCCTCTGAAAACCGTAGCCATTGTGCCAGGTCTAAAAACCATTGTC  750
Qy   747  TTTAGGTGCTGCGAGCGCTAAAACCGTAGCCATTGTGCCAGGTGTGAGAGACCATCGTC  806
Db   751  GGTGCTGTCATTGAATCGTGTAAAAAATCTACGCGATGTGATAATTTGACAATGTTTCC  810
Qy   807  GGGCGCCGTCATCGAATCGGTGAAGAATCTGCGCGCAGTCGTGATTATCCTGACCATGTTCTCC  866
Db   811  CTGTCGGTGTTCGCGCTGATGGGCCTACAAAATCTATATGGTGTTCTAACACAAAGTGC  870
Qy   867  CTGTCGGTGTTCGCGTTGATGGGCGTGGTCTCACGGAGTTGT  926
Db   871  ATTAAACGAATTCCCCTGACGGCAGTTGGGCGCAATCTGACCGATGAAAAATGGTTTCTA  930
Qy   927  ATCAAGAAGTTCCCGTCGGGACGGTTCCTGGGGCAATCTGACGAGAACTGGGACTAT  986
Db   931  CACAATAGCAACAGTTCCAATTGGTTTACGGAGAACGATGGCGAGTCATATCCGGTGTG  990
Qy   987  CACAATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGGCATCTCATTTCCGTTCCGTATGC  1046
Db   991  GGGAATGTATCCGGTCGGGGACAATCGGGGGCGGAAGATTACGTCGCCTGGGCTTCGGC  1050
Qy  1047  GGCAATATATCCGGTCGGGGCAATGCGACGATTACGTCGCCTGAGGGTTTGGT  1106
Db  1051  CCCAATCCCAACTACACCACCAGTTTCGACTCATTCGGTTTGGGCTTTCCGGTCGGCG  1110
Qy  1107  CCGAATCCGAATTATGGCTACACCAGCTTCGATTCGTTCGGGTTTCCTGTCCGTCCGCC  1166
Db  1111  TTTCGTGTCTCATGACCCAAGATTCTCGGAGGATCGTATACGACGTGCTGCTCAAGCAGCT  1170
Qy  1167  TTCCGGCTGATGACACAGGACTTCTGCGGAGGATCGTATACCGACGTTCCACCAGCAGCAGT  1226
Db  1171  GGACCCTGGCACATGTGTTCTTTATAGTCATCATCCTCCTAGTGGTTCATTCTCATCTTGTG  1230
Qy  1227  GGACCATGGCACATGTGTTCTTTCATATCTCATCATCCTCCTAGTTCATTCATATCATCTTGTG  1286
Db  1231  AATTTGATTTGGCCATTGTGGCGGGAGGCGATCCGAGGAGCTGGAGAGCGGCAGCGCAAGAA  1290
Qy  1287  AATTTGATTTGGCCATTGTTGCGGGAGGCGATCGGAGAGCTGGAGAGCGGCAGCGCAAGAA  1346
Db  1291  GAAGAGGGCTGCCGAAGCGCGGGGATCCGAGTCGAGAGCTGAAGAGCGGGCAGCGCAAGGCG  1350
Qy  1347  GAAGAGGGAGGAGGAGCGGGATACGTGAAGCGGAAGAAGAGCTGAAGAGCCGCAAAGCG  1406
Db  1351  GCCAAACTGGAGGAGGCGCGGGCCAATGGGCCAATGGCGGCTCAGGATGCAGCGGATGCC  1410
Qy  1407  GCCAAGCTGGAGGAGCGCGGCCAGCGCAATGCCAGCAGGGCTCAGGCGCGTGCGCCCC  1466
Db  1411  GCTGCGGATTGGCCATGCTGTTGTCCATGTGTTCTTATGACGGAGGAAGGCCAAGAA  1470
Qy  1467  GCTGCGAGCTGCACTGCAGCTGTCTTCATCATCTTCTTCATCTTGCCGTTATCAGCTAT  1526
Db  1471  AATTTGATTTGTTGGCGGGAGGCGATCCGAGTCGAGAGCGGCAGCGCAAGAA  1530
Qy  1527  GAGCTATTTGTTGTTGGCGGGAGGGCGAGCTGGAGAGCGGAAGATGTCCATT  1586
Db  1531  CGCAGCGTCGAAGTGGAATCGGAGTCGGTGAGCGTTATTGTATAGCGTATCCAGCACCACC  1590
Qy  1591  ACAGCGAC-CC--GCTACTAAAGTCCGTAAAGTTAGCACGACTTCCTTATCCTTACCTGGT  1647
Db  1647  ACAGCACACGAGCTACCCAAAGTCGTAAAGTCGACGACATCCTTATCCTTACCTGGT  1706
Qy  1648  TCACCATTAACCTACGCCGGGGATCACGTAGTTCACCACAAGTACACCAATACGGAAATGGG  1707
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Db  2764 ATGGGTGCATTGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTTGCCGTG 2823
         |||||| || |||||||||||||||||||||||||||||||||||||||||| || |||
Qy  2832 ATGGGCGCTTGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTTGCCGGTG 2891

Db  2824 ATGGAATGCAACTTTCGGAAAGAACTATATTGACCACAAGGATCGCTTCAAGGACCAT 2883
         |||||||||||| || |||||||| |||| |||||||||||| ||||| || |||
Qy  2892 ATGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTCCGGATGGC 2951

Db  2884 GAATTACCGCGCTGGAATTCACCGACTTCATGCCAGCTTCATGATGTGTTCCGAGTG 2943
         ||||||| ||  ||  |||||||||||||||||||||||||||| ||||||||| |||
Qy  2952 GACCTGCCGCCGCTGGAACTTCACCGACTTCATGCCAGCTTCATGATGTGTTCCGGGTG 3011

Db  2944 CTGTGCGGAGTGGATGGATCGAGTCCATGTGGACTGCGATGTATGTGGGCGATGTCAGCTGT 3003
         || |||||||||||||||||||||||| ||||||||||||||||||||| ||||||||||
Qy  3012 CTCTGCGGAGAATGGATCCAGTTGCCATGTGGGACTGCGATGTGGGCGGCGATGTCTCGTGC 3071

Db  3004 ATACCCTTCTTGTCCACGGTCTGTAGATCGGCAATTTGTGGTTCTTAATCTTTCTTA 3063
         || |||||| |||||||||  ||| || |||||||  | ||||| |||| |||||
Qy  3072 ATTCCCTTCTTCTTCCCACCGTGTCATCGGCCAATCGGTGTCGTGTACTTAACCTTTCTTA 3131

Db  3064 GCTTTGCTTTGTTCCAACTTCGGTTCATCTAGTTATCAGCCCCGACTGCCGACAATGAT 3123
         |||||||||||  ||||||||||||||||||||||||| ||||| ||| || |||||
Qy  3132 GCCTTGCTTTGTTCCAATTTGGCTCATCTAGCTATCAGCGGCGCCGACTGCCGATAACGAT 3191

Db  3124 ACCAATAAAATAGCAGAGGCCTTCAATCGTATTGCTCTGTTTAAGAACTGGGTGAAACGT 3183
         |||||||||||||| |||| |||| || ||||  | |||  |||||||||||||||| |||
Qy  3192 ACGAATAAAATAGCCGAGGCCTTCAATCGGTGTTAGTTTTAAAGAACTGGGTTAAGCGT 3251

Db  3184 AATATTGCCGATTGTTTAAGTAATTGACAAATAAATTGACAAATCAAATAAGTGACCAA 3243
         ||||||||| ||  | |||| |||||  |||||  | ||||| || ||||||||||||||
Qy  3252 AATATTGCTGATTGTTTCAAGCTATAACGTTAACAAATCATTCACGATCAAATAAGTGATCAA 3311

Db  3244 CCATCAG------------A-A-CA-------TGG--CGAT-A--ATG------- 3265
         ||||||                 | ||        | |  |  |  |||
Qy  3312 CCATCAGGTGAGGGTGTGAGAGGACCAACCAGATCAGTTTGGATTTTGGAGCGGAAGCGGTGACAC 3371

Db  3266 -AACTGGAGTGGGTGGTGCTCATGCAGAAATCATGGGCCATGGAAATCATGGGCCGTTGATCGAACGGTATGAAG 3324
          |||||||||||||||| |||||||| ||||||| |||||||||| |||||||| || |||||| ||||||||||
Qy  3372 GAACTGGAGCGGTGCCACCTGGCCCACGAGATCCTCGCCCGCCGAGATCCTCATGCAGAAGAGGGATCAAG 3431

Db  3325 GGCGAGACCCAGCTGAGGTGGGCCATTGGCGATGGCATGGACTTCACGGATACATGGCGAT 3384
         ||||| |||||||||||| |||||||| ||||||||| || || |||||||||||||||
Qy  3432 GAGCAGACCACGCTGGGTGGGCCATCGGGGATCGGCATCGGGAATTCAACGGATACACGGCAA 3491

Db  3385 ATGAAAAACAACAACAGCCCAAGAAATCAAAATCCATAAACAACAACAACATGATTGGAAAC 3444
         ||||||||| ||||||||||||| || |||||||   | |||||||||||||| || ||
Qy  3492 ATGAAGAACAACAACAGCCCAAGAAATCCAAAATCCATAAACAACAACAACATGATTGGCAAC 3551

Db  3445 TCAATAAACCACCAAGAACAATAGACTGGAACATGAGCCATAGAGGTTTGTCCATA 3504
         ||||| ||||||||||||||| ||||||||||||||| ||||||| ||||||| |
Qy  3552 TCAATTAACCACCAAGAACAATGGACTGGAACATGAGCGCATAGAGGTTTGTCCTTA 3611

Db  3505 CAGGACGATGAATCGGCCAGCATTAACTCATATGGTAGCCATTCAGACCATTCAAG 3564
         ||||||||| |||||||||| ||| |||||||||||||||||| |||||||||||
Qy  3612 CAGGACGACGAATCGGCCAGCATTAACTCATATGGTAGCCATTCAGACCATTCAAG 3671

Db  3565 GACGAGGACCACAAGGGCCAGCGCCGAGGGCGAGAACGGACGTCAGC 3624
         ||||||||||||| |||||||| || || |||||||| ||||||||
Qy  3672 GACGAGGACCACGAGGGCCAGCGGCCGCGGCGAGGACGCGGACGCCAGC 3731

Db  3625 AAAGAGGACCTCGGGCCTCAAGGGCGACGGCGGAGGGCGGATGAGGGCCCG 3684
         |||||||||| |||||||| || ||||||||||||||||| |||||||
Qy  3732 AAGGAGGATTTAGGTCTCGACGGAGGAACTCGGACCGGAGCGGGCGGAGGCCCG 3791

Db  3685 CTGGATGGTGACATCATCCATGCCCAAAGACGACGAGAATAATGACTATCCG 3744
         || ||||| ||| ||| |||||  |||||| | ||||||| | ||||||
Qy  3792 CTCGACGGTGGATATCATTATTCATGGCGTTCGGGGAGGATATACTCGATGAATATCCA 3848

Db  3745 GCCCAAATGCGTTCCCGACTCGTACTACAAGAAGTTCCCGATCTTGGCCGCGAGGAC 3804
         |||| || || |||||||| |||||||||||||||||| |||||||||| ||||||
Qy  3849 GCTGATTGCTGCCCCGATTCGTACTACAAGAAATTTCCGATCTTAGCCGGTGGTGACGATGAC 3908
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Db  3805 TCGCCCGTCTCGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCATTTAATTGAAAAT 3864
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Qy  3909 TCGCCCGTCTCGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCATTTAATTGAAAAT 3968

Db  3865 AAATATTTGAAACGCCAGTTATCCATGATGTTAATGAGTAGCTTAGCTTTGGCCTTA 3924
         |||||||||||| ||||||||| |||||||||||| |||||||||||||||||||
Qy  3969 AAATATTTGAAACAGCGTTATCACTATGATTTTTAAATGAGTAGCTTAGCTTTTGGCATTA 4028

Db  3925 GAAGAGTTCATTACCGATCGACCTGTCATGCAGGAGATACTGCTACTACATGGACAGG 3984
         ||||||| ||| | ||||||| |||||||||||| ||||||||||||||||||||||
Qy  4029 GAAGATGTACATCTGCCACAAAGACCCATACTGCAGGGATTTATTACTATATGGACAGA 4088

Db  3985 ATATTACGGTGATATTCTTTTGGAGATGTTGATCAAATGGTTGATCAAATGGTTAAG 4044
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Qy  4089 ATATTACGGTTATATTCTTGTCTTGAAATGTTAATGAGATGGTTGGCGGCTTCAAA 4148

Db  4045 GTCTACTTCACCAATGCCTGGTGTTGGCTGGATTGTCGTGATTGCGTCGTGGTTGGA 4104
         || ||||| ||||||| || |||| ||||||||| |||||||||||| |||||
Qy  4149 GTGTACTCACCAACGCGGTGGTGTTGGCTGTTGCGTCGTGTTCCGTATGCGTCGTT 4208

Db  4105 AATTGGTTGCCGTTGGTCGGCTTAAATGAATATAGCCGTGTTAGATCAATGGCACA 4164
         |||| || || | |||| || ||| ||||| |||||| || |||||||||||||
Qy  4209 AACTTCGTGCTTCACTGTTGGACGTCGGTATTCAAGCCTCAAGCACTATGCGAACG 4268

Db  4165 CTGCGCGCCCTAAGGCCATTGCGTCGTGCTCTGTGCTCCGAGTGGAGGTATGAAAGTTGTCGTG 4224
         || || || | |||| || ||| || |||||| || || |||||||||||||| || |||
Qy  4269 TTAAGAGCACTGAGACCCACGTGCCATGTCCCGTATGCCGCATGGCCATGAGCGTGTCGTT 4328

Db  4225 AATGCGCTCGTTCAAGCTATACCGTCCATCTTCAATGTCTATTGGTGTGTCTGATATTT 4284
         || || |||||||||| |||||||||||||||| | || ||||||||||||||
Qy  4329 AATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTCTATTGGTGTGTCTCAATATTT 4388

Db  4285 TGGCTTATTTTGCCATTATGGGAGTACAGCTTTTTGCTGGAAATATTTTAAGTGTAAA 4344
         |||| ||  ||| |||| |||| ||||||| |||||||| |||| ||||||| |||
Qy  4389 TGGCTTAATTTTTGCCATATGGGGTGTACAGCTTTTTGCTGGAAAATATTTTAAGTGTGACAC 4448

Db  4345 GATGGTAATGACACTGTCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT 4404
         || |||||| || |||| |||||||||  |||  ||||| ||||||||||||||||
Qy  4449 GACATGAATGGCACGAAGCTCAGCCACGAACATCACCAAATCCAATGCCAATGCCTGCCGAGAGC 4508

Db  4405 GAAAACTACACCTGGGAAAATTCGGACAACTGAACTTCGGTAATGGGTAATGCGTATCTC 4464
         | || |||||| ||||||||||||| || |||||||||||||||| || || |||||
Qy  4509 GAGAACTACACGTGGGTGGTGAATTCAGCCATCAGTGAATTCGATCATCATGTCGATCGTATCTG 4568

Db  4465 TGTCTATTCAAGTGGCCACCTTTAAGGGCTGGATCCAGATGCCATTGAACGATGCCATTGAT 4524
         |||| | |||||| |||||||| || ||||| |||||| |||||||||||||| |||||
Qy  4569 TGCCTTTTCAAGTGGCCACCTTTCAAAGGCTGGATCCAAGTGGATCACAAATCGATGCTATCGAT 4628

Db  4525 TCACGAGGTGGACAAGCAGCCGATCCGAGAAACCAATATCTCAAATGTTATTATTTTC 4584
         || |||||| |||||||||| || ||||||||| || | ||| |||||||||||| |
Qy  4629 TCACGAGGTGGACAACGAACCAATTCGTCGAAACGAACAACTCTACATGTTATTATTTTTC 4688

Db  4585 GTATTCTTCATTATTTGGTGTTATTCATTGTGTTTCATTGGTGTTATCATT 4644
         |||||||||||||||||||| ||| |||||| ||| ||||| || | |||
Qy  4689 GTATTCTTCATCATATTTTGGTGTTATCATTGTGTTTCATTGGTGTTATCATT 4748

Db  4645 GATAATTTAATGAACAAAGAAGAAAGCAGGTGGATCATTAGAAATGTTCATGACAGAA 4704
         |||||||||||| || ||||||||||||||||||||| ||||||||||||||||||
Qy  4749 GATAATTTAATGAACGAACAAAGAAGAAAGCAGGTGGATCATTAGAAATGTTCATGACAGAGA 4808

Db  4705 GATCAGAAAAAGTACTATAAGTCTATGAAAAAGAATGGCTCTAAAAACCATTAAAAGCC 4764
         ||||||||||| |||||| ||| |||||||||||| |||||||||||| ||||||| ||
Qy  4809 GATCAGAAAAAGTACTATAAATGTCATGAAAAAAGAGTGGCCTAAAAAACCATTAAAAGCC 4868

Db  4765 ATTCCAAGACCGAGTGGCACCACAAGCAATAGTTACAGATAAAAAA 4824
         ||||||||| | |||| || || |||| ||| ||| || |||||
Qy  4869 ATTCCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAA 4928

Db  4825 TTCGATAATAATCATTATGTTGTTCATTGGTGGTTGCCTCAAAACATGTTCCGACAAACTCAATGGGATATTCGG 4884
         |||||||| ||||||| ||||| |||| ||| || ||||| ||| ||| |||||| ||||||||
Qy  4929 TTCGATATAATCATTATGTTATTATTCATTGGTGCTGAACATGTTCACCATGAACATGTCTGACCCGGATATTCGG 4988

Db  4885 TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAACTCAATGGGATTATTCGTAGTT 4944
         ||||| ||||||||||| ||||||||||||| |||||||| ||||||||||||||| |||
Qy         GCTGATTGCTGCCCCGATTCGTACTACAAGAAATTTCCGATCTTAGCCGGTGATGAC 
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ID   US-08-608-618-1 STANDARD; DNA; UNC; 6318 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/08608618
CC   Sequence 1, Application US/08608618
CC   GENERAL INFORMATION:
CC     APPLICANT: Soderlund, David M.
CC     APPLICANT: Knipple, Douglas C.
CC     APPLICANT: Ingles, Patricia J.
CC     TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC     TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
CC     TITLE OF INVENTION: HOUSE FLIES
CC     NUMBER OF SEQUENCES: 19
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC       STREET: P.O. Box 1051, Clinton Square
CC       CITY: Rochester
CC       STATE: New York
CC       COUNTRY: USA
CC       ZIP: 14603
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, Version #1.30
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/608,618
CC       FILING DATE:
CC       CLASSIFICATION: 530
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Timian, Susan J.
CC       REGISTRATION NUMBER: 34,103
CC       REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: 716-263-1600
CC       TELEFAX: 716-263-1636
CC   INFORMATION FOR SEQ ID NO: 1:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 6318 base pairs
CC       TYPE: nucleic acid
CC       STRANDEDNESS: single
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA
SQ   SEQUENCE 6318 BP: 1712 A; 1347 C; 1597 G; 1662 T; 0 OTHER.
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Query Match        56.2%;  Score 3662; DB 19; Length 6318;
Best Local Similarity 84.7%;  Pred. No. 0.00e+00;
Matches 4979;  Conservative  0;  Mismatches 813;  Indels  84;  Gaps  21;
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Db   151 ATACGATATGATGACGAGGAGGAAGATGAAGGTCCACAGCCGGATCCCACACTTGAACAG 210
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Qy   207 ATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCCTACACTTGAACAG 266

Db   211 GGTGTGCCTATACCTGTTCGAATGCAGGGCAGCTTCCCGGCCTCCACTCCT 270
          |||||||||||||||||||||  ||||||||||||||||||||||||||||||
Qy   267 GGTGTGCCAATACCTGTTCGATTGCAGGGCAGCTTCCCGGGAATTGGCCTCCACTCCT 326

Db   271 CTCGAGGATATCGATCCCTACTACAGTAACTAATTGTAGTAGTAATAAGTAAAGGA 330
          ||||||||||||||||||||||  |  ||||||||||||||| |  |||| |||||||
Qy   327 CTCGAGGATATCGATCCCTACTACAGCAATGTACTGACATTGTGACAATTCGTAGTTGTAAGCAAAGGA 386

Db   331 AAGGATATTTTCGTTTTCTGCCTCAAAAGCAATGTGGCTGCTCGATCCATTCAATCCG 390
          ||       ||||||||||||||||  ||||||||||||||||||||||||||||||||
Qy   387 AAAGATATTTTTCGCTTTCTGCGATCCATCAAAAGCAATGTGGATGCTCGATCCATTCAATCCG 446

Db   391 ATACGTCGTGTAGCCATTATATTTTAGTGCATCCCTTGTTTGTTATTCATTATCACC 450
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Qy   447 ATACGTCGTGTGGCCATTTACATTCCAGTGCATTCCCTTGTTTGTTATTCATTATCACC 506

Db   451 ACTATTCTAACTAATTGTATTTAATGATAATGCCGACAGCCGACCGGTCGAATCCACA 510
          |||||||||||||||| |||  |||||  ||||||||||||||||||||| |||||||
Qy   507 ACAATTCTCGTCCAACTGCATCCTGATGATAATGCCGACAACGCCCACACGCCCACGGTTGAGTCCACT 566
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Qy 4989 TACGATGCGTCGGACACGCTATAACGGTCCTAGACTATCTCAATGCGATATTCGTAGTT 5048
         ||||||  ||    ||||||  |||  ||||  |||||   ||| ||||||||||||||
Db 4945 ATTTCAGTGGCCGAATGTCTATTAAAAATATTCGCTTTACGATACTACTATTTCAAAGAG 5004

Db 5049 ATTTTCAGTCCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATTTATTGAG 5108
         ||||||||   |  ||||||||||||||||||||||||||||||||    ||||  ||
Qy 5005 CCATGGAATTTATTTGATGTAGTAGTAGTTGTCATTTTATCCATCTTAGCTCTTGTACTTCAGC 5064

Qy 5065 CCATGGAATTTATTTGATGTAGTAGTAGTTGTCATTTTATCCATCTTAGCTCTTGTACTTAGC 5124
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db 5109 GACATCATTGAGAAGTATTTCGTATCGCCGACACTGCTTCCGTCGTGTGTGGCCAAA 5168

Db 5125 GACATCATTGAGAAGTATTTCGTATCGCCGACACTGCTTCCGTCGTGTGTGGCCAAA 5184
         ||||||||||||||||||||||||||||||||||||||||||| |||| |||||||
Qy 5169 GATATTATCGAGAAGTACTTCGTTCGTGTCCGAGGGTATCCGGACGTTGCTTCGTCCCG 5228

Qy 5185 GTGGGTGCGTGTCCGTTAGTCAAGGGTGCCAAGGGTATCCGGACGTTGCTTCGTCCCG 5244
         ||||||||||| |  |||   ||||||||||||||||||||||||||||||||||| ||
Db 5229 GTGGGCGGTGCCTTCGACTGGTGAAGGGAGCCAAGGGCATTCGGACGCCGCTTCCTCCGCG 5288

Db 5245 TTAGCCATGTCGTTGCCTGCCTTATTCAACATTGTCTGTTGCTCTTGGTGATGTTC 5304
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Qy 5289 TTGGCCATGTCGTCGCCGCCCCTGTTCAACATCTGCCTGCTGTTGCTCTTGGTCATGTTC 5348

Qy 5305 ATCTTTGCTATCTTTGGCATGTCCTTCTTCATGCATGCTCAAAGAAGCGGCATAAAT 5364
         ||||||||||||||||||||||||||||  |||| |||||||||| ||||||||||| ||
Db 5349 ATCTTTGCCATTTCGGCATGTCGTTCTTCATGCACGTGAAGCACGTGAAGGAGAGCGGCATTAAC 5408

Db 5365 GCTGTGTATAATTTAAGACATTTGGCCAAAGTATGATATTGCTGTTTCAGATGTCTACC 5424
         | ||||||| |  |||| |||||||||||| |  |  |||| |||||  ||||| |||||
Qy 5409 GACGTCTACAACTTCAAGAGCATTTGGCCAGAGATTCGTTTCAGAGTCGCACG 5468

Qy 5425 TCAGCCGGTTGGGATGGTGTTAGATGCCATTATCAATGAGGAAGATTGCGATCCCACCC 5484
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5469 TCAGCCGGTTGGGATGGTGTACTGGACGCGCCAATTGTGGTTCAGGGACTGTTGGAATTACGTTTCTC 5528

Db 5485 GACAACGACAGAAGGGCTATCGGGCAATTGTGGTTCAGGGACTGTTGGAATTACGTTTCTC 5544
         ||| ||| |||  |||||||||||||||||||||||||||||||||||||||||||||||
Qy 5529 GACAGCGACAAAGGGCTATCCGGGCAATTGTGGTTCAGGGACCGGTTGGAATAACGTTCTC 5588

Qy 5545 CTTTCATATCTAGTTATAAGCTTTTTGATAGTTATTAATATGTAACATTGCTGTCATTCTC 5604
         |||||||||||| ||||||||||||||||  |||| ||||||||||  |||||||||||||
Db 5589 CTCTCATACCTAGTTATAAGCTTTTTTGATAGTTATTAATATGTACAATTGCTGTCATTCTC 5648

Db 5605 GAGAACTATAGCCAGGTACCAGGGATGGTACAGGAGGGTCTCACCGGACGACTATGAT 5664
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Qy 5649 GAGAACTATAGTCAGGCCACCGAGAGACGTGCAAGAGGGTCTAACCGGACGACGACTACGAC 5708

Qy 5665 ATGTACTACGAGATTTGGCAACAATTGGCGCAGCCCTGCTGGACGCGCCGGCTGGACATCCGGAGG 5768
         |||||| ||| |||||||||||||||||| ||||| |||| | ||   ||||||||||||||
Db 5709 ATGTACTATGAGATCTGGCAATTCGATCCGGAGCGGCGCGCTGCGGACGCGCCGGGCTATCCGGAGG 5768

Db 5725 CAGCTGTCCGAGTTCCTGGACGTACTGGAGCGCCCCCGTGAGATCGGGGT 5784
         |||||||||| ||||||||||||||||||||||||||||||||||||||||
Qy 5769 CAGCTGTCCGAATTCCTGGACGTACTGGAGCGCCCCCGTGAGATCGGGGT 5828

Qy 5785 TACAAAATCATATCGATGGACATGCCGATATGTCGGGGCGATATGTCGGTGGAT 5844
         |||||||||||||||||||||||||||||||||||||||||||| || |||||
Db 5829 TACAAGATCATATCGATGGACATGCCGATATGTCGGGGCGACATGTGGTGGAT 5888

Db 5845 ATATTGGATGCCCTGACCAAGGACTTCTTCTGCTTTTTTGCGTGTCGGTGT 5904
         |||||||| |||||||||||  ||||||||||||||||||| |||||||
Qy 5889 ATCCTCGACGCCCCTTACGGAAAGACTTCTTTCTTCGCGCCGACACCGGTGTCGTCG 5948

Qy 5905 ACACTGTGGCGCGGCGTGAGGAGTACTGGCCCAAGGACTACGCCCAAGCTGATACGGACGAATGCCAA 5960
         |||||||||||||||||||||||||||||||||||||||| | |||
Db 5949 GGTGAGATTGGTGAGATAGGCGCCCCCGGTATACGGGAGCGGGTACGACGCCCTACGAGGGGCTAGC 6008

Db 5949 ... ...
Qy 6009 ACGCTGTGGCGGTCAGCGTGAGGAGTACTGCCCCGGCTAATCCAGCACCGGTTGAGTCCACT 6064
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RESULT 9

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Db  511 GAGGTGGATATTCACCGGAATCTACACATTTGAATCAGCTGTAAAGTGATGGCACGAGGT 570
        |||||| ||||||||||| |||||||||||||||||||||||||||||||||||||||||
Qy  567 GAGGTGATATTCACCGGGAATCTACACATTTGAATCAGCTGTAAAGTGATGGCACGAGGT 626

Db  571 TTCATTTTATGCCCGTTACGTATCTTAGAGATGATGCATGGAATTGGCTGGACTTCGTAGTA 630
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  627 TTCATTTTATGCCCGTTACGTATCTTAGAGATGATGCATGGAATTGGCTGGACTTCGTAGTA 686

Db  631 ATAGCTTTAGCTATGTGACCATGGGCATAGATTTAGGTAATCTCGCAGCTTTGAGAACA 690
        ||||||||||||||||| ||||||||||||||||||||||||||| || |||  |||||
Qy  687 ATAGCTTTAGCTATGTGACCATGGGCATAGATTTAGGTAATCTCGCAGCCCTGCGAACG 746

Db  691 TTTAGGGTACTGCGAGCTGAAAACCGTAGCCATTGTGCCAGGTCTAAAAACCATTGTC 750
        |||||||||||||||| ||||||||||||||||||||||||| |  ||||||||||||
Qy  747 TTTAGGGGTGCTGCGAGCGGCTTAAAAACCGTAGCCATTGTGCCAGGCTTAAAGACCATCGTC 806

Db  751 GGTGCTGTCATTGAATCTGTAAAAAATCTACGCGATGTGATAATTTTGACAATGTTTCC 810
        |||||| || ||||| |||| |||||||||||||||||||||||||||||||||||||||
Qy  807 GGGCGCCGTCAATCGGTGAAGAATCTGCGCGATCTGGGCCATGGAATCTGACCATGTTCTCC 866

Db  811 CTGTCGGTGTTCGCGCTACGAAATCTATATGGGGTCTTCTAACACAAAAGTGC 870
        ||||||||||||||||||||||||||||||||||||||||||  | |||||||
Qy  867 CTGTCGGTGTTCGCGCTGCGGGTTGATGGGGCAATGCCTACTATATGGGGCTGCTGCAGGAAGTGC 926

Db  871 ATTAAACGATTCCCCTGGACGGCAGTTGGGCAATCTGACCGATGAAAACTGGTTCTA 930
        || ||||||||| ||||||||||| |||| ||||||||||||| |||| |||||||
Qy  927 ATCAAGAGTTCCCGACGGTTCCTGGGCAATCGACCGAGAACTGGGACTAT 986

Db  931 CACACAATAGCAACAGTTCCAATTGGTTACGGACGAACGGCGAGTCATATCCGGTGTGC 990
        || || ||||||||| ||| |||||||||| ||||| ||||  |||||||||| |||||
Qy  987 CACAATCGCAATGCTCCAATTGGTATCCGAGGACTCTGGGAATCTGGGCATCTCCATTCCGTTATGC 1046

Db  991 GGGAATGTATCCGGTGCGCGGACAATGCGCGAGGATTACGTCCTCCCAGGGCTTCCGG 1050
        ||||| || |  ||||||| |||||||| |||||||||||  |||||||||||||| ||
Qy 1047 GGCAATATCCGGTGCGCGGTTGCGACGATTACGTGTGCCTGGGTTTGGT 1106

Db 1051 CCCAATCCCAACTACGACTACACCAGTTCGATTCATTCGGTTGGGCTTTCCTGTCTCGGCG 1110
        |||||||||||||||||||||||||||||||||| | |||||||||||| |||| |  |
Qy 1107 CCGAATCCGAATTATGGCTACACACGCGATTCATTCGGTTCGATTGGGCTTTCCTGTCTGTG 1166

Db 1111 TTTCGTCCATGACCCCAAGAGTTTCTGGGGAGGATCTGTATCAGCAGCTTGCTGCAAGCAGCT 1170
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Qy 1167 TTCCGGGCTGATGACAACAGGACTCTGGGGAGGATCTGTATGGCAGCAGTGTTCGGCCACAGT 1226

Db 1171 GGACCCTGCACATGTGTTCTTTATAGCTCTTAATCTCCTAGGTTCTCATCTTGTG 1230
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Qy 1227 GGACCATGCACATGCTGGCCAATGGCCAGTCTCAAGGCATCGAAATCTTTTGT 1286

Db 1231 AATTTGATTTTGGCCATTCTGCCATGTCTTATGACGAATTCCAAAAGAAGGCCGAAGAA 1290
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Qy 1287 AATTTGATTTTGGCCATTCTGCCATGTCTTATGACGAATTGCAAAGGAAGGCCGAAGAA 1346

Db 1291 GAAGAGGCTGCCCGAGGAGCGCGATACGAGAGAAGCTGAAGAAGCGGCAGCCAAGGCG 1350
        |||||||||||||||||||||||||||| ||||| |||||||||||| |||||||| ||
Qy 1347 GAAGAGGCTGCCCGAGGAGCGCGATACGGAGAAGCTGAAGAAGCGGCAGCTGCGCCCAAAGCG 1406

Db 1351 GCCAAACTGGAGAGGCGGGCCAATGACCGGCTCAAGCGGCTCAGGGATGCC 1410
        |||||||||||||||| |||||||||||||||||||| ||||||| || ||
Qy 1407 GCCAAGCTGGAGAGGCGGGCCAATGCGCAGGCAGCGCTCAGGCGATGCGCCGCC 1466

Db 1411 GCTGCGGCAGCTGCATCCCGAGAATGGCAAAGTCCCACGTACTCTTGCATTAGCTAT 1470
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Qy 1467 GCTGCGGCAGCTGCATCCGGAAATGGCCAAGAGTCCCGACGTATTCTTCTGCATCAGCTAT 1526

Db 1471 GAACTGTTTGTTGGTGGCGAGTGGAAGCGGCAACGATGGCAACAAGAGACAAGAAGATGTCCATA 1530
        ||||||||| | || ||||||||||||||||| |||| |||||| | ||||||| |||||||
Qy 1527 GAGCTGTTTGTTGGCGGCGGAGTGGAAGCGGCAACGATGACAACAAGAGAGAAGATGTCCATT 1586

Db 1531 CGGCACCGTCGAAGTGGATGGCGAGTCGGTGAGCGTTATCACAAAGACACCAGCACCTACC 1590
        |  |||| ||| ||| ||||  |  ||||| ||||||||||| ||||||||||||||||||
Qy 1587 CGGAGCGTCGAGGGTGGAGTGGGAGTCGGTGAGCGTTATACAAAAGACAACACCAGCACCTACC 1646

Db 1591 ACAGCAC--CC--GCTACTAAAGTCCGTCAAGTTAGCACCGACTTCCTTATCCGTTACCTGGT 1647
        |||||||  ||  ||| || |||| || |||||| | || ||||||| ||  ||||| |
Qy 1647 ACAGCACACCAAGCTACCAAAGTTCGTAAAGTGATGGCACGACGTATCCTTATCCTTACCTGGT 1706
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Qy 1647 ACAGCACACCAAGCTACCAAAGTTCGTAAAGTGATGGCACGACGTATCCTTATCCTTACCTGGT 1706
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Db 1648 TCACCATTTAAACTACCTACGGCCGGGATCACGTAGTTCACCACAAGTACACAATACGAAAGTGG 1707
        || |||||||| | ||| | ||||| ||||| |||| || | | |||||||||||||||||
Qy 1707 TCACGGTTTAAACATACGCCAGCGAGGGATCTCTCACAAGTTCTCACAAGTACACACACTCATCG 1766

Db 1708 CGTGGACGTTTGGTATACCAGTTAGGCATCGCAAGCCATTGGTACTGCAAACATATCAG 1767
        |  |||||||  |||||||||||||| |||||||| ||||||||  || |  |||||||
Qy 1767 CGTGGCCGCTTGGTATACCCGGTTAGGCATCGTAAGCCATTGGTATTGTCAACATATCAG 1826

Db 1768 GATGCCCAGCAGCATTTGCCCTATGCCGTATGCGATGACTCGGTAACCACCAATGTCCGAA 1827
        |||||| |||||||| ||||| |||||||||| ||||| |||  | |||||  |||||||
Qy 1827 GATGCCCAGCAGCACTTGCCCTATGCCGTAGGACTCGTAGGCGTCGTCACCCCCGATGTCCGAA 1886

Db 1828 GAGAATGGTGCCATTATAGTACCAGCCTACTATTGTAATTGAATTTAGGTTCAGACATTCTTCA 1887
        |||||||||  ||||||||| |||| | || |  |  |||| || | |||||||| ||||| |
Qy 1887 GAGAATGGGCCATCATAGTGCCCGTGTACTATGGCTCCGACACTCATCG 1946

Db 1888 TATACCTCGCATCAATCAATCAAGAATCTCGTATACACATCGGTGATTATTGGTGGCATG 1947
        |||||||||||||||||| |||| |||| |||||| || |||||| | ||  |||||| |
Qy 1947 TATACCTCGCATCAGTCAGTCAAATATCGTATACCTCACATGGCGATCTCACGTCGGGCATG 2006

Db 1948 GCGGCCATGGTGCGCAGTGGCAGCTGCCAATCTACCGATGCCGCAGTTGCCGACACACACG 2007
        ||   | || || ||| |||||||||||||||||| ||| || ||||||| |||||||||
Qy 2007 GCCGTCATGGGCGTCAGCGGCAGCTGCCAATCGACCGATGCCGCAGTTGCGCAACACACG 2066

Db 2008 AATCAATCAATCCGGTGCTGCAACCAATGGTGGAGTAGTACGGCTCGGTGGTGGCTATCCC 2067
        |||||||||| || |  |||| ||| |||| |||   || | |  | | ||| |||||||
Qy 2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGCACCA--C--CTG-TC-TGGACA--CC 2114

Db 2068 GATGCCAATCACAAGGAACAAAGGGATTGAAATGGTCAGGATTATCACAGACGAAGCT 2127
        |||||||||| |||  |||  ||| ||  | |||||  |||| | | |||||||||||
Qy 2115 AATCAATCAGT---GATCATCGCACTACGAATTGGCCTGGACTGGCACGGACGGACGAAGCT 2171

Db 2128 GGCAAAATAAAACACCACGACAATCCTTTATCGAGCCGTCCAAACTCAAACAGTGGTA 2187
        ||||| ||||| |||||||||||| |||||||||| ||||||||||| |||||||||
Qy 2172 GGCAAGATTAAACATCGACAATCCTTTTATCGAGCCGTCCAGACAGACACAAACGGTGGTT 2231

Db 2188 GACATGAAAGATGTTATGGTCTTAAATGATATGCATCATTGACAACGGCCGTCGGCGCATAGT 2247
        || |||||||||||||||||| | |  |  |||||||||||||||| ||||||||||||||
Qy 2232 GATATGAAAGATGTGATGGTCCTGAATGATCATCGAACATCATCGAACAGGCCGTCGGCGCACAGT 2291

Db 2248 CGTGCTAGTGAACGAGTG--------------------AGGACGATGACGAAGAT 2283
        |||||||||||||||||                     |||||||||||||||||
Qy 2292 CGGGCAAGCGATCGCGGTGTCTCCGGTTGTCCGTTTACTATTCCCAACGAGGACGATGACGAGGAT 2351

Db 2284 GGTCCCACATTCAAGGACATCGCCTCGCCGAATACATCCTAAAGGCCGAAAATCTTTTGT 2343
        |||||| ||||||| |||| | ||||| |||  |||| ||||||||||| ||||||||||
Qy 2352 GGGCCCACGTTCAAAGACACTCGAAGTGATCCTCAAAGGCATCGATGTGTTTTGT 2411

Db 2344 GTATGGGACTGTTGTGGGTGTGGTTAAAATTTCAGGAATGGGTGTCTTTATTGTGTTC 2403
        ||| | |||||||||||||||||| | |||| ||||| || |||||||||| ||| |
Qy 2412 GTGTGGGACTGTTGCTCGGGTTTGGTTGAAATTTCAGGAGTGGTATCGGGTTATCGTCATCGTCTTC 2471

Db 2404 GATCCATTCGTGGAGCTCTTCATTAACCCTGTGTATTGTGGTCAATACGATGTTATGGCC 2463
        ||| |||||||| |||||| || || |||||  ||||| || ||||| ||||| || ||
Qy 2472 GATCCCTTCGTGGAGCTCTTCATCATCACCGCTGTGTCGTGTCAACCGATGTTCATGGCA 2531

Db 2464 ATGGATCATCACGACGATATGGTGTAACTTGAAAATGTGGTAACTATTC 2523
        ||| ||||| |||||||| || | |||  ||||| |||| || || |||
Qy 2532 ATGGATCACCACGATATGAACAACAAGGAGATGGAACGCGTGCTGCAACTATTC 2591

Db 2524 TTCACGGCCACTTTGCCGATTGAGGCCAGCATGAAACTGATGCCGAAGTAC 2583
        |||| | |||||  | |||| |||| ||||||| | |||||||   ||||||
Qy 2592 TTCACGGCCACCTTTGCCGATCGGAGGCCATCATGGGCCCCAGTAC 2651

Db 2584 TACTTCCAGGAAGGCTGGAACATTTGTGGGCCTTGTCTCTGCTGGAA 2643
        ||||||||||||  ||||  |||| | |   | | | || | ||||
Qy 2652 TATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGGCCCTATTGGAA 2711

Db 2644 TTGGGCCTGGAGGGTGTCCAGGGGCTCTCGTGGTTGAGAAGTTTGTTCGTTGGT 2703
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Qy  2712  CTGGGACTCGAGGGTGTCCAGGGTCTGTCCGTATTGCGTTCCTTCGATTGCTGCCGTGTA  2771
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Db  2704  TTCAAATTGGCAAAATCATGGGCCACCACTACTCATTTGCGATTATGGGCCGGACA  2763

Qy  2772  TTCAAACTGGCCAAGTCTTGGCCCCACACTTAATTTACTCATTTACTCATTTCGGATCTATGGGACCGCCACC  2831
          ||||| ||||| ||| ||||||||||||||| ||||||||||||||||||||||||||
Db  2764  ATGGTGCATTGGTAATCTGACATTTGTACTTGACTTTGGATTATCATCTTCATCTTTGCCGGTG  2823

Qy  2832  ATGGGCGCTTGGTAATCTGACATTTGTACATTTGACTTGCATTATCATCTTCATCTTTGCCGGGTG  2891
          |||| |||||||||||||||||||||| ||| ||||| |||||||||||||||||||||
Db  2824  ATGGGAATGCAACTTTCGGAAAGACCAATATTGACCACAAGGATCGCTACAAGGACCAT  2883

Qy  2892  ATGGGAATGCAACTGTTCCGGAAGAATTATCACATTCACAAGACCGCTTTCCGGATGGC  2951
          |||||||||||||  ||  ||||  || |||||||  |||||  ||||  ||||| ||
Db  2884  GAATTGCCGCCGCCGGTGGAACTTCACCGACTTGGAATTTCATGCACAGCTTCATGATTGTGTTCCGAGTG  2943

Qy  2952  GACCTGCCGCCGCCGGTGGAACTTCACCGACTTGGAATTTATGCACAGCTTCATGATTGTGTTCCGGGGTG  3011
          ||| ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  2944  CTGTGCGGAGAGTCGATCGAGTCCATGTAATGTGGGCGATGTCAGCTGT  3003

Qy  3012  CTCTGCGGAGAATGGATCGAGTCCATGTCGGGACTGGGACGATGTCTCGTGC  3071
          || |||||||| | ||||||||||||||  | |||| ||||||||  ||
Db  3004  ATACCCTTCTTCTTCTGGCCACGGTCGTGATCGGCAATCTTGTGGTTCTTAAATCTTTTCTTA  3063

Qy  3072  ATTCCCTTCTTCTTCTGCCACCGTTGTCATCGGCAATCTGTGTGGTGTACTTTAACCTTTTCTTA  3131
          || ||||||||||||||| |||| ||| |||||||||  |||||| | ||||| |||||||||
Db  3064  GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTTATCAGCCCCGACTGCCGACAATGAT  3123

Qy  3132  GCCTTGCTTTTGTCCAATTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGAT  3191
          || ||||||||||||||  || | ||||||| ||||||| |||||||||||| || |||
Db  3124  ACCAATAAAAATAGCAGAGGCCTTCAAATCGTATTGCTCGTTTTAAGAACTGGGTGAAACGT  3183

Qy  3192  ACGAATAAAATAAAGCCGAGGCCTTCAAATGGAATTGGCCGCCTCATCAAGAGGGGATCAAG  3251
          || ||||| || || |  || |||||||||  ||  ||   |   | ||||  ||   ||
Db  3184  AATATTGCCGATTGTTTTAAGTTAATTGAAATAAAATGACAAATCAAATAAGTGACCAA  3243

Qy  3252  AATATTGCTGATTGTTTCAAGTTAACGTTAACAAATTGACAAATCAAATAAGTGATCAA  3311
          ||||||||  ||||||| |||||||  |||| |||| ||||||||||||||||| |||
Db  3244  CCATCAG------A-A-CA------TGG--CGAT-A--ATG---  3265

Qy  3312  CCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTTGGAGCGAGAGCAGCATGGTGACAAC  3371
          |||||||                              |||   | ||
Db  3266  -AACTGGAGTTGGGTCATGACGAAATCATGGGCGGATGGCCATTGATCAAAAGGGTATGAAG  3324

Qy  3372  GAACTGGAGCTGGGCCACGCGAGCTTCATCAAGAGGGGATCAAG  3431
          ||||||||  ||||  |  | | |  |  ||
Db  3325  GGCGACCCAGCTGAGGTGGCCATTGGCCATTGGAGTTCACGGATACATGGCGAT  3384

Qy  3432  GAGCAGCGCAACTGGAGGTGGCGGCAACTGGGATCGGCCATCGGGGATCGGGGATCAAG  3491
          ||||||| |||||||||||||||| |||||| |||||||| | |||| | |  | |||
Db  3385  ATGAAAAACAAGCCGAAGAAATCATAAACAACACGATGATTGGAAAC  3444

Qy  3492  ATGAAGAACAACAAGCCGAAGAAATCTAAATAACGCAACGATGATTGGCAAC  3551
          ||||| ||||| ||||||||||||||  |||||| |||||||||||| |||
Db  3445  TCAATAAACCACCAAGAAGCAATAGACTGGACAATGAGCTAAACCATCATAGGTTGTCCATA  3504

Qy  3552  TCAATTAACCACCACCAAGAAGCAATAGACTGGACACGAGGGGATCAAG  3611
          ||||| |||||||| |||||||||||||||||||||
Db  3505  CAGGACGATGACACTGACTAACTAACTCATTAGTAGCCTAGCTTCAGACCATTCAAG  3564

Qy  3612  CAGGACGATGACACCGCCGAGGGCGAGGGCGAGGGCCGACGTCAGC  3671
          |||||||||||||  |  || |||| |||||||  ||||||||||
Db  3565  GACGAGAGCCACCAAGGGCCGCGAGGCGACGAATCCGGACGAGGGCGAC  3624

Qy  3672  GACGAGAGCCAAGGGCCGCGAGGGCGACGATGAGGGGCCAG  3731
          |||||||||||| ||||||||||  ||||  || |  |||
Db  3625  AAAGAGGACCTCGGCCTCGACGGGCCCAAAAACGAATCGCGAGGGCCCG  3684

Qy  3732  AAGGAGGATTAGGTCTCGACGAGGACGAGGAACTGGCAATCCGGAGGAGGGCCCG  3791
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Db  3685  CTGGATGGTGACATCATCATTGATTACTCAGCGATAATCGGATGAATATCCA  3744

Qy  3792  CTCGACGGTGATATCATTATTCATGCACA---CGACGAGGATATACTTCGATGAATATCCA  3848


Db  3745  GCCGACTGTTCCCCACTCGTACTACACAGAAGTTCCGATCGTTGGCCGCGACGAGGAC  3804
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Qy  3849  GCTGATTGCTGCCCCGATTCCGTACTACTATAAGAAATTTCCGATCTTAGCCGTGACGATGAC  3908

Db  3805  TCGCCGTTCTGCAAGGATGGGCAATTACGACTGGGCAATTTCAAAAACTTTGAAAAT  3864
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Qy  3909  TCGCCGTTCTGCAAGGATGGGCAATTACGACTTTTCAATTAATTGAAAAAT  3968

Db  3865  AAATATTTGAAACCGCAGTTATCACTATGATTTAATGAGTAGCTTGGCCTTA  3924
          |||||||||||||  | || |||||||||| |||| |||||| ||||||||
Qy  3969  AAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTGGCATTA  4028

Db  3925  GAAGATGTTCATTTACCCGATCGATCGTCATGCAGGATATATTGTTACTACTACGAGG  3984
          ||||| ||||   |||| |||| |||| |||| ||||||| |||| ||||||| |||
Qy  4029  GAAGATGTACATCTGCCACAAAGACCCATACTGCAAATGTTGGCCCTGGCCTTTAAG  4088

Db  3985  ATATTACGGTGTATATCTTTTTGGAGATGTTGATCAAATGGTTGATCAAATGTTCAATCAAGTA  4044
          |||||||| |  ||| |||||| |||||| | ||   |    | |||| || ||
Qy  4089  ATATTACGGTTATATTCTTCTGGAAATGTTAATCAAGTGGTTGGCGTTGGCGTCGTTCAA  4148

Db  4045  GTTTACTTCACCAATGCCTGGTGTTGCTGGCTCATGTCATCGTCATCGCTTATA  4104
          |||||||||||||| ||||| ||||| |||||||  || | ||   || |||
Qy  4149  GTGTACTTCACCAACGCCGTGGTTGGTTGCTCGTCATTTCGTGATTCGCTTATC  4208

Db  4105  AATTGGTTGCCGTTTGGCTGCCGTTGTGGGCGTTAAATGATGATAGCCGTGTGTTTAGATCAATGAT  4164
          ||||| ||| | |||   ||| ||||| | || ||| | ||| ||||| ||  || |  |
Qy  4209  AACTTCGTTGCTTCACTTGTTGGAGCTGGTGTATTCAAGGCTTCAAGACTATGCGAACG  4268

Db  4165  CTGCGCGCCTAAGGCCATTGCCGTGTCTGTCTAGATGGAGGTATACCGTCATCTTCAATGTGCTCATCTC  4224
          ||  ||   || ||||  ||| |  |||| | |  | || |||||||  ||||||||||||   |
Qy  4269  TTAAGAGACTGAGACCAGTCCCGATGCCCGATGCCATGCAGGGCCATGGTCGTTGGTTAAGCGT  4328

Db  4225  AATGCGCTGGTTCAAGTTACACCGTCATCTTCAATGTCCATTGGTGTGTCTGATATT  4284
          ||||| |||||||||| ||| |||| || |||||||  ||||| |||||| || |||
Qy  4329  AATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTCCATGGTGTGTCTAATATTT  4388

Db  4285  TGGCTTATTTTGTCCATTATGGAGTACAGCTTTTGCTGGAAAATATTTTAAGTGTAAA  4344
          |||||| |||  ||||||| |||| | |||||||| |||  ||||| ||||||| | |
Qy  4389  TGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTAAGTGCCAAAGT  4448

Db  4345  GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT  4404
          || || || |   ||| |  |||||  |||||||||||||  |   | ||||| |||||
Qy  4449  GACATGAATGGCCACGCAAGCTCAGCCGACCCACCAACGCAATCCTGCAATCCTGCAGAGC  4508

Db  4405  GAAAACTACACCTGGAGAAATTCGGCAATGAACTTCGGATCATGGTAATGCCGTCATCTG  4464
          ||||||||||| ||| ||| | || |  || ||  | |||||  |||| | || | |||
Qy  4509  GAGAACTACACGTGGTGTGCGAATTCAGCAATGAATTCGATCATGCAATCATCTGGTAATTAATT  4568

Db  4465  TGTCTATTCAAGTGGCACCTTTAAGGCTGGATCCTGGATGGCCATTGAT  4524
          || |||||||||||||  || || |||  ||  | ||| || ||||||
Qy  4569  TGCCTTTTCCAAGTGGCACCCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGAT  4628

Db  4525  TCACGAGGTGGACAAGCAGCCGATCCGAGAAACCAATATCTATTATATTTC  4584
          ||||||||||||| ||| ||||||||||| ||| ||||| |||||||||||
Qy  4629  TCACGAGGTGGACAAGCTGGACAAGCAACCATTCGTGTTCATGTATTTATATTTC  4688

Db  4585  GTATTCTCATTATTTTGGATCATTTTCCACACTCATTCTTGTTCATTGGTTTATCATT  4644
          ||||||||||| |||| ||||| ||| |||| |||| ||||||||||||||  ||| |
Qy  4689  GTATTCTCATCATATTTGGATCCTTTTTCACACTCGTTGGTTTCATTGGTTTATCATT  4748

Db  4645  GATAATTTTAATGACAAGTACTACATCGATGAAAAACCATTAAAAGCC  4704
          |||||||||||||| |||||||||||| ||||||| |  || |||||
Qy  4749  GATAATTTTAATGAGTACTCATCATAGTGATCGATGAAAAGAAATGTTCATGCCTAAAAACCATTAAAAAC  4808

Db  4705  GATCAGAAAAGTACTATAATGCTCTAAAACCATTAAAAGCC  4764
          |||||||||| ||||||| |||  ||||||||||||  |||
Qy  4809  GATCAGAAAAGTACTATAATGTCTATGAAAAAGAATTGGGCCTAAAAAACCATTAAAAGCC  4868

Db  4765  ATTCCAAGACCAAGGTGGCCGACCACCAAGCAATATTCGACGACTATCCG  4824
          ||||||||||| |||||||||||||||||| |||| |   | |||  |
Qy  4869  ATTCCAAGACCAAGGTGGCCGACCACCAAGCAATAGTCTTTGAAATAACCGATAAGAAA  4928
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         ||| || ||||||||||||||| ||||||| |||||||||||||| |||||| ||||
Qy  6009 ACGCTGTGGCGTCAGCGTCGTGAGGAGTACTGCGCGCCGGCTAATCCAGCACGCACGCCTGGCG 6064
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RESULT  10
ID   US-08-608-618-2 STANDARD; DNA; UNC; 6318 BP.
AC   xxxxxx
DT
DE   Sequence 2, Application US/08808618
CC   Sequence 2, Application US/08808618
CC   GENERAL INFORMATION:
CC     APPLICANT: Soderlund, David M.
CC     APPLICANT: Knipple, Douglas C.
CC     APPLICANT: Ingles, Patricia J.
CC     TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
CC     TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
CC     TITLE OF INVENTION: HOUSE FLIES
CC     NUMBER OF SEQUENCES: 19
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC       STREET: P.O. Box 1051, Clinton Square
CC       CITY: Rochester
CC       STATE: New York
CC       COUNTRY: USA
CC       ZIP: 14603
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, Version #1.30
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/608,618
CC       FILING DATE:
CC       CLASSIFICATION: 530
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Timian, Susan J.
CC       REGISTRATION NUMBER: 34,103
CC       REFERENCE/DOCKET NUMBER: 19603/600 (CRF D-1657)
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: 716-263-1636
CC       TELEFAX: 716-263-1600
CC   INFORMATION FOR SEQ ID NO: 2:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 6318 base pairs
CC       TYPE: nucleic acid
CC       STRANDEDNESS: single
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA
SQ   SEQUENCE 6318 BP; 1713 A; 1349 C; 1592 G; 1664 T; 0 OTHER.

Query Match          56.2%;  Score 3660;  DB 19;  Length 6318;
Best Local Similarity 84.7%;  Pred. No. 0.00e+00;
Matches 4978;  Conservative 0;  Mismatches 814;  Indels 84;  Gaps 21;
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Db  151 ATACGATATGATGACGAGGACGAGGAGGTCCACAGCCGGATCCCAACGCCGGATCCCAACTTGAACAG 210
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Qy  207 ATCCGATATGATGACGAGGACGAGGAGGTCCACAACCGGATCCTACACTTGAACAG 266
Db  211 GGTGTGCCTATACCTGTTCGAATGCAGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT 270
        |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  267 GGTGTGCCAATACCTGTTCGAATGCAGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT 326
Db  271 CTCGGAGGATATCGATCCCTTCACAGTAACAATGTGACATTGTAGTAATAAGTAAGGA 330
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Qy  327 CTCGGAGGATATCGATCCCTACTACAGCAATGTACGACATTCGTAGTTGTAAGCAAGGA 386
Db  331 AAGGATATTTCGTTTCTGCCTCAAAAGCAATGTGGCTGCTCGATCCATTCAATCCG 390
        || ||||||| ||| |||||| |||||||||||| |||||||||||||||||||||
Qy  387 AAAGATATTTTCGCTTTCTGCATCAAAAGCAATGTGGATGCTCGATCCATTCAATCCG 446
Db  391 ATACGTCGTGTAGCCATTATTATTTTCGTTATTTCGTTATTCATTATCACC 450
        |||||||||| |||||||  || |||||||||| |||||||| |||||||||
Qy  447 ATACGTCGTGTGGCCATTTACATTCTAGTGCATCCTAGTTTCCTATTATTTCCTATTCATCATCACC 506
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Db  4825 TTCGATAATCATTATGTTGTTCATTGGCTTAAACATGTTTACCATGACCCTCGATCGG 4884
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Qy  4929 TTCGATAATCATTATGTTGTTCATTGGCTGAACATGTTCACCATGACCCTCGATCGT 4988
Db  4885 TACGACGCCTCCGAGGCTACAACAATGTCCTCGACAAACTCAATGGATATTCGTAGTT 4944
         |||||  ||||| |||  |||| || | |||||||   | ||||| |||||||||||||
Qy  4989 TACGATGCGTCGGACACGTATAACGCGGTCCTAGACTACTTTCAATGCGATATTCGTAGTT 5048
Db  4945 ATTTTCAGTGGCGAATGTCTATTAAAAATATTCGCTTACGATATCACTATTCAAAGAG 5004
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Qy  5049 ATTTTCAGTTCCGAATGTCTTATTAAAAAATTCGCTTTACGATATCACCATTTATTGAG 5108
Db  5005 CCATGGAATTTATTTGATGTAGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTCAGC 5064
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy  5109 CCATGGAATTTATTTGATGTAGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTTAGC 5168
Db  5065 GACATCAATTGAGAGAAGTATTCGTATCGCCGACACTGCTCCGTGGTGAGAGTGGCCAAA 5124
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Qy  5169 GATATTAATCGAGAAGTACTTCGTCGTCCGAGTGGGTCCGGTGGCGTGTGGCGAAA 5228
Db  5125 GTGGGTCGTGTCCTCGTTTAGTCAAGGGTGCCAAGGGTATCCGACGTTGCTGTTCGCG 5184
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Qy  5229 GTGGGCCGTGTCCTCCTCGACTGGTGAAGGGACCAAGGGCCATTCGGACACTGCCTCTTCGCG 5288
Db  5185 TTAGCCATGTCGTTGCCTCGCCTATTCAACATTTGTCTGTTCTTGGTGATGTTC 5244
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Qy  5289 TTGGCCATGTCGTCGCCGGCCCTGTTCAACATCTGCCTGCTGTTCCTGGTCATGTTC 5348
Db  5245 ATCTTTGCCATCTTCGGCATGTCCTTCTTCATGCATGATCAAAGAGGAAGAGAGCGGCATAAAT 5304
         ||||||||||| || ||||||| |||| |||||| | | |||| ||||||||| |||||| ||
Qy  5349 ATCTTTGCCATTTCGGCATGTCGTTCTCATGCAGCGTGAAGAGAGCGGCATTAAC 5408
Db  5305 GCTGTGTATAATTTAAGACATTTGGCCAAAGTATGATATTGCTGTTTCAGATGCTACC 5364
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Qy  5409 GACGTCTACAACTTCAAGAGACCTTGGCCAGAGCATGCTCTTTCAGATGTGCACG 5468
Db  5365 TCAGCCGGTTGGGATGGTGTGTTAGATGCCATTATCAATGAGGAAGATTGCGATCCACCC 5424
         |||||||||||||||||||| | | ||||||||||||||||||||||| | ||||||||||
Qy  5469 TCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGATCCGATCCACCC 5528
Db  5425 GACAACGACAAGGGCTATCCGGGCAATTGTGGTTCAGCGACTGTTGGAATTACGTTTCTC 5484
         |||| |||||| ||||||||||||  |||| ||||||| | |  | ||||| ||||||||
Qy  5529 GACAGCGACAAAGGCTATCCGGGCTACTGGATTGGTTCAGCAATAACCGTTTCTC 5588
Db  5485 CTTTCATATCCTAGTTATAAGCTTTTTGATAGTTATTAATATGTCGTCATTCTC 5544
         || ||||| |||||||||||||||||| |||||||||||||||||||||||||
Qy  5589 CTCTCATACCTAGTTATAAGCTTTTTTGATAGTTATTAATATGTCGTCATTCTC 5648
Db  5545 GAGAACTAGCCAGGCTACGGAGGATGTACAGAGGGTCTCACCGACGACGATTACGAT 5604
         |||||||| | |||| || |||||  || ||||| |||| ||||||||||| |||| |
Qy  5649 GAGAACTATAGTCAGGCCACCGAGGACGTCAAGGGGCTCAACCGACGACGACTACGAC 5708
Db  5605 ATGTACTACGAGATTGGCAACAATTGGCAACAATCGGCCACCGGAGGGCACCCAGTACATACCGATCCGATGAT 5708
         ||||||||||||||  |  |   | |  | |||  |||||||||||||||||||||||||||| | |||||||
Qy  5709 ATGTACTACGAGATCTGAGAATCCGATCCGGAGGGCACCCAGTACATACGGTATGAT 5768
Db  5665 CAGCTGTCCGAGTTTCTGGACGTGCTGGAGCGCCGCGTCTGAGCGCTGGAGATCCGGAACAAG 5724
         |||||||||||| | ||||||||| |||||||||| | |  ||| ||||||||||||||||||
Qy  5769 CAGCTGTCCGAATTCCTGGACGTACTGGAGCGCCGACCCGGACGTCTGGAGATCCGGAACAAG 5828
Db  5725 TACAAAATCATATCGATGGACGACATACCCATCGTCTGCGGTGACTTGTCTGTGTGGAT 5784
         ||||| ||||||||||||||||||||||| |||||||||||||||||||||| ||||
Qy  5829 TACAAGATCATATCGATGGACGACATACCTGTCTGCGGTGACTTGTCTGTCTGCGAC 5888
Db  5785 ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCCGACACGGTAATCCGATGGAGGACG 5844
         ||  | ||  ||||| || ||||||||||||||||||||||| || ||||| ||||||
Qy  5889 ATCCCTCGACCCCCTTACGAAAGACTTCTTTGCGCCGACACCGGATAGGAGGAGACG 5948
Db  5845 GGTGAAATTGGTGAGATAGGCGCGCACCGGACGATATCCGGTGTCGTCG 5904
         ||||| |||||||||||||||| |  || |||| || |||||| |||| |
Qy  5949 GGTGAGATTGGTGAGATAGGCGGAGGGCTACGGAGCCCGTCTCATCA 6008
Db  5905 ACACTGTGGCGCCAGCGTGAGGAGTACTGCGCGCCGGCTAATCCAGCACGCACGCACGAATGCGTGGCG 5960
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Db   451 ACTATTCTAACTAATTGTATTTAATGATAATGCCGACAACGCCCACGGTCGAATCCACA  510
         ||  ||||| ||  |||| ||| |||||||||| ||||||||||||||| || ||||| |
Qy   507 ACAATTCTCGTCAACTGCATCCTGATGATAATGGCCGACAACGCCCACCGTGAGTCCACT  566

Db   511 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT  570
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   567 GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT  626

Db   571 TTCATTTATGCCCGTTACGTACTTAGAGATGCATTGGAATTGGCTGGACTTCGTAGTA  630
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   627 TTCATTTATGCCCGTTACGTACTTAGAGATGCATTGGAATTGGCTGGACTTCGTAGTA  686

Db   631 ATAGCTTAGCTTATGTGACCATGGCATAGATTTAGGTAATCCTCGCAGCTTTGAGACA  690
         ||||||||||||||||||||||||||||||||||||||||||||||| | ||  ||| |
Qy   687 ATAGCTTAGCTTATGTGACCATGGTATAGATTTAGGTAATCCTCGCAGCCCTCGGAACG  746

Db   691 TTTAGGGTACTGCGAGCTCTGAAAACCTAGCCATTGTGCCAGGTCTAAAAAACCATTGTC  750
         ||||||||| |||  ||||| || ||| ||||| ||||||| ||| ||     |||| |
Qy   747 TTTAGGGTGCTGGAGCGCGTTAAAACCGTAGCCATTGTGCCAGGTTCTGAGAACCATCGTC  806

Db   751 GGTGCTGTCATTGAATCTCGCCGATGGGCCTACAAATCTATATGGTGTTCTAACACAAAGTGC  810
         ||  |||| |||| |||| |||||||||||||  || |  | | || ||||||||| |||
Qy   807 GGCGCCGTCATCGAATCGGTGAAGAATCTGCGGGCCTACAGTGCCCGTGTACTATTCCTGACCATGTTCTCC  866

Db   811 CTGTCGGTGTTCGCGCTGATGGGCCTACAAATCTATATGGTGTTCTAACACAAAGTGC  870
         ||||||||| |||||||||| |||||||| | | || | |||   ||||||||||||
Qy   867 CTGTCGGTGTTCGCGTGATGGGCCTACAGATCTATATGGCGTGTCCCGAGAAGTGC  926

Db   871 ATTAAACGATTCCCCTGGACGGCAGTTGGGCCAATCTGACCGATGAAAACTGGTTTCTA  930
            |||||  |||||||| ||||||||||||||||||||||||||||||||||||||||
Qy   927 ATCAAGAGTTCCCGGTGGACGGTTCCTGGGCAATCTGACCGACGAGAACTGGGACTAT  986

Db   931 CACAATAGCAACAGTTCCAATTGGTTACGGGAGAACGATGGCGAGTCATATCCGGTGTGC  990
         ||||| ||| ||| |||||||||| | | ||||||| ||||||||| ||  ||||| ||
Qy   987 CACAATAGCCAATAGCTCGTTCTTATATAGTCATTGGTTCATTCTCCGGTTATGC  1046

Db   991 GGGAATGTATCCGGTCGGGACAATGCGGCGAAGATTACGTCGCCTGCGAGGGCTTCGGC  1050
         |||||||| ||||||||||| ||||||| ||||||||||||||  |||| ||||| ||
Qy  1047 GGCAATATCCGGTGCGGGGCAATGCGACGATTACGTCGCGCTTCGGTTGCGAGGGGTTTGGT  1106

Db  1051 CCCAATCCAACTACGACTACCAGTTTCGACTCATTCGGATGGCCTTTCCTGTCGCC  1110
         || |||| | || || || |||| ||| ||| | ||  | || ||||||||||| ||
Qy  1107 CCGAATCCGAATTATGCCTACCAGCTTCGTATCGTATGGCGTTCGGTATGGCCTTTCCTGTCCGCC  1166

Db  1111 TTTCGGTCTCATGACCCAAGAGATTCTCGGGAGAATCTGTATCAGCACGTGCTGCAAGCAGCT  1170
         |||| ||| |||| |||||| | |||||||||| |||  ||  || ||||  ||||| ||
Qy  1167 TTCCGGCGTGATGACAGGAGGCTCTGGGAGGATCTGTACCAGCTGTGTTGCGGCCGCC  1226

Db  1171 GGACCCTGGCACATGTGTTCTTTATAGTCATTCATCATCTTCCTAGGTTCATTCTTATCTTGTG  1230
         |||||| |||||||| ||| |||| | | ||||||| |||||| ||||||||||||||||||||
Qy  1227 GGACCAATGGCACATGCTGTCGTTCTTTATAGTCATTCATCTTCTTAGGTTCATTCTTATCTTGTG  1286

Db  1231 AATTTGATTTTGGCCATTGTTGCCATGTCTTATGACGAATTGCAAAAGAAGGCCGAAGAA  1290
         |||||||||||||||||| ||| ||| || ||||||| ||||||||||||||||||||||
Qy  1287 AATTTGATTTTGGCCATTGTTGCCATGTCTTATGACGAATTGCAAAAGAAGGCCGAAGAA  1346

Db  1291 GAAGAGGCTGCCGAAGAGGAGGCGGATCCGAAGCTGAAGAGGCGGCAGCCAAGGCG  1350
         |||||||||||||||||||||||||| |||| |||||||||||||||||||  ||||
Qy  1347 GAAGAGGCTGCCGAAGAGGAGGCGGCGCCGAAGCTCAAGCGGCTCAGCGCGGATGCG  1406

Db  1351 GCCAAACTGGCACTGGCAGAGGAGCGCCTCAAGCGGCTCAGGATGCGGCGGATGCC  1410
         |||||| |||||| |||  |||||||| ||||||||||||||| |||| |||||||||
Qy  1407 GCCAAGCTGGCACTGGCGGAGAGGCGACAGCCAGCTCAGGAGCGCCGAAGATGCCGCC  1466

Db  1411 GCTTCGCTGCAGCTCTGCCATGGCAAAGATGCCCACGTACTCTTGCATTAGCTAT  1470
         || |||| || |||||||||||||| || |||||||||||||||||||||||||||
Qy  1467 GCTTCGCTGCACTGCAGCTCCGACGTATTCTTGCATCAGCTAT  1526

Db  1471 GAACTGTTTGTTGGCGGCGAGAAGGGCAACGATGACAACAAGAGTATGTCGATA  1530
         || |||| ||||| |||||||||||||||||||||| |||||  | || |||||
Qy  1527 GAGCTGTTATTGTTGGCGGCGAGAAGGGCAACGATGACAACAACAAGAGAGTGTCCATT  1586
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Db  1531 CGCAGCGTCGAAGTGGAATCGGAGTCGGTGAGCGTTATACAAAGACAACCAGCACCTACC  1590
         || ||| |||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Qy  1587 CGGAGGCGCGAGTGGAGTCGGAGTCGGTGAGCGTTATACAAAGACAACCAGCACCTACC  1646

Db  1591 ACAGCAC-CC--GCTACTAAAGTCCGTCAAGTTAGCACGACTTCCTTATCCTTACCTGGT  1647
         | |||| | ||    ||| ||||| ||||||||| || |||||||||||| ||||| |||
Qy  1647 ACAGCACCACCAAGTTCGTAAAGTTCGTAAAGTGAGCACGACAATCCTTATCCTTACCTGGT  1706

Db  1648 TCACCATTTAACCTCACGCCGGGATCACGTACGTAGTTCACACAAGTACACAATACGAAATGGG  1707
         |||  |||||||| || | || ||||| ||| |||  | ||| | | ||||  |||| |||||
Qy  1707 TCACCGTTTAACATACGGAGGGGATCACGTAGTTCTCACAAGTACACGATACCGGAACGGA  1766

Db  1708 CGTTGGACGTTTGGTATACCAGGTAGGCGGATCCCAAGCCATTGGTACTGCAAACATATCAG  1767
         |||||| ||||||||||||| |||||| |||||||||||||||||| ||| ||||||||||
Qy  1767 CGTGGCCGCTTTGGTATACCAGGTAGGCGATCCGTAGGCCATTGTATTGTCAACATATCAG  1826

Db  1768 GATGCCCAGCAGCATTGCCCTATGCCGATGACTGGAGCTCGAATGACGTCAACACCAATGTCGAA  1827
         ||||||||||| |||||||| || | |||||| ||||||| |||||||||||| |||||||||||
Qy  1827 CGTGGCCCGCTTTGGTATACCCGCGACGACTGGAAGCCGTAAGCCATTGTGTCACCCCGATGTCCGAA  1886

Db  1828 GAGAATGGTGCCATTATGTACCAGCCTACTATTGTAATTGAATTTGACAATGTTCTCA  1887
         |||||||||| | ||| ||| || || ||||| | | || ||||||| | |||| ||
Qy  1887 GAGAATGGGGCCATCAGTGCCCGTGTACTAGTCCCGACTCAGTGCAATCGAATCTAGGCTCCCGACACTCATCG  1946

Db  1888 TATACCTCGCATCAATCAAGAATCTGTATACATCACATGGTCGATTTATTGGGTGGCATG  1947
         ||||| ||  ||||||| | || |||||| || || |||||| |||| ||||||||| ||
Qy  1947 TATACCTCGCATCAGTCCGAATATCGTATACCTCACATCGGGATCGATCTCACGGAGAGTGC  2006

Db  1948 GCGGCCATGGTGCCAGCACAATCGGTCCAGCACACCGCAGTCGCAGTGCCAACACCACGC  2007
         || ||||||| || ||||||| ||  ||| ||||| ||| || ||  |||| || |||||
Qy  2007 GCCGTCATGGCGTCAGCACAATGCCAGCCAGCACACCGCCAAATTGCGCAACGCCAACACCACCGC  2066

Db  2008 AATCAATCAATCGTGCTGCAACCAATGGCAACCATGGGGTCAGTAGTACGGCGTGGCTATCCC  2067
         |||||||| | |  |||| |  |||||  |  |||  |   |  |  || ||  | |||||||
Qy  2067 AATCAATCAGT-GG-GC-GCCACCAC--CTGTC--TTGGA--C-A--CC  2114

Db  2068 GATGCCAATCACAACAAAGGAACAAAGGGATTATGAAATGGGTCAGGATTATACAGACGAAGCT  2127
         ||||||| |  ||||||  |  | |||||  |  ||||  ||||||| |  |||| | |  || |
Qy  2115 AATCACAAGCTC---GATCATCGCGACTACGCAATCCTTTTATCGGAGCGGGCCCGTCCAAACTCAAACGGTGGT  2171

Db  2128 GGCAAAATAAAACACCAGACAATCCTTTTATCGGAGCGGGCCCGTCCAAACTCAAACAGTGGTA  2187
         ||||| ||| | | |||| || ||| ||| ||| ||||| |||| |||| | |||| ||||||
Qy  2172 GGCAAGATTAAACATCATGACAATCCTTTTATCGGAGCGGGCCCGTCCAAACTCAAAACCGGTGGTT  2231

Db  2188 GACATGAAAGATGTTATGGTCTTAAAATGATTATCATTGAACAGAAGCCGGTCGGCATAGT  2247
         || |||||| | ||| || ||  ||||| | || |  |||  |  || |||| |||||||
Qy  2232 GATATGAAAGATGTGATGGTCCTGAATGACATCATCGACAGGAAGCCGGTGGTCGGCGGCACAGT  2291

Db  2248 CGTGCTAGTGAACGAGGTG----------AGGACGATGAACGAAGAT  2283
                                      |||||| |||| ||| | |
Qy  2292 CGGGCAAGCGGATCGCGGTGTCTCCGTTGTCCGTTTACTATTCCCACAGAGGACGATGAACGAGGAGAT  2351

Db  2284 GGTCCCACATTCAAGGACATCGCCCTCGAATATATCCTAAAGGCATCTAAAGCCATCGAAATCTTTTGT  2343
         |||||||| ||| | || |  ||  |  | | | | ||  || || | | ||| |||| ||||| |||
Qy  2352 GGGGCAAGCGGATCGCGGTGTCTCCGTTGTCCGTTTACTATTGCCCACAGAGGACGATGAACGAAGAT  2411

Db  2344 GTATAGGGACTGTTGTTGGGGTGGTTAAAATTTCAGGAATGGGGTCTTCCTTTATTGTGTTC  2403
         | ||  | |  |  || || ||| ||    ||||  || | ||  | |  || | |  | | |
Qy  2412 GTGTGGGGACTGTTGCTGGGGTTGGTTTGAAATTTCAGGAGTGGGTTGAAATTTCAGGGAGTGGCTTATCTTCGCTCATCGTCTTC  2471

Db  2404 GATCCATTCGTCGAGCTTCATTACCCTGTGTATTGTGGTCAATCAGTTCATGGCC  2463
         | ||||| | |||||| |||  |  ||| || |||| ||| || |||| ||||||
Qy  2472 GATCCCTTCGTCGAGCTCTTCATCACCGTGTGGTCAACGATGGTTCAACACGATGGTTCATGGCA  2531

Db  2464 ATGGATCATCACGACGACGAATCCCGATGACATCAAGGCCATGATGACGGAGTACTTTC  2523
         |||||| ||||||| |  | ||  | |   ||  || | | ||||  ||| ||||||||
Qy  2532 ATGGATCACCACGATATGAACAAGGACAAGGAGAGAATGGCCAGAAACTGGTCAACTATTC  2591

Db  2524 TTCACGGCCGCACTTTGCATCCGGAAGACTTTTGCCAATTGGCCATGGCCCAAGTAC  2583
         ||||||||| | ||| |||||| ||| || ||||| | || | || ||||||||||||
Qy  2592 TTCACGCGCCACCTTTGCCATCGGAAGGCCACCATGAATGGCCCATGCCTCGCTGCTGGAA  2651

Db  2584 TACTTCCAGGAAGGCTTGGAACATTTCATTATTGTGGCCTTGCTGTCTGCTGGAA  2643
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Qy  3732  AAGGAGGATTAGGTCTCGACGAGGAACTGCCCAAAACGACGAGCAGGAGGGCGAATGCGAGGAGGGCCCG  3791
          ||  ||||||||  |||| |||| || |||| ||  |||| ||   ||  | ||||| |||||||||||
Db  3685  CTGGATGGTGACATTATCATTCATTCATTCGGTTGTTGAGAAGTTTCGTTTGCTTCGTGTA          3744

Qy  3792  CTCGACGGTGATATCATTATTCATCATGCACA---CGACGAGGATATACTCGATGAATATCCA        3848
          |||||| | ||   ||  ||  ||||   |||      |  ||   |  | ||  || || ||
Db  3745  GCCGACTGTTCCCCGACTCGTACTACAGAGAAGTTCCGATCTTGGCCGCGACGAGGAC            3804

Qy  3849  GCTGATTGCTGCCCCGATTCGTACTATAGAAATTCCGATCTTAGCCGGTGACGATGAC          3908
          ||||| ||| |  | ||   ||   ||     || |   | | || |  ||| ||  |
Db  3805  TCGCCGTTCTGCCAAGGATGGGCCAATTTACGACTTTTCAATTAATTGAAAAT                3864

Qy  3909  TCGCCGTTCTGCCAAGGATGGGCCAATTTACGACTTTTCAATTAATTGAAAAT               3968
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  3865  AAATATTTGAAACCGCAGTATCACTATGATTTAATGAGTAGCTTTGGCCTTA                3924

Qy  3969  AAATATTTGAAACAGCTGTTATCACTACTGTACTACACATGGACAGG                    4028
          |||||||||||| ||  |  ||||||| || ||||||| | || |||
Db  3925  GAAGATGTTCATTACCCGATCGACCTGTCATGCAGGATATACTGTACTACACATGGACAGG      3984

Qy  4029  GAAGAGTAGCATCTGCCACAAAGACCCATACTGCAGGATATTTTATACTATATGGACAGA       4088
          ||||| || ||| | ||| |||  | ||| | | ||   ||||||| ||| || || |
Db  3985  ATATTTACGGTGATATTCTTTTGGAGATGTTGGCCGATCAAATGGTTGGCCCTGGCCTTAAG    4044

Qy  4089  ATATTTACGGTTATATTCTTCTTGAAATGTTAATCAGGTGGTTGGCGTCGGTCGTT          4148
          |||||||||||  |||| | || | |  | || ||  | ||  | |||| |||| ||
Db  4045  GTCTACTTCACCAATGCCTGGTGTTGGCTGATTGCTGATGTTCGTGATTGCTATCGCTATC      4104

Qy  4149  GTGTACTTCACCAACGCCGTGTGTTGGCTCGATTTGCGATTGCTATCGCTATC             4208
          |||||||||||||||||||||||||||| ||||| |||| |||||||||||||
Db  4105  AATTTGGTTGCCGTTTGGTCGGGCTTAAATGATGATAGCCGTGTGTTAGATCAATGCGCACA    4164

Qy  4209  AACTTCGTTGCTTCCACTGTTGGAGCTGGTGTATTCAAGACTCAAGACTATGGAACG         4268
          ||  ||||||||| || |||||| | |||||| ||| ||  |||||  |  ||||||
Db  4165  CTGCGCGCCCTAAGGCCATTCATCTGTCGTCTCTAGATGGAGGTGCCCGGGTG              4224

Qy  4269  TTAAGAGCACTGAGACCACTACGTGCCATGCCCGTATGCAGGGCGTCGGGTCGTCGTT        4328
          |  |  |||||||| |   | |||||||   | | |||||||   | | | |||||||
Db  4225  AATGCGCTGGTTCAAGCTACACGTCCATCTCATTCAATGTGCTATCTGTGTGTGCTATATTT    4284

Qy  4329  AATGCGGTGTACAACGCGTATCGACATGAATTCGATCGATGTGCTAATATTT              4388
          |||||||  ||||| | | | |||| || ||  || | ||||||| |||||||
Db  4285  TGGCTTATTTTGCTGGAGTAAGTGGAAAATATTTTAAGTGTAAA                      4344

Qy  4389  TGGCTTAATTTTGCCCATAAATGGGTTGCTGGAAAATATTTTAAGTGCAG                4448
          |||||||||||||| |||||||||| | |||||||||||||||||| ||
Db  4345  GATGTGTAATGACACTGTCTGAGCCATGAATCATACCGATCAATCATTATATTTC           4404

Qy  4449  GACATGAATGGCACGAAGCTCAGCCGACGAACCAATTCGTGAAACGAACATCCAATCACAGT    4508
          || |||||||| || |||||||||| | |||||||||  |||||||| || | |||||||||
Db  4405  GAAAACTACACCTGGGAAATTCGGCAATGAACTTCGATGGTAGGTAATGCGTATCTC          4464

Qy  4509  GAGAACTACACGTGGGAATTCAGCAATCAGAATTTCGATCGATGTGGTAACGCGTATCTG      4568
          | ||||||||| |||||| || || | ||||| || || | ||| ||| || ||||| |
Db  4465  TGTCTCTATTCAAGTGCCACCTTTAAGGCCATTGGAAACATGCCATTGAT                4524

Qy  4569  TGCCTTTTCAAGTGCCACCTGCAAGGCTGGATACAAATCATGACGATGCTATCGAT          4628
          ||||| | |||||||||||| |||| | ||  | |||| |||| | || || || ||
Db  4525  TCACCGAGGTGGACAAGCAGCCGATCCGAGAAGAACCAATATCCACATGTATTATATTTC      4584

Qy  4629  TCACCGAGGTGGACAAGCAGCAACCAATTCGTGAAACGAACATCGACACTACACATATTTC     4688
          ||||||||||||||||||||| | |||||| |||||| || || | || | ||| |||||
Db  4585  GTATTCTTCATTATTGGATCATTTTCACACTCGTTCATTTGGTTATCATT                4644

Qy  4689  GTATTCTTCATCATTTGGATCCTTTTTCACACTGTTCATTGGTGTTATCATT              4748
          |||||||||| ||| |||||| |||||| ||||| |||| || ||||||||
Db  4645  GATAATTTAATGAACAAAAGAAGAAAAGCAGGTGAAATGTTCATGACAGAA                4704

Qy  4749  GATAATTTTAATGAGCAAAGAAAAAGAAAAATGTTCATGACAGAA                     4808
          |||||||| |||| |||| |||||| |||||||||||||||||||
Db  4705  GATCAGAAAAAGTACTATAATGCTATGAAAGATGGCTCTAAAAAAGCC                   4764

Qy  4809  GATCAGAAAAAGTACTATAATGCTATGAAAGATGGCTCTAAAAAACCATTAAAAGCC         4868
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Qy  2652  TATTTCCAGGAGGAGGCTGGAACATCTTCGAACTTCATTATTCGTGGCCCTATCGCCATTGGAA   2711
          ||  ||||||||  |||| |||| ||  |||| ||   | | ||  |||| ||| | |||||||
Db  2644  TTGGGCCTGGAGGGTGTCCAGGGCCGTGCCGTTTCGGTTGTTGAGAAGTTTCGTTTGCTCGTGTA 2703

Qy  2712  CTGGGACTCGAGGGTCGAGGGCCGTGCTGGTCGTATTGCGTTCCTTTCGATTGCTGCTGCGTGTA 2771
          |||||||||||||||||||||||| | |  ||| || || |  | || ||| ||   |  ||
Db  2704  TTCAAATTGGCAAAATCATGGCCCACACTCAATTACTCATTTCGATTATGGGCCGGACA         2763

Qy  2772  TTCAAACTGGCCAAGTCTTGGCCCACACTTAATTTACTTACTCATTTCGATTATGGGACGCACC   2831
          ||||| ||||| ||| ||||||||||||| |||| || || |||||||||||||||  || |||
Db  2764  ATGGGTGCATTGGTAATCGACATTGTACTTGTACTTTGCATTATCATCTTCATCTTGCCGTG     2823

Qy  2832  ATGGGCGCCGTTTGGGTAATCGACTTGTGCATTGTGCATTTGCATGTCATCTTCATCTTTGCCGGTG 2891
          ||||| ||||||||||||||| || |||| ||| || ||| |||| ||| |||||| |  || |||
Db  2824  ATGGGAATCAACTTTTCGGAAGAACTATATTGACCACCAAGGATCGCTTCAAGGACCAT         2883

Qy  2892  ATGGGAATCAACTTTTCGGAAATCAACTATATTGACCACCAAGGATCGCTTCAAGGACGACC     2951
          |||||||||||||||||||||| |||||||||||| |||| ||||| | ||  |||  | ||
Db  2884  GAATTACCGCCGCTGGAACTTCACCGAGCTTCATGATGTTGTTCCGACGTG                2943

Qy  2952  GAATTACCGCCGCTGGAACTTCACCGAGCTTCACGATGTTGTGTTCCGACGTG             3011
          |||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  2944  CTGTCGCGGAGAGTGGATCGAGTCGCATGTGGGCCGATGCTCAGCTGT                   3003

Qy  3012  CTCTGCGGGAGAATGGATCGAGTCGCATGTCGATGCCATGTCAGCTCGTCGTGC            3071
          || |||||||||| ||||||||||||||||| |||| ||||||||| || || |
Db  3004  ATACCCTTCTTCTGGCCACGGTCGTGTTCTTAATCTTTCTTA                        3063

Qy  3072  ATACCCTTCTTCTGTGCCACGGTCGTGTTCTTAATCTTGTGGTACTTAACCTTTTCTTA       3131
          |||||||||||||| |||||||||||||||||||||| |||| ||||||| ||||||||
Db  3064  GCTTTGCTTTGTTGTCCAATTTTGGCTCATCAGTTTCATCAGTAGTTATATCAGCGATGAT     3123

Qy  3132  GCTTTGCTTTGTTGTCCAATTCTGGCTCATCAGCTTGCTATCGTCAGTTTCATCAGTAACGAT   3191
          |||||||||||||| ||||||||||||||||| || | | || |||||||||||||| | |||
Db  3124  ACCAATAAAAATAGCAGAGGGCCTTTTAAGAACTGGGTGAAACGT                     3183

Qy  3192  ACGAATAAAAATAGCGAGGCCGAGGCCCTCATCGATTTTTAAGAACTGGGTTAAGCGT        3251
          || ||||||||||| || |  |||| |  | || |||||||||||||||| ||||| ||
Db  3184  AATATTGCCGATTGTTTAAGTTAATTGACAAATAAATTGACAAATAAGTGATCAA           3243

Qy  3252  AATATTGCTGATTGTTTCAAGTTTAATACGTTAATAACAAATCAAATAAGTGATCAA         3311
          |||||||| |||||||| ||| |||||||| |||||| ||||| |||||||||||||
Db  3244  CCATCAG------------TGG--CGAT-A--ATG                                3265

Qy  3312  CCATCAGGGTGAGAGGACCAACCAGATCAGTTGGATTGGAGCGAAGAGCCATGTTGACAAC     3371
          |||||||  |  |  | | || | ||| ||  ||  | |||||| |||| || | || |||
Db  3266  -AACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTCAGATTTGTCATCATTTCCATA    3324

Qy  3372  GAACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTCAGATTTGTCAGCATTTCCCTTA   3431
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||
Db  3325  GGCGAGACCCAGCTGGAGTGGCATTGGCCATGGCATGAGTTCACGATACATGGCGAT          3384

Qy  3325  GGCGGATGACACTGCCAGCTGGATGGTGGCCATGGCATGAGTTCACGATACATGGCGCGAC     3491
          |||| ||| |   | |||||||| ||| |||||||||||||||||||||||||||| | ||
Db  3385  ATGAAAAACAACAGCCAAGACCCGAGAAATCATGACAACAACAACGACGATGATGAAAC      3444

Qy  3492  ATGAGAAGACACAGCCGACACTGCCCAGCATTAACTTAACTGGAATAATATCCAACGATGCTATCGAT 3551
          ||||  |  ||| |||| |||| |||||||||| ||||| |||| ||||| |||||||||||| ||
Db  3445  TCAATAAACCACCAAGAACAATGACTGGAACATAGAGCTAAAACCATAGAGTTTTGTCCATA     3504

Qy  3552  TCAATTAACCACCAAGAACAATGACTGGAACATAGAGCTAAAACCATAGAGGTTTCCCTTA     3611
          ||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||| ||
Db  3505  CAGGACGATGACACTGCCAGCACTTAACTCATATGGTAGCCATAAGAATCGACCATTCAG     3564

Qy  3612  CAGGACGACGACACTGCCAGCATTAACTCATATGTGTAGCCATAAGAATCGACCATTCAAG     3671
          ||||||||| ||||||||||| ||||||||||| ||||||||||||||||||||||||| |
Db  3565  CAGGACGCCCACAAGGCCCAGCGGCCAGCCATCGGAAACGACACGTCAGC                3624

Qy  3672  GACGAGAGCCCACAAGGCCCAAGGGGCCACAAGGGCCAGCGGCCGAGACGACGGCGCGCCAGC   3731
          |||||||||| |||||||||| |  ||||||||  |||||||| || |||||| | | |||||
Db  3625  GACGAGAGCCGAGGAGGGCGAGGAGGGCGAGGAGCCGAGGAGGGCGAGGAGGGCCCAG        3684
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Db   5845 GGTGAAATTGGTGAGATAGCCGGCGCGACGACACCGAGGGCTATGATCCGGTGTCGTCG 5904
          || ||||||||||||||||||||| || |||||  |||| || |||||||||  ||| ||
Qy   5949 GGTGAGATTGGTGAGATAGCCGGCGCCCCGCCCGGATACGGAGGGCTACGAGCCGTCTCATCA 6008

Db   5905 ACACTGTGGCGCGCCAGCGTGAGGAGTACTGCGCCAAGCTGATACAGAATGCGTGGCG 5960
          || |||||| |||||||||||||||||||||||||||| || |||| |||| ||  ||||
Qy   6009 ACGCTGTGGCGTTGGCGGCGTGAGGAGTACTGCGCCCGCTAATCCAGCACGCGCCTGGCG 6064
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RESULT 11
ID   US-08-808-793-26 STANDARD; DNA; UNC; 1237 BP.
AC
DT
DE   Sequence 26, Application US/08808793
CC   Sequence 26, Application US/08808793
CC   GENERAL INFORMATION:
CC     APPLICANT: Soderlund, David M.
CC     APPLICANT: Ingles, Patricia J.
CC     TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
CC     TITLE OF INVENTION: AND USE THEREOF
CC     NUMBER OF SEQUENCES: 32
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
CC       STREET: Clinton Square, P.O. Box 1051
CC       CITY: Rochester
CC       STATE: New York
CC       COUNTRY: USA
CC       ZIP: 14603
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, Version #1.30
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/808,793
CC       FILING DATE:
CC       CLASSIFICATION: 435
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 60/034,361
CC       FILING DATE: 24-DEC-1996
CC       CLASSIFICATION: 435
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: US 60/012,649
CC       FILING DATE: 01-MAR-1996
CC       CLASSIFICATION: 435
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Braman, Susan J.
CC       REGISTRATION NUMBER: 34,103
CC       REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: 716-263-1636
CC       TELEFAX: 716-263-1600
CC   INFORMATION FOR SEQ ID NO: 26:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 1237 base pairs
CC       TYPE: nucleic acid
CC       STRANDEDNESS: single
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: cDNA
SQ   SEQUENCE 1237 BP; 310 A; 309 C; 293 G; 325 T; 0 OTHER.

Query Match             7.2%;  Score 472;  DB 21;  Length 1237;
Best Local Similarity  76.6%;  Pred. No. 0.00e+00;
Matches   679;  Conservative   0;  Mismatches 207;  Indels   0;  Gaps   0;

Db    187 ACAACTGTTCGCTGGCAAATATTCAAGTCGTCGACCTCAACCACCACGACGTTGAGCCA 246
          ||||| ||||||| |||||||||||| | |||| || |||| ||||||||| |||||||
Qy   4415 ACAGCTTTTGCTGGAAAAATATTTAAGTGCGAGACATGAATGGCACGAAGCTCAGCCA 4474

Db    247 CGAAAATCATCCAGACGCGGAATGCGTGCATCTTAGAGAACTACACCTGGGAGAACTCACC 306
          ||| || |||||||||| ||| | |||  ||||||||||||||||||||||||| | |||
Qy   4475 CGAGATCATACCAAATCGCAATCCTGCGAGAGCCGCGGAGAACTACACGTGGGTGAATTCAGC 4534
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Db   4765 ATTCCAAGACCGAGGTGGCGACCACACGCAATGTCCTCGACAAACTCAATGGATATTCGTAGTT 4824
          |||||||||||||||||||||||||||||||||||| ||||  |||||| ||| ||||||||||
Qy   4869 ATTCCAAGACCAAGTGGCGACCACCAGCAATAGTCTTTGAAATAGTAGTAACCGATAAGAAA 4928

Db   4825 TTCGATAATAATCATTATGTTGTTCATTGGCTTAAACATGTTTACCATGACCCTCGATCGG 4884
          |||||||||||| || ||| |||||||||| | ||||| ||| |||||||  |||||||||
Qy   4929 TTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATCGT 4988

Db   4885 TACGACGCCTCCGAGGCGTACACACAATGTCCTCGACAAACTCAATGGATAATTCGTAGTT 4944
          ||||||  || ||||||| ||| ||||||||||||| ||| |||| |||||||||||||||
Qy   4989 TACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGGATATTCGTAGTT 5048

Db   4945 ATTTCAGTGGCGAATGTCTTATTAAAAATTCGCTTACGATATCACTATTCAAAGAG 5004
          ||||||||||||||||||| |||| ||| ||||||| | ||| || |||||||||
Qy   5049 ATTTCAGTTCCGAATGTCTTATTAAAAAATATTCGCTTTACGATATCACTATTTATTGAG 5108

Db   5005 CCATGGAATTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTTACTCAGC 5064
          ||||||||||| ||||||||||||||| |||||||||||| ||||||||||||||||||
Qy   5109 CCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTTACTTAGC 5168

Db   5065 GACATCATTGAGAAGTATTCGTATCGCCGACACTGCTCCGTGTGGTGAGAGTGGCCAAA 5124
          ||| |  ||||||||| |||| ||||||||||||||||||||| |||||| ||||||
Qy   5169 GATATTATCGAGAAGTACTTCGTGTCGCCGACCCTCCGAGTGGTGCGTGTGGCGAAA 5228

Db   5125 GTGGGTCGTGTCCTGCGTTTAGTCAAGGGTGCCAAGGGTATCCGGACGTTGCTGTTGCCG 5184
          ||||| |||||||||| ||||| |||| ||| || ||||||||| || ||| |||| ||||
Qy   5229 GTGGGCCCGTGTCCTGCGACTGGTGAAGGAGCCAAGGGCATTCGGACACTGCTCTTCCGCG 5288

Db   5185 TTAGCCATGTCGTTGCCTCCTTATTCAACATTTGTCTGTTGCTGTTCCTTGGTGATGTTC 5244
          ||||||||||| ||| ||| |||| || | || |  |||| |  |||| ||||| ||||||
Qy   5289 TTGGCCATGTCGTTGCCGGCCCCGTTCAAACATCTGCCCTGCTGCGTTCCTTGGTCATGTTC 5348

Db   5245 ATCTTTGCTATCTTGGGATGTCCTTCTTCATGCGATGTCAAAGAGAGAGAGCGGCATAAAT 5304
          ||||| || | ||| |  |||||| |||||||||||||||| |||| ||| ||||| || |
Qy   5349 ATCTTTGCCATTTTCCGCATGTCGTTCTTCATGCGATGGAGGAGCGCGGCATTAAC 5408

Db   5305 GCTGTGTATAATTTAAGACATTGGCCAAGTATGGCCAAAGTATTGCTGTTTCAGATGCTACC 5364
          |||| |||| |||  |||| |||||||| ||| || ||||| |||||||||| |  |||||
Qy   5409 GACGTCTACAACTTCAAGACCTTGGCGCAATTGTGGTTCAGCGAATGTGCGACG 5468

Db   5365 TCAGCCCGGTTGGGATGTGTGTTAGATGCCATTATCAATGAGGAAGAATTGCGATCCACCC 5424
          || ||||| ||||||||| ||||| | ||||||||| |||||| ||| |  ||||||||||
Qy   5469 TCAGCCCGGTTGGGATGTGTGTTACGGACGCCATTATCAATGAGGAAGCATGCGATCCACCC 5528

Db   5425 GACAACGACAAGGGCTATCCGGGCAATTGTGGTTCAGCGACTGTTGGAATTACGTTTCTC 5484
          ||||| ||||||||||||||| |||||||||||||||| | |||||  ||| | ||||||
Qy   5529 GACACGGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTGGAATAAACGTTTCTC 5588

Db   5485 CTTTCATATCCAGTTGATTATAAGCTTTTTGATAGTAATTATAATACATTGCGTGTCATTCTC 5544
          |||||||| || |||||||||||||||||| |||||||| |||| ||| |||||||||||||
Qy   5589 CTCTCATACCCAGTTGATTATAAGCTTTTTTGATAGTTATTAATATGTACATTGCTGTGTCATTCTC 5648

Db   5545 GAGAACTATAGCCAGGCTACGGAGGATGTACAGAGGGGTCTCACCGACGATTATGAT 5604
          |||||||||| ||||||| ||||||||||||| ||| || |||||| ||| ||||| ||
Qy   5649 GAGAACTATAGTCAGGCTCAAGAGAGGTCTAACCGACGCTCAACCGACGACTACGAC 5708

Db   5605 ATGTACTACGAGATTTGCAACAATTCGATCCGGAGCCACCCAGTACCCAGTACATACGATACGAC 5664
          |  ||||| | ||| || ||||||||||||| ||||| |||||||||||| |||||||||||
Qy   5709 ATGTACTATGAGATCTGCAACAATTCGATCCGGAGGGCCACCCAGTACATACGCTATGAT 5768

Db   5665 CAGCTGTCCGAGTTCCTGGACGTGTCGGACGTGCTGACGAGATCCGCTCGACAAGCCGAACAAG 5724
          |||||||||||| |||||| |||||||||||| |||| ||| ||| |||||||||||||||||
Qy   5769 CAGCTGTCCGAATTCCTGGACGTACTGGACGTGCTGCAGATCCGCAGATCCCACAAACCGAACAAG 5828

Db   5725 TACAAAATCATATCGATGGACATGCCGATAATGTCGGGGCGACATGATGTACTGTGTGGAT 5784
          ||| ||| ||||| ||| ||| ||| |||||||||| | ||||| |||| ||||||||||
Qy   5829 TACAAGATCATATCGATGGACATGCCGATTAATGTCGGGTGACCTCATGTACTGCGTGGAC 5888

Db   5785 ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCCGAAGGTTAATCCGATCGAGGAGACG 5844
          || ||| ||||||||||| |||||||||||| |||| |||| | ||||||||||||||||
Qy   5889 ATCCTCGACGCCCTTACGAAAGACTTCTTTGCGGAAGGCAATCGATCCGATACCGGGAGAGACG 5948
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CC   COUNTRY: U.S.A.
CC   ZIP: 94304-1397
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/09/024,020A
CC   FILING DATE: 16-FEB-1998
CC   CLASSIFICATION: 536
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US 60/039,447
CC   FILING DATE: 26-FEB-1997
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: CLARK, JANET P.
CC   REGISTRATION NUMBER: 34,799
CC   REFERENCE/DOCKET NUMBER: R0020B-REG
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (650) 852-3097
CC   TELEFAX: (650) 855-5322
CC   INFORMATION FOR SEQ ID NO: 1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 5977 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
SQ   SEQUENCE 5977 BP: 1478 A; 1554 C; 1600 G; 1345 T; 0 OTHER.

Query Match            5.5%;  Score 356;  DB 23;  Length 5977;
Best Local Similarity 65.1%;  Pred. No. 0.00e+00;
Matches  899;  Conservative    0;  Mismatches  471;  Indels  12;  Gaps  9;
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Db   4195 ATCAACTTTGACAATGTCGGAGCAGGTACCTGGCCCTTCTTCAAGTGGCAACCTTCAAA 4254
          || ||| ||  ||  || ||   || ||  ||||| ||   |||||||| ||||||||||
Qy   4536 ATGAATTTCGATCATGTAGGTAACGCGTATCTGTGCCTTTCCAAGTGGCCACCTTCAAA 4595

Db   4255 GGCTGGATGGACATCATGATGTATGCGGCGTGTAGATTCCGAAAGCCAGAGCCTGAC 4314
          |||||||| | |||||||| || |  || |   | |||| |||| ||| || |  ||
Qy   4596 GGCTGGATACAAAATCATGACGATGCTATCGATTCACGAGAGGTGGACAAGCAACCAATT 4655

Db   4315 TACGAGGGCAACATCACATGTACATCGTCATCTTCATCATCTTCGGCTCCTTC 4374
          |||| | | ||||||| ||||||  |   || |||||||| ||| || | |||
Qy   4656 CGTGAAACGAACATCTACATGTATTATATTCGTATTCTTCATCATATTTGGATCCTTT 4715

Db   4375 TTCACCCTCAACCTGTCATCGGTGTCATCATCGACAACTCAACCAGCAGAAGAAAAG 4434
          ||||| || |||  || |  | |||  ||||||||| ||| | | |  ||||||| |
Qy   4716 TTCACTCAATCTGTTCATTGGTGTTATCATTGATAATTTTAATGAGCAAAAGAAAAA 4775

Db   4435 TTTGGAGG-TCAG--GACATCTTCATGACAGAGGAACAGAGAGAATCAGAAGAA 4491
          || ||| | ||    |||| |||||||||||| || || || | |||||| |||
Qy   4776 GCAGGTGGATCATCATTAGAAATGTTCATGACAGAGAATCAGAAAGTACTACAATGCCATG 4835

Db   4492 AAAAGCTGGGCTCCAAGAAGCCACAGAGAGCCCATCCCCCGACCCTTGAACAAATCCAA 4551
          |||||  ||    ||| |   ||   | || ||| | |  ||  |||||  ||  |||
Qy   4836 AAAAGATGGGGCCTAAAAACCATTAAAAGCCATTCCAAGACCCAAGGTGGCGACCACA 4895

Db   4552 GGGATTGTCTTGATTTGTCACTCAACAGCTTGCTCAACAGCTTGTCGATCATGTGATGTGTCATC 4611
          ||| | | || || | ||  | ||| || || || || ||  ||   ||||||||| ||| |||
Qy   4896 GCAATAGTCTTTGAAATAGTAACGGATAAGAAATTCGATATGATCATTATGTTATTCATT 4955

Db   4612 TGCCTAACATGGTGACAAATGGTGGACAGACACTCAGAGCAGATGGAGAAC 4671
          || | |||  |  |||  | ||  | || | |||  | ||||| | || ||
Qy   4956 GGTCTGAACATGTCACCATGACCCTCGATCGTCGATGCGTCGGCACGTATAAGCGCG 5015

Db   4672 ATTCTTTACTGGATTAATCTGGTCTTTGTCATCTTCTTGTAGTATTTCGTAGTTATTTTTCAGTTCGATTAAA 4731
          || |||| || ||  |||   ||  ||| || |   |||||| || ||  ||| || |  |||| | ||||||
Qy   5016 GTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTCAGTTCGAATGTCATTAAAA 5075

Db   4732 ATGTTGCCTTGAGACACTACTATTCACCATTGGCTGGAACATCTTTGACTTTGTGGTG 4791
          || || | ||| | | |||||  | || || | | | || |   |  |||  ||  |
Qy   5076 ATATTCGCTTTACGGATATCACTATTTTGGTATTGATGGAATTTATTTGATGTAGTAGTT 5135
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Db    307 GATGAACTTTGACCATGTCGGCAAGGCGTATCTCTGCCTGTTCCAAGTGGCCACCTTCAA 366
          ||| ||  |||| |||||| |  ||  ||||||| ||||  |||||||||||||||||||
Qy   4535 AATGAATTCGATCATGTAGGTAACGCGTATCTGTGCCTTTCCAAGTGGCCACCTTCAA 4594

Db    367 GGGATGGATACAGACGATCATGACGCTATTGATTCGAGAGAGTGGGCCGGCAACCTAT 426
          |||||||||||   |||||||||||  ||||||||   ||||||||   |||||| |
Qy   4595 AGGCTGGATACAAAATCATGACGATGCTATCGATTCACGAGAGGTGGACAAGCAACCAAT 4654

Db    427 ACGCGAGACGAACATCTACATGTACCTGTACTTCGTGTTCTTCATCATATTTGGCTCATT 486
          || | ||||||||||||||||||||  |  |||| || |||||||||||||||| || ||
Qy   4655 TCGTGAAACGAACATCTACATGTATTATATTCGTATTCTTCATCATATTTGGATCCTT 4714

Db    487 CTTCACCTCAACCTATTCATCGGTGTGATCATCGACAACTTAACGAACAGAAGAAGAA 546
          ||||| |||||| | |||||| ||||| ||||| || ||||| || | ||||| |||
Qy   4715 TTTCACACTCAATCTGTTCATTGGTGTTATCATTGATAATTTTAATGAGCAAAAGAAAAA 4774

Db    547 AGCCGGCGGCAGCCTTGAGATGTTCATGACGTGAGGACCCAGAAGAAATACTACAATGCCAT 606
          ||| ||||| |||| | ||||||||||||| | ||  |  |||| || || || ||||| |
Qy   4775 AGCAGGTGGATCATTAGAAATGTTCATGACGAAGAAGATCAGAAAGTACTATAATGCTAT 4834

Db    607 GAAGAAAATGGGTTCTAAAAAACCTTTAAAAGCTATCCGAGACCGAAGTGGCGGCCACA 666
          |||| ||||||| | ||||| |  ||||||||| || | |||| || |||||| |||||
Qy   4835 GAAAAAGATGGGGCCTAAAAACCATTAAAAGCCATTCCAAGACCCAAGGTGGCGACCACA 4894

Db    667 AGCGATCGTGTTCGAGATAGTGACGGACAAGAAGTTCGACATGATCATCATGTGTTCAT 726
          ||| || || | ||| ||||| |||||  || | ||||| |||||||| |||| | |||
Qy   4895 AGCAATAGTGTCTTTGAAATAGTAACGGATAAGAAATTCGATATGATCATTATGTTATTCAT 4954

Db    727 CGGCCTCAACATGTGACGATGACGCTCGATCACTACCAGCGCGGAGACCTTCAGCAC 786
          | | || |||||| ||| ||||| | ||||| | | |||| | |||||  ||| |
Qy   4955 TGGTCTGAACATGTCACCATGACCCTCGATCGTCGATGCGTCGGCACGTATAAGC 5014

Db    787 TGTCCTCGACTACCTCAACATGATATTCATCGTGATATTCGTGATATTCAGTTCGATTAAA 846
          |||| | |||||  ||||  |||||||||| ||| |||||    |||||||||||| ||||
Qy   5015 GGTCCTTAGACTATCTCAATGCGATATTCGTAGTTATTTCAGTTCGAATGTCATTAAA 5074

Db    847 AATGTTCGGCCTTAGCGTACCAGTTACTTGTTGAGCCATGGAACTTGTTCGATTTCGTAGT 906
          || |||||  || |  ||| | || | || || |||  ||||  | | ||| ||| ||||
Qy   5075 AATATTCGCTTTACGGATATCACTATTTTGGTATTGATGGAATTTATTTGATGTAGTAGT 5134

Db    907 AGTCAATTTCTCAATTCTTAGTTTGGTATTGAGTGATATTATAGAAAAATATTTGTGTC 966
          ||||| |||| |  || ||||  |||||| || ||||||||| |||||  ||| ||||
Qy   5135 TGTCATTTTATCCATCTTAGGTCTTGTACTTAGCGATATTATCGAGAAGTACTTCGTGTC 5194

Db    967 ACCCACGTTACTGAGGGTGGTGAGGTAGCGAAGGTCGCGAAGGTCGTGTTGCGTCTCGTGAA 1026
          | | || | |  |||||||| || ||||| ||| | | |||| | || | |  ||| ||||
Qy   5195 GCCGACCCTGCTCCGAGTGGTGCCGAGTGGCGAAAGTGGCGAAAGTGCCGTGTCCTTCGACTGGTGAA 5254

Db   1027 GGGTGCGAAGGGTATCCGCAAGCGTATTGTTCGGGCTGGCCACGCG 1072
          ||| |||||||| ||| |  | |||||||| | | ||| |||| |
Qy   5255 GGGAGCCAAGGGCATTCGGACACTGCTCTCGCGGACACTGCCCATGTCG 5300
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RESULT 12
ID   US-09-024-020A-1 STANDARD; DNA; UNC; 5977 BP.
AC   xxxxxx
DT
DE   Sequence 1, Application US/09024020A
CC   Sequence 1, Application US/09024020A
CC   GENERAL INFORMATION:
CC   APPLICANT: DELGADO, STEPHEN G.
CC   APPLICANT: DIETRICH, PAUL S.
CC   APPLICANT: FISH, LINDA M.
CC   APPLICANT: HERMAN, RONALD C.
CC   APPLICANT: SANGAMESWARAN, LAKSHMI
CC   TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
CC   TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
CC   NUMBER OF SEQUENCES: 42
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: JANET PAULINE CLARK
CC   STREET: 3401 HILLVIEW AVENUE, MS A2-250
CC   CITY: PALO ALTO
CC   STATE: CA
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CC   CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: JANET PAULINE CLARK
CC      STREET: 3401 HILLVIEW AVENUE, MS A2-250
CC      CITY: PALO ALTO
CC      STATE: CA
CC      COUNTRY: U.S.A.
CC      ZIP: 94304-1397
CC   COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/09/024,020A
CC      FILING DATE: 16-FEB-1998
CC      CLASSIFICATION: 536
CC   PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 60/039,447
CC      FILING DATE: 26-FEB-1997
CC   ATTORNEY/AGENT INFORMATION:
CC      NAME: CLARK, JANET P.
CC      REGISTRATION NUMBER: 34,799
CC      REFERENCE/DOCKET NUMBER: R0020B-REG
CC   TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (650) 852-3097
CC      TELEFAX: (650) 855-5322
CC   INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC         LENGTH: 6007 base pairs
CC         TYPE: nucleic acid
CC         STRANDEDNESS: single
CC         TOPOLOGY: linear
CC      MOLECULE TYPE: DNA (genomic)
SQ   SEQUENCE 6007 BP: 1490 A; 1559 C; 1609 G; 1349 T; 0 OTHER.
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Query Match    5.5%;   Score 356;  DB 23;     Length 6007;
Best Local Similarity 65.1%;  Pred. No. 0.00e+00;
Matches 899;  Conservative 0;  Mismatches 471;  Indels 12;  Gaps 9;
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Db  4225 ATCAACTTTGACAATGTCGGAGCAGGGTACCTGCCCTTCTTCAAGTGGCAACCTTCAAA 4284
           | |||||||||||||||||||| ||| ||| |||||  |||| |||||||||||||||
Qy  4536 ATGAATTTCGATCATGTAGGTAACGCGTATCTGTCCTTTTCCAAGTGGCCACCTTCAAA 4595

Db  4285 GGCTGGATGGACATCATGTATGCGGCTGCTGTAGATTCCGAAAGCCAGACGCAGCCTGAC 4344
           ||||||||||   | |||||||| ||| ||||||| | ||||||||||||||||||
Qy  4596 GGCTGGATCAAAATCATGAACGATGCTATCGATTCACGAGAGTGGACAAGCAACCAATT 4655

Db  4345 TACGAGGGCAACATCACATGTACATCTACACTTCGTCATCTCGGCTCCTTC 4404
           ||    |||| || || |||||||||| |||| | | ||||||| ||||||||
Qy  4656 CGTGAAACGAACATCTACATGTATTTATATTTCGTATCATCATATTTGGATCCTTT 4715

Db  4405 TTCACCCTCAACCTGTTCATCGACTGTCATCATCGACAACTTCAACCAGCAGAAGAAAAAG 4464
          ||  ||| ||| | ||||||||||| || | | ||||| | ||| |||||||||||||||
Qy  4716 TTCACACTCAATCTGTTCATTGGTGTTATCATTGACAAGATCAGAAGAAGTACTATAAGTCTATG 4775

Db  4465 TTTGGAGG-TCAG--GACATCTTCATGAGGAACAGAGAGAACAATGCCATG 4521
          |||  ||| ||||    | | ||||||| |||| | |||| || |||| |||||
Qy  4776 GCAGGTGGATCATTAGAAATGTTCATGACAGAGATCAGAAAAAGTACTATAAATGCTATG 4835

Db  4522 AAAAAGCTGGGCTCCAAGAAGCCACAGAGAGCCCCATCCCCCGACCCTTGAACAAAATCCAA 4581
          ||||| ||| |||| | || |||  |||||||||  | |||| |||||||||  ||||||
Qy  4836 AAAAAGATGGGCTCTAAAAAACCATTAAAAGCCATTCAAGACCAAGGTGGCACCACACA 4895

Db  4582 GGGATTGTCTTTGATTTCGTCACTCAACACCTTTGACATTGTGATCATGATGCTCATC 4641
          |||| |||||| | |||| || |||  ||| |||| ||| |||||| || | ||||
Qy  4896 GCAATAGTCTTTGAAATAGTAACCGATAGAAAATTCGATATAATAATCATTATTGTTATTCATT 4955

Db  4642 TGCCTTAACATGGTGACAATGATGGTGGAGACAGACACTCAGGCAAGCAGATGGAGAAC 4701
          || || || |||| ||  | ||||| | ||| ||| ||| | ||| || ||||||||
Qy  4956 GGTCTGAACATGTCGATCCCTCGAATCGTTACGATCGTTCGGAACACACGTGTCGTCAAA 5015

Db  4702 ATTCTTTACTGATTAATCGGTCTTTGTCATCTTCTTCACCTGCGAGTGTGTGCTCAAA 4761
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Db  4792 GTCATCCTCCTCCATTGTGGGAATGTTCCTGGCTGATATCATTGAGAAGTACTTCGTCTCC 4851
          ||||| ||| ||| ||| ||   ||     ||  ||  ||||||||||||||||||
Qy  5136 GTCATTTTATCCACTCTAGGTCTTGCTTTGTACTTAGCGATAATCGCGTGATCTCGTGTCG 5195

Db  4852 CCAACCCTATTCCGAGTATCCGATTGGGCCCGTATTGGGCGCCATCTTGCGTCGTCATCAAG 4911
          ||||||||||||||| || ||| |   || ||  ||||| |  |||||||| ||  | |||
Qy  5196 CCGACCCTGCTCCGAGTGGTGCGTGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAG 5255

Db  4912 GGCGCCAAAGGGATCCGCACCCTGCTCTTTGCCTTAATGATGTCGCTGCCCGCCCCTGTTC 4971
          || ||||||  | || |  ||||||||| || |||||| ||   ||   ||||||||
Qy  5256 GGAGCCAAGGGCATTCGGACACTGCTCTTCGGCCATGCGCTGCTGCCGGCCCCTGTTC 5315

Db  4972 AACATCGGCCTCCTGCTCTTCCTCGTCATGTTCATCTCTCCATTTTGGCATGTCCAAC 5031
          |  ||||  |   |||  | || ||| || |||||||| |||| |||| | || |||
Qy  5316 AACATCTGCCTGCTCGTCTGTCATGTTCCATTTTCCGGCATGTCGTTC 5375

Db  5032 TTCGGCATACGTGAAGCACGAGGCGCGCATTGACGACATGTTCAACCTTCGAGACATTTGGC 5091
          |||| ||| | |||| ||| |||||  ||  || |||  ||| || | ||||||||||||
Qy  5376 TTCATGCACGTGAAGGAGAAGGAGAGGCGCCATTAACGACGTCTACAACTTCAAGACCTTTGGC 5435

Db  5092 AACAGCATGATCGTTTGTTCCAGATACACAACGTCTGCTGGCTGGGATGGCCTGCTGCTG 5151
          | ||||| || |||   || | | | |  | | |  |||||| |||||| ||  | |||
Qy  5436 CAGAGCATGATCCTTCAGATGTCGACGTCAGCCGGTTGGGATGTGTACTGGAC 5495

Db  5152 CCAATCCTGAACCGCCCCCCTGACTGACGTTGGACAAAGAGCACCCAGGGAGTGGCTTC 5211
          || |  | ||||| ||    | |  | | |  || |  || | | | ||| || || |||
Qy  5496 GCCATTATCAATGAGGAGGC--A-TGC-GATCC-ACCC--GA-CAGCGACAAAG--GCTAT 5546

Db  5212 CCAATGTCTGGAACCGCCTCGGTGGGCCATCTTCGGTGAGCTACATCATCATC 5271
          || |||||   | ||| ||||| |||| | ||  |  | ||| || || || |||
Qy  5547 CCGGGCAATGTGGTTCAGCGAACGTTGGGAATAACGTTTCTCCCTCATACCTAGTTATA 5606

Db  5272 TCCTTCCTGATTGTGGTGAACATGTACATCCCCATCATCCTGGAGAACTTCAGCGTGGCC 5331
          ||||  ||  |||| |||| | | || | ||||| ||| ||||||| |||||||||||
Qy  5607 AGCTTTTTGATAGTATGTAATTAATATGTACATTGTCTGCATTCTCGAGAACTATAGTCAGGCC 5666

Db  5332 ACCGAGGAGAGCGCCGCCAACCCTCGAGTGAGGATGACTTCATGAGACTATAGTCGG 5391
          ||||| | | | | ||  ||| ||||  ||| || | | || ||  || |||||
Qy  5667 ACCGAGGACGTGCAAGAGGTCAAGAGGTCTAACCGAGGACTACGACATGTCTAAGCATGAGATCGG 5726

Db  5392 GAGAAGTTTGACCCAGAGCACCCACCCGGAGGGCACCCAGTCACTCGTTCCGAATTCCTG 5451
          |  |||||  ||||||  ||| || |||| | | || ||||| | |||| ||||||||
Qy  5727 CAGCAATTCGATCCGGAGGGGCACCCAGTCACTGGCTATGAATGGCAGTTCGTCCGAATTCCTG 5786

Db  5452 GACGCCCTGGAGCACGCCGGCTCCGAGTACCCAGCCCATGCGCCATG 5511
          |  ||||| | |||| || ||||   | ||| | | ||| || |||||
Qy  5787 GACGTACTGGAGCCCCCGCTGCGCGAATCGAACCGGACAAGTACAGATCATATCGATG 5846

Db  5512 GACCTGCCCATGGTGAGCGAGGAGATCGCATCGCTACCTACTGCTTGGACAATCTTTCGCCTTCACC 5571
          ||   ||||||| || | |  |   | | | ||||| | |  | || ||  |||||  |||||
Qy  5847 GACATACCCATCTGTCGCGGTGACCTCATGTACTGCTGACGCGCCCTTACG 5906

Db  5572 AA 5573
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Qy  5907 AA 5908
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RESULT 13
ID  US-09-024-020A-2 STANDARD; DNA; UNC; 6007 BP.
AC  xxxxxx
DT
DE  Sequence 2, Application US/09024020A
CC  Sequence 2, Application US/09024020A
CC  GENERAL INFORMATION:
CC     APPLICANT: DELGADO, STEPHEN G.
CC     APPLICANT: DIETRICH, PAUL S.
CC     APPLICANT: FISH, LINDA M.
CC     APPLICANT: HERMAN, RONALD C.
CC     APPLICANT: SANGAMESWARAN, LAKSHMI
CC     TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
CC     TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
CC     NUMBER OF SEQUENCES: 42
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APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
  ADDRESSEE: JANET PAULINE CLARK
  STREET: 3401 HILLVIEW AVENUE, MS A2-250
  CITY: PALO ALTO
  STATE: CA
  COUNTRY: U.S.A.
  ZIP: 94304-1397
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/024,020A
  FILING DATE: 16-FEB-1998
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/039,447
  FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
  NAME: CLARK, JANET P.
  REGISTRATION NUMBER: 34,799
  REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (650) 852-3097
  TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
  LENGTH: 6556 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
SQ  SEQUENCE 6556 BP: 1620 A; 1727 C; 1736 G; 1471 T; 2 OTHER.

Query Match          5.5%;  Score 356;  DB 23;  Length 6556;
Best Local Similarity 65.1%;  Pred. No. 0.00e+00;
Matches 899;  Conservative   0;  Mismatches 471;  Indels 12;  Gaps 9;

RESULT 14
ID   US-09-024-020A-7  STANDARD; DNA; UNC; 6556 BP.
AC   xxxxxx
DT   
DE   Sequence 7, Application US/09024020A
CC   Sequence 7, Application US/09024020A
CC   GENERAL INFORMATION:
CC     APPLICANT: DELGADO, STEPHEN G.
CC     APPLICANT: DIETRICH, PAUL S.
CC     APPLICANT: FISH, LINDA M.

```
CC  Sequence 8, Application US/09024020A
CC  GENERAL INFORMATION:
CC    APPLICANT: DELGADO, STEPHEN G.
CC    APPLICANT: DIETRICH, PAUL S.
CC    APPLICANT: FISH, LINDA M.
CC    APPLICANT: HERMAN, RONALD C.
CC    APPLICANT: SANGAMESWARAN, LAKSHMI
CC    TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
CC    TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
CC    NUMBER OF SEQUENCES: 42
CC    CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: JANET PAULINE CLARK
CC      STREET: 3401 HILLVIEW AVENUE, MS A2-250
CC      CITY: PALO ALTO
CC      STATE: CA
CC      COUNTRY: U.S.A.
CC      ZIP: 94304-1397
CC    COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC    CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/09/024,020A
CC      FILING DATE: 16-FEB-1998
CC      CLASSIFICATION: 536
CC    PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 60/039,447
CC      FILING DATE: 26-FEB-1997
CC    ATTORNEY/AGENT INFORMATION:
CC      NAME: CLARK, JANET P.
CC      REGISTRATION NUMBER: 34,799
CC      REFERENCE/DOCKET NUMBER: R0020B-REG
CC    TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (650) 852-3097
CC      TELEFAX: (650) 855-5322
CC  INFORMATION FOR SEQ ID NO: 8:
CC    SEQUENCE CHARACTERISTICS:
CC      LENGTH: 6826 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC    MOLECULE TYPE: DNA (genomic)
SQ  SEQUENCE 6826 BP: 1726 A; 1764 C; 1780 G; 1554 T; 2 OTHER.
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Query Match       5.4%;   Score 354;  DB 23;  Length 6826;
Best Local Similarity  65.0%;  Pred. No. 0.00e+00;
Matches  898;  Conservative  0;  Mismatches 472;  Indels 12;  Gaps  9;

Db  4168 ATCAACTTTGACAATGTCGGAGCAGGGTACCTGCCCTTCTTCAAGTGCAACCTTCAAA 4227
         | || |||| || ||| || || ||| || ||  | ||||||  ||||| | ||||||
Qy  4536 ATGAATTTCGATACATGTAGGTAACGCGTATCCTGTGCCTTTTCCAAGTGGCCACCTTCAAA 4595

Db  4228 GGCTGGATGACATCATGTATGCGGCTGTAGATTCCGGAAGCCAGAGACGAGCAGCCTGAC 4287
         ||||||||| ||| ||||| ||| ||||  |||| || ||| ||  ||   |||| || | 
Qy  4596 GGCTGGATACAAATCATCATGAACGATGCTATCGATTCACGGAGGTGGACAAGCAACCAATT 4655

Db  4288 TACGAGGGCAACATCTACATGTACTACTTCGTCATCATCTTCGGCTCCTTC 4347
         | ||| | || ||||||||| |  |  || |||||| ||| ||| || |||
Qy  4656 CGTGAAACGAACATCTACACTATTTATATTTCGTATTCTTCATCATATTTGGATCCTTT 4715

Db  4348 TTCACCCTCAACCTGTTCATCGTGTCATCACTGACACTTCAACCAGCAGAGAAAAG 4407
         |||| | |||| ||||||| | || ||| || |  ||| ||||| || ||| |||||
Qy  4716 TTCACACTTCAATCTGTTCATTGGTTGTTATCATTTTAATGAGCAAAAGAAAAA 4775

Db  4408 TTTGGAGG-TCAG--GACATCTTCATGAGAGAGAACAGAGAAGAGTACTATAATGCCATG 4464
         |||||| | || |     || || ||| || | ||| || ||  | |||||||||| ||||
Qy  4776 GCAGGTGGATCATTAGAAATGTTCATGACAGGATCAGAAGAAGATCAGAAAAGTAGTATAATGCTATG 4835

Db  4465 AAAAAGCTGGGCTCCAAGAAGCCACAGAGACCCATCCCCGACCCTTGAACAAAATCCAA 4524
         ||||||  |||||| || |  ||| ||| | |  ||  |||| | |||  || | |||
Qy  4836 AAAAAGATGGGCTCTAAAAAACCATTAAAAGCCATTCAAGAACGACCAAGGTGGCGACCACA 4895
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Qy  4956 GGTCGGAACATGTTCACCATGACCCTCGATCGTTACGACGTCGGGACACACGTGTATAACGCG 5015
         | ||  | ||| ||   ||   |  |  || |  ||  |  || |  |  | || ||||  ||
Db  4819 ATTCTTTACTGGATTAATCTGGTCTTGTCATCTTCTCACCTGCGAGTGTGTGCTCAAA 4878

Qy  5016 GTCCTAGACTATCCAATGCAGATATTTCGGTATATTTCAGTTCCGAATGTCATTAAAA 5075
         |  | |  |    |  |  | |||| || | |||   | || | | ||| ||| ||||
Db  4879 ATGTTGCCTGAGACACTACATTCACCATTGGCTGGAACATCTTTGACTTTGTGTG 4938

Qy  5076 ATATTCGCTTTACGGATATCACATATTTTATTGAGCCATGGAATTTATTGATGTAGTAGTT 5135
         |  ||||| ||  | | | || ||  |  |  |||   || ||| |  | |||| |||| ||
Db  4939 GTCATCCTCCATTGTGGGAATGTTCCTGGCTGTGATATCATTGAGAAGTACTTCGTCTCC 4998

Qy  5136 GTCATTTTATCCATCTTAGGCTCTGTACTTGGCGATATTATCAACTTATCCGTGTGTCG 5195
         || ||  | | |  || ||| |  || ||||| |  ||  ||  | | || |||||| ||
Db  4999 CCAACCCTATTCCGAGTTATCCGAGTCGCCGATCTGCCGTCTGCATGTCTGATCAAG 5058

Qy  5196 CCGACCCTTCCGCTGCTGGTGCGCGTGTCCTTGCGCCCGCGTTC 5255
         |||   || ||| || || |  || ||   ||||| || |||||
Db  5059 GGGCCCAAAGGGATCGGCACCCGGCCCTCTTGTTCGCTGCGCCCCCGTTC 5118

Qy  5256 GGAGCCAAGGGCATTCGGACACTGCTTCTCCGCGTGTTGGCCATGTCGCCGGCCCTGTTC 5315
         |||||||||||| ||  || | |||| ||||  ||  ||| ||||  ||  || | || | 
Db  5119 AACATCGGCCTCCTGCTCTCTCGTCATGTTCATTTTCCATTTTGGCATGTCCAAC 5178

Qy  5316 AACATCTGCCTGCTGCTCGTTCCTGGCTGTTTCATCTTCGGCCATGTCCATCGTTC 5375
         |||| || | || ||||  | |||  |  |  ||| ||  | ||||| || |||||
Db  5179 TTCGCATACGTGAAGCACGACGAGGCCGGCATTGACGACATGTTCAACTTGGC 5238

Qy  5376 TTCATGACGTGAAGGAGAAGACGGCATTAACGACGTCTACACAACTTTCAAGACCTTTGC 5435
         |||| || |||||  |  ||| |||  ||| ||  | || || ||||||||||  |||||
Db  5239 AACAGCATGATCTGTTGTTCCAGATCACAACGTCTGGCTGGCCGTGGCTGCTGTG 5298

Qy  5436 CAGAGCATGATCGTCCTTGCTCTTTCAGATGTCGACGTCAGCCGGTTGGGATGGTGTACTGGAC 5495
         || ||||||||| |   || | ||| ||| |  || ||||||| | ||||| || |||| || 
Db  5299 CCAATCCTGAACCGCCCCCCTGACTGCGCAGCTTGGCACAAAGAGACACCCAGGGAGTGGCTC 5358

Qy  5496 GCCATTATCAATGAGGAAGC--A-TGC-GATCC-ACCC-GA-CAGCGACAAAG--GCTAT 5546
         ||| || |   |||| | || | ||| || ||  |  | || |   ||| ||| | |||
Db  5359 AAAGGGGACTGTGGGAACCCCTCGGTGGAACCCTCGGTCCATCCTCTCTAGTTATA 5418

Qy  5547 CCGGGCAATGTGGTGGTCAGCGAGCCGTTCAGCGACCGTTGGATAACGTTTCTCCCTCATACCTAGTTATA 5606
         ||  || || || |    || |  || | | |  ||| ||| || |  ||| | ||  |  | |||||||
Db  5419 TCCTTCCTGATTGTGGTGAACATGTGAACATGTACATCCGCCATCCGCTGGAACTTCTCGAGAACTTCAGCGTGCC 5478

Qy  5607 AGTTTTTGATAGTTATTATTAATATGTACATTGCTGTCATTCGAGAACTATAGTCAGGCC 5666
         |||||||||| |  |||||| |  |||| |||   ||| ||||| ||  |  |  || ||
Db  5479 ACCGAGGAGAGCGCCGACCTCTGAGTGAGGAGATCGTCTAACCGGTCTTATGAGATCTGG 5538

Qy  5667 ACCGAGGAGAGCGCTGCAAGAGGGTCAAGCGGTACCAGACGTGTAAGCTGGCCTATGAGATCTGG 5726
         ||||||||||||| | |  || | | ||||   | || ||   ||||||| | ||||||||||||
Db  5539 GAGAAGTTTGACCCAGAGGGGCACCCACCACCGTCCAGCTGCTGCAGCGTCATCACCTATCCTGTGTCGTCGCCATG 5598

Qy  5727 CAGCAATTCGATCCGGAGGGCACCCAGTACATACGTCTATGATCAGCTGTCGTCAGGCTCATCGCCATG 5786
         ||||| |||||  ||||||||||| ||| |||| | | ||| |||| || |  || |||| ||||||||
Db  5599 GACCGCCTGGAGCACGCTCCGAGCTGCCGGGCAGCTCCAAGCCCATCGGCTCATCGCCATG 5658

Qy  5787 GACGTACTGGAGCCCCCGCTGCAGATCGCGCAATCCCACTGCTTGACACCTCCTTTTTGCGCCTTACC 5846
         ||||| |||||  ||| ||| || ||  | | | ||||  ||  ||| || | ||  ||||| |||
Db  5659 GACGTGCCCATGGTCAGCGGAGATCGCATCCATTGCTGCCTGCGAGATGCCACATCCTACCGCAATCCCTCAACATCCTCCTGATCG 5718

Qy  5847 GACATACCCATCTGTCGTCGTGACTACGTGCGTGGCGACATCCTGCGACATCCCTCAACATCCTCCTGATACG 5906

Db  5719 AA 5720
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Qy  5907 AA 5908
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RESULT 15
ID  US-09-024-020A-8 STANDARD; DNA; UNC; 6826 BP.
AC  xxxxxx
DT
DE  Sequence 8, Application US/09024020A
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Wed Jul 8 10:17:00 1998

US-08-554-424-7.rmp

Search completed: Wed Jul 8 04:28:31 1998
Job time : 9438 secs.

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Db  4525 GGGATTGTCTTTGATTTCGTCACTCAACAAGCCTTTGACATTGTGATCATGATGCTCATC 4584
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Qy  4896 GCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATTATGTTATTCATT 4955

Db  4585 TGCCTTAACATGGTGACAATGATGGTGAGACAGACACTCAGAGCAGATGGAGAAC       4644
          | ||| |  | || | ||  | |   | |   | |||| ||  |||| |||| |
Qy  4956 GGTCTGAACATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGACACGTATAAACGCG 5015

Db  4645 ATTCTTTACTGGATTAATCTGGTCTTTGTCATCTTCTTCACCTGCGAGTGTGTGCTCAAA  4704
          | || | ||  || |||  ||  | |  || |  | | ||  |   | |||  | |||
Qy  5016 GTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTCAGTTCCGAATGTCTCATTAAAA 5075

Db  4705 ATGTTTGCCTTGAGACACTACTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTG     4764
          |   |||||| || | |   |     |  |  || | || |    | | ||| | |  | |
Qy  5076 ATATTCGCTTACGATATCACTATTTTATTGAGCCATGAAATTATTTGATGTAGTAGTT   5135

Db  4765 GTCATCCCTCCATTGTGGGAAATGTTCCTGGCTGATATCATTGAGAAGTTACTTCGTCTCC 4824
          |  || | |  ||| | ||    |   ||   |||| |  ||  |||||||| ||||| ||
Qy  5136 GTCATTTTATCCATCTTAGGTCTTGTACTTAGCGATATTATCGAGAAGTACTTCGTGTCG 5195

Db  4825 CCAACCCTATTCCGAGTTATCCGATTGGCCCGTATTGGGCGCATCTTGCGTCTGATCAAG  4884
          |       |||||| ||   |||    || | || |  | | | || ||||| |  |||
Qy  5196 CCGACCCTGCTCCGAGTGGTGTGCCGTGTGTGGCGAAAGTGGGCCGTCCTTCGACTGGTGAAG 5255

Db  4885 GGGCCAAAGGGATCCGCACTCTGCTCTTTGCTCGATGATGTCGCTGCCCGCCCTGTTC   4944
          |  | |  ||| | |  || |||   | | | || || || ||  |  | || | |||
Qy  5256 GGAGCCAAGGCATTCGGACACTGTCTCTCGCGTTGGCCATGCTGCTGCTGCCGGCCCTGTTC 5315

Db  4945 AACATCGGACCGCCTCCTGCTCTTCCGTCGTCATGTTCATCTTCTCCATTTTTGGCATGTCCAAC 5004
          |  |||||  || | |||||| ||||  |  ||||||  | || |  | |||  |||| |
Qy  5316 AACATCTGCCTGCTGCGTTCCTTGGTCATGTTCATCTTTCGCATTTTCGGCATGTCGTTC 5375

Db  5005 TTCGCATACGTGAAGCACGAGGCCGGCATTGACGACATGTTCAACTTCGAGACATTTGGC 5064
          |||  |   | |      | || |   ||| | || ||| |  |  | | || || | |||
Qy  5376 TTCATGCACGTGAAGGAGAAGCGGCATTAACGACGTCTACAACTTCAAGACCTTTGGC 5435

Db  5065 AACAGCCATGATCTGTTTGTTCCAGATCACAACGTCTGCTGGCGTGGGATGGCCTGCTCCTG 5124
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Qy  5436 CAGAGCCATGATCCTGCTCTTTCAGATGTCGACGTGCAGCCGGTGGTGTGTACTGGAC 5495

Db  5125 CCAATCCTGAACCGGCCCCCCGCTCCGACTGCAGCTTGACAAAGAGCACCAGGGAGTGGCTTC 5184
          || |  || | | |  |  |  ||    | | |  |  | | || | |  |||||   |
Qy  5496 GCCATTATCAATGAGGAGGC--A-TGC-GATCC-ACCC-GA-CAGCGACAAAG--GCTAT 5546

Db  5185 AAAGGGGACTGTGGGAACCCTCGGTGGCATCTCTCTTGTGAGCTACATCATCATC      5244
          || |||   | || |   |  ||  | | |||  | | || |    |   | ||  |
Qy  5547 CCGGGCAATTGTGTTCAGCGACCGTTGAATAAACGTTTCTCCCTCTCATACCTAGTTATA 5606

Db  5245 TCCTTCCTGATTGTGGTGAACATGTCAACATTCATCGCCATCATCCTGGAGAACTTCAGCGTGGCC 5304
          |   | ||  || | | |  | ||| ||| | || || | |  | | ||||| || |
Qy  5607 AGCTTTTGATAGTATTTAATATGTTGCATTCTGCTGTCATTCTCGAGAACTATAGTCAGGCC 5666

Db  5305 ACCGAGGAGGCGGCCGACCCTGCCGACCCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGG 5364
          ||||||| |  | |  ||| | |  |||| | | || |  ||  | |   |  |||||||| |||
Qy  5667 ACCGAGGACGTGCAAGAGCGTCTAACCGACGACTACGACATGTACTATGAGTACTATGAGATCTGG 5726

Db  5365 GAGAAGTTTGACCCAGACGCCACCCAGTTCATCGAGTACTGTAAGCTGCAGACTTTGCC 5424
          |  ||  | ||| ||| || | | |  ||   |||  |  | || ||   |||  |  ||
Qy  5727 CAGCAATTCGATCCGGAGGCACCCAGTACATACGCTATGATCAGCTGCGAATTCCTG 5786

Db  5425 GACGCCCTGGAGCACCCGCTCCGAGTACCCAAGCCCAACACCATCGAGCTCATCGCCATG 5484
          ||||  || | || | |   | | |  |||  ||| |   | ||||| || | ||||||
Qy  5787 GACGTACTGGAGCCCCGCCCCGTCGAGATCACCACCAACAAGCCGATCATATCGGATG 5846

Db  5485 GACCTGCCCATGGTGAGCGGAGATCCCATCCGCTTGGACATCCTTTTCGCCTTCACC 5544
          || ||   |  |||| | |   ||   |||    ||||   | | || |||  | |
Qy  5847 GACATACCCATCTGTCGCGGTGACCTCATGTCGCGTCGCAATCCTCGACGCCCTTACG 5906

Db  5545 AA 5546
          ||
Qy  5907 AA 5908
```

prior art DoT 11/10/94

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|‾\  /|  |‾‾|  |‾‾|  |‾‾|  |‾‾|  |‾|  |‾|
| \/ |  |--|  |__|  |__|  |  |  |  |
|    |  |      \__|  |  \  |__|  |  |  (TM)
***********************************
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Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_nn    n.a. - n.a. database search, using Smith-Waterman algorithm

Run on:     Tue Jul 7 18:44:09 1998;  MasPar time 7952.09 Seconds
                                        1366.703 Million cell updates/sec

Tabular output not generated.

Title:        >US-08-554-424-7
Description:  (1-6513) from US0855424.seq
Perfect Score: 6513    1 TCTAGACGTTGGCCGCATAG.........ACGGCGAGTATTAGCTCTAGA 6513
                         AGATCTCGCAACCGGCGTATC.........TGCCCTCATAATCGAGATCT
N.A. Sequence:
Comp:

Scoring table:  TABLE default
                Gap 6

Nmatch  STD :   Dbase 0:  Query 0

Searched:       457396 seqs, 834342348 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:       embl154
                1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
                7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_vi

Database:       genbank106
                13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat
                19:gb_ph 20:gb_pl 21:gb_pr1 22:gb_pr2 23:gb_ro 24:gb_st
                25:gb_sy 26:gb_un 27:gb_vi

Statistics:     Mean 12.782;  Variance 6.793;  scale 1.882

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 6513 | 100.0 | 6513 | 18 | I74672 | Sequence 7 from patent | 0.00e+00 |
| 2 | 6513 | 100.0 | 6513 | 18 | I33685 | Sequence 7 from patent | 0.00e+00 |
| 3 | 6513 | 100.0 | 6513 | 18 | I25433 | Sequence 7 from patent | 0.00e+00 |
| 4 | 5992 | 92.0 | 6883 | 15 | DROSODCHA | Drosophila melanogaste | 0.00e+00 |
| 5 | 3676 | 56.4 | 6318 | 15 | MDU38813 | Musca domestica insect | 0.00e+00 |
| 6 | 3676 | 56.4 | 6899 | 15 | MDPARA | M.domestica mRNA for v | 0.00e+00 |
| 7 | 3664 | 56.3 | 6315 | 15 | MDU38814 | Musca domestica insect | 0.00e+00 |
| 8 | 1912 | 29.4 | 6096 | 15 | BGU73584 | Blattella germanica pa | 0.00e+00 |
| 9 | 1912 | 29.3 | 6096 | 15 | BGU73583 | Blattella germanica pa | 0.00e+00 |
| 10 | 1592 | 24.4 | 2144 | 15 | DVU26343 | Drosophila virilis sod | 0.00e+00 |
| 11 | 1441 | 22.1 | 5068 | 15 | BGU71083 | Blattella germanica pa | 0.00e+00 |
| 12 | 696 | 10.7 | 986 | 15 | U83872 | Haematobia irritans pa | 0.00e+00 |
| 13 | 694 | 10.7 | 986 | 15 | U83874 | Haematobia irritans pa | 0.00e+00 |
| 14 | 485 | 7.4 | 1840 | 15 | DMU26715 | Drosophila melanogaste | 0.00e+00 |
| 15 | 448 | 6.9 | 947 | 15 | U83871 | Haematobia irritans pa | 0.00e+00 |
| 16 |  | 6.8 | 446 | 15 | U83873 | Haematobia irritans pa | 1.15e-270 |
| 17 |  | 6.0 | 391 | 15 | SQDNACH | Squid sodium channel m | 1.23e-255 |
| 18 |  | 5.7 | 372 | 23 | MMU26707 | Mus musculus voltage-g | 1.58e-248 |
| 19 |  | 5.6 | 363 | 23 | RNSCIII | Rat mRNA for brain sod | 2.00e-241 |
| 20 |  | 5.4 | 354 | 23 | RATSCP6A | Rattus norvegicus sodi | 7.57e-240 |
| 21 |  | 5.4 | 352 | 23 | RATSCAL | Rat cardiac specific s | 5.79e-232 |
| 22 |  | 5.3 | 342 | 21 | HUMHBAX | Human voltage-gated so | 3.55e-231 |
| 23 |  | 5.2 | 341 | 17 | FRBSCAS2 | Fugu rubripes mRNA for | 3.55e-231 |
| 24 |  | 5.2 | 341 | 21 | HUMSKM1A | Homo sapiens skeletal | 3.08e-227 |
| 25 |  | 5.2 | 336 | 23 | RATNACHI | Rattus norvegicus sodi | 3.08e-227 |
| 26 |  | 5.2 | 336 | 23 | RNSCPIIR | Rat brain mRNA for sod | 1.16e-225 |
| 27 |  | 5.1 | 334 | 23 | RATNCHVS | Rat skeletal muscle vo | 1.16e-211 |
| 28 |  | 4.9 | 316 | 23 | RNU79568 | Rattus norvegicus volt | 1.66e-211 |
| 29 |  | 4.9 | 316 | 15 | ACU66915 | Aplysia californica so | 1.66e-211 |
| 30 |  | 4.9 | 320 | 23 | RNSCPIR | Rat brain mRNA for sod | 1.19e-214 |
| 31 |  | 4.9 | 320 | 23 | RATNACHI | Rattus norvegicus sodi | 1.19e-214 |
| 32 |  | 4.9 | 320 | 21 | HUMHH1A | Human cardiac tetrodot | 1.66e-211 |
| 33 |  | 4.9 | 316 | 23 | AF000368 | Rattus norvegicus volt | 1.66e-211 |
| 34 |  | 4.8 | 313 | 15 | DMU26714 | Drosophila melanogaste | 3.76e-209 |
| 35 |  | 4.7 | 312 | 15 | OCU35238 | Oryctolagus cuniculus | 2.29e-208 |
| 36 |  | 4.7 | 306 | 16 | ECU35943 | Equus caballus skeleta | 1.17e-203 |
| 37 |  | 4.7 | 308 | 21 | HSVASCAS | H.sapiens mRNA for vol | 3.16e-205 |
| 38 |  | 4.6 | 302 | 15 | HIU32390 | Haematobia irritans ex | 1.61e-200 |
| 39 |  | 4.6 | 298 | 23 | RNU53833 | Rattus norvegicus sodi | 2.20e-197 |
| 40 |  | 4.5 | 296 | 23 | RNSNS | R.norvegicus mRNA for | 8.11e-196 |
| 41 |  | 4.5 | 296 | 9 | A58853 | Sequence 1 from Patent | 8.11e-196 |
| 42 |  | 4.5 | 296 | 9 | A58859 | Sequence 7 from Patent | 8.11e-196 |
| 43 |  | 4.5 | 296 | 9 | A58857 | Sequence 5 from Patent | 8.11e-196 |
| 44 |  | 4.4 | 284 | 23 | MMSNS | M.musculus mRNA for SN | 2.00e-186 |
| 45 |  | 4.3 | 279 | 15 | DMU26716 | Drosophila melanogaste | 1.62e-182 |

ALIGNMENTS

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RESULT        1
LOCUS         I74672        6513 bp  DNA              PAT      23-DEC-1997
DEFINITION    Sequence 7 from patent US 5688917.
ACCESSION     I74672
NID           g3010813
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE     1  (bases 1 to 6513)
  AUTHORS     Arena,J.P., Feng,G., Hall,L.M., Liu,K., Van Der Ploeg,L.H.T.,
              Wang,P. and Warmke,J.W.
  TITLE       Process for functional expression of the para cation channel
  JOURNAL     Patent: US 5688917-A 7 18-NOV-1997;
FEATURES             Location/Qualifiers
     source          1..6513
                     /organism="unknown"
BASE COUNT     1681 a   1548 c   1702 g   1582 t
ORIGIN

Query Match      100.0%;  Score 6513;  DB 18;  Length 6513;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 6513;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db     1 TCTAGACGTTGGCCGCATAGACAATGACACGAAGATTCCGACTCGATATCTGAGGAAGAAC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1 TCTAGACGTTGGCCGCATAGACAATGACACGAAGATTCCGACTCGATATCTGAGGAAGAAC 60

Db    61 GCAGTTGTTCCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCCATTGCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 GCAGTTGTTCCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCCATTGCCG 120

Db   121 CTGAACATGAAAAGCCAGAAGGAGCTGGAAAGAAAGAGAGCCGAGGGAGGAGTGCCCGGAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CTGAACATGAAAAGCCAGAAGGAGCTGGAAAGAAAGAGAGCCGAGGGAGGAGTGCCCGGAT 180

Db   181 ATGGTCGCAAGAAATCCGATATGATGACGAGGAAGGTC 240
          ||||||||||||||||||||||||||||||||||||||
Qy   181 ATGGTCGCAAGAAATCCGATATGATGACGAGGAAGGTC 240
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Exact Match
-- no appl--

Left column:

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Db   241 CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCCAGCT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCCAGCT   300

Db   301 TCCCGCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC   360
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Qy   301 TCCCGCCGGAATTGGCCTCCACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC   360

Db   361 TGACATTCGTAGTTGTAAGCAAAGAAAAGATATTTTTCGCTTTTCTGCATCAAAAGCAA   420
         |||||||||||||||||||||||||||||||||||||| ||||||||
Qy   361 TGACATTCGTAGTTGTAAGCAAAGAAAAGATATTTTTCGCTTTTCTGCATCAAAAGCAA   420

Db   421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTCTAGTGCATC   480
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Qy   421 TGTGGATGCTCGATCCATTCAATCCGATACGTCGTGTGGCCATTTACATTCTAGTGCATC   480

Db   481 CATTATTTTCCCTATTCATCATCACCACACAATTCTCGTCAACTGCATCCTGATGATAATGC   540
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Qy   481 CATTATTTTCCCTATTCATCATCACCACACAATTCTCGTCAACTGCATCCTGATGATAATGC   540

Db   541 CGACAACGCCCACCGGTTGAGTCCACTGAGTCGATATTCACCGGAATCTACACATTTGAAT   600
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Qy   601 CAGCTGTTAAAGTGATGGCACGAGGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATG   660

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Qy   661 CATGGAATTGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT   720

Db   721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCCGTTAAAACCGTAGCCA   780
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Qy   721 TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCCGTTAAAACCGTAGCCA   780

Db   781 TTGTGCCAGGTTGAAGACCATCGTCGGCGCCGCCGTCATCGAATCGGTGAAGAATCTGCGCG   840
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Qy   781 TTGTGCCAGGTTGAAGACCATCGTCGGCGCCGCCGTCATCGAATCGGTGAAGAATCTGCGCG   840

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Qy   841 ATGTGATATCCTGACCATGTTCTCCCGTGTTCGCGTTGATGGGCCTACAGATCT   900

Db   901 ATATGGGCGTGCTCACCGAGAAGTGCATCAAGAAGTTCCCGCTGACGGTTCCTGGGGCA   960
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Qy   901 ATATGGGCGTGCTCACCGAGAAGTGCATCAAGAAGTTCCCGCTGACGGTTCCTGGGGCA   960

Db   961 ATCTGACCGACGAGAACTGGACTATATCACAATCGCCAATAGCTCCAATTGGTATTCCGAGG  1020
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Qy   961 ATCTGACCGACGAGAACTGGACTATATCACAATCGCCAATAGCTCCAATTGGTATTCCGAGG  1020

Db  1021 ACGAGGGCATCTCATTTCGGTATGCGGCAATATCCGGTGCGGGCAATGCGACGACG  1080
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Qy  1021 ACGAGGGCATCTCATTTCGGTATGCGGCAATATCCGGTGCGGGCAATGCGACGACG  1080

Db  1081 ATTACGTGTGCCGCTGCCAGGGGTTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT  1140
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Qy  1081 ATTACGTGTGCCGCTGCCAGGGGTTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT  1140

Db  1141 CGTTCGGATGGGCTTTCCTGTCGTCCGCCTTCCTGTCGCTGCGGCTTTCGTCCGTCGGGAGGATC  1200
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Qy  1141 CGTTCGGATGGGCTTTCCTGTCGTCCGCCTTCCTGTCGCTGCGGCTTTCGTCCGTCGGGAGGATC  1200

Db  1201 ACGAGGGCACTGGTGTTGCGCGCCGCCGACCATGGCACATGTCGTTCTTTATAGTCATCA  1260
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Qy  1201 ACGAGGGCACTGGTGTTGCGCGCCGCCGACCATGGCACATGTCGTTCTTTATAGTCATCA  1260

Db  1261 TCTTCCTAGGTTCATTCGTATCTTGTGAATTTGATTTGGCCATTGTTGCCATGTCGTATG  1320
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Qy  1261 TCTTCCTAGGTTCATTCGTATCTTGTGAATTTGATTTGGCCATTGTTGCCATGTCGTATG  1320
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Right column:

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Db  1321 ACGAATTGCAAAGGAAGGCCGAAGAGGAAGAAGAGGCTGCCGAAGAGGAGGAGGCGATACGTGAAG  1380
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Qy  1321 ACGAATTGCAAAGGAAGGCCGAAGAGGAAGAAGAGGCTGCCGAAGAGGAGGAGGCGATACGTGAAG  1380

Db  1381 CGGAAGAAGCTGCCGCCGCCGCCAAAGCGGCCAAGCGGCCCAAGCTGGAGGAGGCGGGCCAATGCGCAGGCTC  1440
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Qy  1561 ACAACAACAAAGAAGAGATGTCATTCGGAGCGTCGAGGTGGAGTCGGTGGTGAGCG  1620

Db  1621 TTATACAAAGACACAACCAGCACCTACCAGCACACCACCAAGCTACCAAAGTTCGTAAAGTGA  1680
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Qy  1621 TTATACAAAGACACAACCAGCACCTACCAGCACACCACCAAGCTACCAAAGTTCGTAAAGTGA  1680

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Qy  1681 GCACGACATCCTTATCCTTACCTGGTTCACCGTTTAACATACGCAGGGGATCACGTAGTT  1740

Db  1741 CTCACAAGTACACGATACGGAACGGACGTGGCCGTTGGTATACCCGGTAGCGATCGTA  1800
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Qy  1741 CTCACAAGTACACGATACGGAACGGACGTGGCCGTTGGTATACCCGGTAGCGATCGTA  1800

Db  1801 AGCCATTGGTATTGTCAACATATCAGGATGCCGAAGAGAATGGGCCCATCAGTGCCCGACGACT  1860
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Qy  1801 AGCCATTGGTATTGTCAACATATCAGGATGCCGAAGAGAATGGGCCCATCAGTGCCCGACGACT  1860

Db  1861 CGAATGCCGTCACCCGATGTCCAAGAGGAATGGGCCATGGGCCGATCAGTGCCGTGTACTATG  1920
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Qy  1861 CGAATGCCGTCACCCGATGTCCAAGAGGAATGGGCCATGGGCCGATCAGTGCCGTGTACTATG  1920

Db  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCAATATCGTATACCT  1980
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Qy  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCAATATCGTATACCT  1980

Db  1981 CACATGGCGATCTACTCGGCGGCCGTCATGGGCGTGCAGCACAATGACCAAGGAGA  2040
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Qy  1981 CACATGGCGATCTACTCGGCGGCCGTCATGGGCGTGCAGCACAATGACCAAGGAGA  2040

Db  2041 GCAAATTGCGCAACCGCAACACACGCCACCAGTGGCGCCACCACCA  2100
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Qy  2041 GCAAATTGCGCAACCGCAACACACGCCACCAGTGGCGCCACCACCA  2100

Db  2101 CCTGTCTCGGACACCACCATGGCCGACTCGCAGAAATTGGCCTGGAGTGCA  2160
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Qy  2101 CCTGTCTCGGACACCACCATGGCCGACTCGCAGAAATTGGCCTGGAGTGCA  2160

Db  2161 CGGACGAAGCTGGCAAGATTAAACATCAGACAATCCTTTATCGAGCACACAC  2220
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Qy  2161 CGGACGAAGCTGGCAAGATTAAACATCAGACAATCCTTTATCGAGCACACAC  2220

Db  2221 AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTG  2280
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Qy  2221 AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTG  2280

Db  2281 GTCGGCACAGTCGGGACGAATCGGGGTGTTCCGTTACTATTTCCCAACAGAGGACG  2340
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Qy  2281 GTCGGCACAGTCGGGACGAATCGGGGTGTTCCGTTACTATTTCCCAACAGAGGACG  2340

Db  2341 ATGACGAGGATGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCA  2400
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Qy  2341 ATGACGAGGATGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCG  2400

Db  2401 ATGTGTTTTGTGTGTGGGACTGTTGCTGGGTTGCTGAAATTCAGGAGTGGTATCGC  2460
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Qy   2401  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  2460
           ATGTGTTTTGTGTGTGGGACTGTTGCTGCTGGGTTTGGTTGGTTGAAATTCAGGAGTGGTATCGC

Db   2461  TCATCGTCTTCGATCCCTTCGTCGTCTGCAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGA  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2461  TCATCGTCTTCGATCCCTTCGTCGTCTGCAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGA  2520

Db   2521  TGTTCATGGCAATGGATCACCACGATATGAACAAGGAGGATGGAACGCGTGCTGCTCAAGAGTG  2580
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Qy   2521  TGTTCATGGCAATGGATCACCACGATATGAACAAGGAGGATGGAACGCGTGCTGCTCAAGAGTG  2580

Db   2581  GCAACTATTTCTTCACCGCCACCTTTGCCATGAGGCCACCATGAAGCTAATGGCCATGA  2640
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Qy   2581  GCAACTATTTCTTCACCGCCACCTTTGCCATGAGGCCACCATGAAGCTAATGGCCATGA  2640

Db   2641  GCCCCAAGTACTATTTCAGGAGGGCTGAACATCTTCGACTTCATTATCGTGCCCTAT  2700
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Qy   2641  GCCCCAAGTACTATTTCAGGAGGGCTGAACATCTTCGACTTCATTATCGTGCCCTAT  2700

Db   2701  CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTCCGTATTGCCGTTCCTTCGAT  2760
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Qy   2701  CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTCCGTATTGCCGTTCCTTCGAT  2760

Db   2761  TGCTCGGTGTATTCAAACTGGCCAAGTCTTGGCCACACTTAATTACTCATTTCGATTA  2820
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Qy   2761  TGCTCGGTGTATTCAAACTGGCCAAGTCTTGGCCACACTTAATTACTCATTTCGATTA  2820

Db   2821  TGGGACGCACCCATGGCGCCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA  2880
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Qy   2821  TGGGACGCACCCATGGCGCCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA  2880

Db   2881  TCTTTGCGGTGATGGGAATGCAACTGTTCGGGAAAGAATTATCATGATCACAAGGACCGCT  2940
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Qy   2881  TCTTTGCGGTGATGGGAATGCAACTGTTCGGGAAAGAATTATCATGATCACAAGGACCGCT  2940

Db   2941  TTCCGGATGGCGACCTGCCGCGCTGGAACTTCACCGACTTCATCGGCCTTCATGATCG  3000
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Qy   2941  TTCCGGATGGCGACCTGCCGCGCTGGAACTTCACCGACTTCATCGGCCTTCATGATCG  3000

Db   3001  TGTTCCGGGTGCTCTGCGGAGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCG  3060
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Qy   3001  TGTTCCGGGTGCTCTGCGGAGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCG  3060

Db   3061  ATGTCTCGTGCAATCCCTTCTTCTTGGCTCTTGTCATCGGCAATCTGTGTGTGTACTTA  3120
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Qy   3061  ATGTCTCGTGCAATCCCTTCTTCTTGGCTCTTGTCATCGGCAATCTGTGTGTGTACTTA  3120

Db   3121  ACCTTTCTTAGCCTTGCTTTGTCCAATTTGGCTCATCTAGCTTATCAGCCGCCGACTG  3180
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Db   3181  CCGATAAGCATACGATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT  3240
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Qy   3181  CCGATAAGCATACGATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT  3240

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Db   3301  TAAGTGATCAACCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTTGGAGCGAAGAGC  3360
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Db   3361  ATGGTGACAACGAACTGGAGCTGGGCCCACGAGGCTGGGCCCGACGGCCTCCATCAAGA  3420
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Qy   3361  ATGGTGACAACGAACTGGAGCTGGGCCCACGAGGCTGGGCCCGACGGCCTCCATCAAGA  3420

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Qy   3421  AGGGGATCAAGGAGCAGAACGCUAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGA  3480

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Qy   3481
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Qy   3481  TACACGGCGACATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACCGAACGA  3540
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Qy   3541  TGATTGGCAACTCAATTAACCACCAAGACAATGGAACACGAGCTAAACCATAGAG  3600

Db   3601  GTTTGTCCTTACAGGACGACGACACTGCCAGCATTCATATGGTAGCCATAAGAATC  3660
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Qy   3601  GTTTGTCCTTACAGGACGACGACACTGCCAGCATTCATATGGTAGCCATAAGAATC  3660

Db   3661  GACCATTCAAGGACGAGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGC  3720
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Qy   3661  GACCATTCAAGGACGAGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGC  3720

Db   3721  GCGACGCCAGCAAGGAGGATTAGTCTCGACGAGGAACTGACGAGGGGCGAATGCG  3780
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Qy   3781  AGGAGGGCCCGCTCGACGGTGATATCATTATTCATGCACACGACGAGGATATACTCGATG  3840

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Qy   3841  AATATCCAGCTGATTGCTGCCCCGATTCGTACTATAAGAAAATTCCGATCTTAGCCGGTG  3900

Db   3901  ACGATGACTCGCGTTCTGCAAGGATGGGCAATTACGACTGAAAACTTTCAATTAA  3960
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Qy   3901  ACGATGACTCGCGTTCTGCAAGGATGGGCAATTACGACTGAAAACTTTCAATTAA  3960

Db   3961  TTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTAATGAGTAGCTTAGCTT  4020
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Qy   3961  TTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTAATGAGTAGCTTAGCTT  4020

Db   4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTATACTATA  4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4021  TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTATACTATA  4080

Db   4081  TGGACAGAATATTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG  4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4081  TGGACAGAATATTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG  4140

Db   4141  GCTTCAAAGTGTACTTCACCCAACCGTGGTGTTGGCTCGATTTCGTGATTGCGTCATGGTAT  4200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4141  GCTTCAAAGTGTACTTCACCCAACCGTGGTGTTGGCTCGATTTCGTGATTGCGTCATGGTAT  4200

Db   4201  CGCTTATCAACTTCGTTGCTTGTTCACTTGTTGGAGCTGGTGGTGTATTCAAGCCTTCAAGACTA  4260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4201  CGCTTATCAACTTCGTTGCTTGTTCACTTGTTGGAGCTGGTGGTGTATTCAAGCCTTCAAGACTA  4260

Db   4261  TGCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGGG  4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4261  TGCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGGG  4320

Db   4321  TCGTCGTTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC  4380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4321  TCGTCGTTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC  4380

Db   4381  TAATATTTGGCTAATTTTGCCATAATGGGTACAGCTTTTGCTGGAAAATATTTTA  4440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4381  TAATATTTGGCTAATTTTGCCATAATGGGTACAGCTTTTGCTGGAAAATATTTTA  4440

Db   4441  AGTGCGAGGACATGAATGGCGAGAACTACACGTGGTGAATTCGATCATCGCAATGCCT  4500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4441  AGTGCGAGGACATGAATGGCGAGAACTACACGTGGTGAATTCGATCATCGCAATGCCT  4500

Db   4501  GCGAGAGCCGAGAACTACACGTGGGTGAATTCAGCAATGAATTTCGATCATGTAGGTAACG  4560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4501  GCGAGAGCCGAGAACTACACGTGGGTGAATTCAGCAATGAATTTCGATCATGTAGGTAACG  4560

Db   4561  CGTATCTGTGCCTTTTCCAAGTGCCCACCTTCAAAGGCTGCACCTTCAAAGGCTGCACCTTCAAATGCTGATCAAATCATGAACGATG  4620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4561  CGTATCTGTGCCTTTTCCAAGTGCCCACCTTCAAAGGCTGCACCTTCAAATCATGAACGATG  4620
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Db 4621 CTATCGATTCACGAGAGGTGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680
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Qy 4621 CTATCGATTCACGAGAGGTGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT 4680

Db 4681 TATATTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCACTCGTTCATTGGTG 4740
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4681 TATATTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCACTCGTTCATTGGTG 4740

Db 4741 TTATCATTGATATTTAATGAGCAAAAGAAAAAGCAGGTGGATCATTAGAAATGTTCA 4800
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Qy 4741 TTATCATTGATATTTAATGAGCAAAAGAAAAAGCAGGTGGATCATTAGAAATGTTCA 4800

Db 4801 TGACAGAGAGATCAGAAAAAGTACTATATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860
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Qy 4801 TGACAGAGAGATCAGAAAAAGTACTATATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT 4860

Db 4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACAGCAATAGTCTTTGAAATAGTAACCG 4920
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Qy 4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACAGCAATAGTCTTTGAAATAGTAACCG 4920

Db 4921 ATAAGAAATTCGATATAATCATTATGTTCATTGGTCTGAACATGTTCACCATGACCC 4980
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Qy 4921 ATAAGAAATTCGATATAATCATTATGTTCATTGGTCTGAACATGTTCACCATGACCC 4980

Db 4981 TCGATCGTTACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGATAT 5040
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Qy 4981 TCGATCGTTACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGATAT 5040

Db 5041 TCGTAGTTATTTCAGTTCCGAATGTCTATTAAAATATTCGCTTACGATATCACTATT 5100
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Qy 5041 TCGTAGTTATTTCAGTTCCGAATGTCTATTAAAATATTCGCTTACGATATCACTATT 5100

Db 5101 TTATTGAGCCATGGAATTTATTGATGTAGTTGTCATTTTATCCATCTTAGGTCTTG 5160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5101 TTATTGAGCCATGGAATTTATTGATGTAGTTGTCATTTTATCCATCTTAGGTCTTG 5160

Db 5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTG 5220
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Qy 5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTG 5220

Db 5221 TGGCGAAAGTGGGCGCCGTGTCCGACTGGTGAAGGAGCCAAGGCATTCGGACACTGC 5280
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Qy 5221 TGGCGAAAGTGGGCGCCGTGTCCGACTGGTGAAGGAGCCAAGGCATTCGGACACTGC 5280

Db 5281 TCTTCCGCGTTGGCCATGCGCCGGCCCCTGTTCAACATCTGCCTCGCTGCTGTCCTGG 5340
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Qy 5281 TCTTCCGCGTTGGCCATGCGCCGGCCCCTGTTCAACATCTGCCTCGCTGCTGTCCTGG 5340

Db 5341 TCATGTTCATCTTTGCCATTTTCGGCATGTCGTTCTTCATGCACGTGATCCTCATGACTG 5400
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Qy 5341 TCATGTTCATCTTTGCCATTTTCGGCATGTCGTTCTTCATGCACGTGATCCTCATGACTG 5400

Db 5401 GCATTAACGACGTCTACAACTTCAAGACGCTTTGGGCCAGACCATTTCAAGACCCTTTCAGA 5460
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Qy 5401 GCATTAACGACGTCTACAACTTCAAGACGCTTTGGGCCAGACCATTTCAAGACCCTTTCAGA 5460

Db 5461 TGTCGACGTCAGCCGGTTGGGATGTGTACTGGACGCATTATCAATGAGGAAGCATGCG 5520
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Qy 5461 TGTCGACGTCAGCCGGTTGGGATGTGTACTGGACGCATTATCAATGAGGAAGCATGCG 5520

Db 5521 ATCCACCCGACAGCGACACCGGCTATCCCGGCGACAAAGGCTATTGTGGTTCAGCCGACCGTTGAATAA 5580
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Qy 5521 ATCCACCCGACAGCGACACCGGCTATCCCGGCGACAAAGGCTATTGTGGTTCAGCCGACCGTTGAATAA 5580

Db 5581 CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTG 5640
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Qy 5581 CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTG 5640

Db 5641 TCATTCTCGAGAACTATAGTCAGGCCACCGTGCAAGAGGGTCTAACCGACGACG 5700
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5641 TCATTCTCGAGAACTATAGTCAGGCCACCGTGCAAGAGGGTCTAACCGACGACG 5700
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Db 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATAC 5760
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Qy 5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATAC 5760

Db 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGACGACGACCCCGCTCGAGATCCACAAAAC 5820
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Qy 5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGACGACGACCCCGCTCGAGATCCACAAAAC 5820

Db 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCCTCGCGGTGACCTCATGTACT 5880
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Qy 5821 CGAACAAGTACAAGATCATATCGATGGACATACCCATCCTCGCGGTGACCTCATGTACT 5880

Db 5881 GCGTGACATCCTCGACGCGCCCTACGAAAGACTTCTTTGCGCGAAGGGCAATCCGATAG 5940
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Qy 5881 GCGTCGACATCCTCGACGCCCCTACGAAAGACTTCTTTGCGCGAAGGGCAATCCGATAG 5940

Db 5941 AGGAGACGGGTGAGATTGGTGAGATAGCGCCCGCCCGGATACGGAGGGCTACGAGCCCG 6000
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Qy 5941 AGGAGACGGGTGAGATTGGTGAGATAGCGCCCGCCCGGATACGGAGGGCTACGAGCCCG 6000

Db 6001 TCTCATCAACCGCTGTGCCGTCAGCGTGAGGGAGTACTGCCCGGCTAATCCAGCACGCCT 6060
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Qy 6001 TCTCATCAACCGCTGTGCCGTCAGCGTGAGGGAGTACTGCCCGGCTAATCCAGCACGCCT 6060

Db 6061 GGCGAAAGCACAAGGCGCGCGCGAGGGAGGTGGGTCCTTTGAGCCGGATACGGATCATG 6120
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Qy 6061 GGCGAAAGCACAAGGCGCGCGCGAGGGAGGTGGGTCCTTTGAGCCGGATACGGATCATG 6120

Db 6121 GCGATGGCGGTGATCCGGATGCCGGGGACCCGGGCGATGAAGCAACGACGCGGCGATG 6180
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Qy 6121 GCGATGGCGGTGATCCGGATGCCGGGGACCCGGGCGATGAAGCAACGACGCGGCGATG 6180

Db 6181 CGCCCGTTGGTGGGAGATGGTAGTGTTAACGGTACTGCAGAAGGAGCTGCCGATGCTCATCC 6240
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Qy 6181 CGCCCGTTGGTGGGAGATGGTAGTGTTAACGGTACTGCAGAAGGAGCTGCCGATGGTCATCC 6240

Db 6241 AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCAGCGGCGGCCGCAGCAGCAGCAG 6300
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Qy 6241 AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCAGCGGCGGCCGCAGCAGCAGCAG 6300

Db 6301 CGGCGGCCGGCCGCGGCGGGTCCCGGAAGTCCGGGCGGGTAGCGCCGGGCGGACAGA 6360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 6301 CGGCGGCCGGCCGCGGCGGGTCCCGGAAGTCCGGGCGGGTAGCGCCGGGCGGACAGA 6360

Db 6361 CCGCCGTTCGTGGAGAGCGACGACGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC 6420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 6361 CCGCCGTTCGTGGAGAGCGACGACGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC 6420

Db 6421 ACTCGCGATCGCCGAGCATCACGTCGCCCACGCGGCCGGATGTCTGAGCCCAGGCC 6480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 6421 ACTCGCGATCGCCGAGCATCACGTCGCCCACGCGGCCGGATGTCTGAGCCCAGGCC 6480

Db 6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513
        |||||||||||||||||||||||||||||||||
Qy 6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513
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BASE COUNT     1681 a   1548 c   1702 g   1582 t
ORIGIN

Query Match        100.0%;  Score 6513;  DB 18;  Length 6513;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 6513;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db     1 TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC   60
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Qy     1 TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC   60

Db    61 GCAGTTTGTTCCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCATTGCCG  120
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Qy    61 GCAGTTTGTTCCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCATTGCCG  120

Db   121 CTGAACAATGAAAAGCAGAAGAGGAGCTGGAAAGAAAGAGAGCCGAGGAGGTGCCGCGAT  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CTGAACAATGAAAAGCAGAAGAGGAGCTGGAAAGAAAGAGAGCCGAGGAGGTGCCGCGAT  180

Db   181 ATGGTCGCAAGAAAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGACGTGAGGTC  240
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Qy   181 ATGGTCGCAAGAAAAAACAAAAGAAATCCGATATGATGACGAGGACGAGGACGTGAGGTC  240

Db   241 CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT  300

Db   301 TCCCGCCGGAATTGGCCTTCCACTCCTCTCGAGGATATATCGATCCTACTACAGCAATGTAC  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 TCCCGCCGGAATTGGCCTTCCACTCCTCTCGAGGATATATCGATCCTACTACAGCAATGTAC  360

Db   361 TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAA  420
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Qy   361 TGACATTCGTAGTTGTAAGCAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAA  420

Db   421 TGTGGATGCTCGATCCATTCAAATCGATACGTCGTGTGCCATTTACATTCTAGTGCATC  480
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Qy   421 TGTGGATGCTCGATCCATTCAAATCGATACGTCGTGTGCCATTTACATTCTAGTGCATC  480

Db   481 CATTATTTTCCCTATTCATCATCACCACAATTCTCGTCAACTGCATCCTGATGATAATGC  540
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Qy   481 CATTATTTTCCCTATTCATCATCACCACAATTCTCGTCAACTGCATCCTGATGATAATGC  540

Db   541 CGACAACGCCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 CGACAACGCCCACGGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT  600

Db   601 CAGCTGTTAAAGTGATGCGACGAGGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATG  660
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Qy   601 CAGCTGTTAAAGTGATGCGACGAGGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATG  660

Db   661 CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661 CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT  720

Db   721 TAGGTAATCTAGCAGCCCTGCGGAACGTTAGGGTGCTGCGAGCGTTAAAACCGTAGGCA  780
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Qy   721 TAGGTAATCTAGCAGCCCTGCGGAACGTTAGGGTGCTGCGAGCGTTAAAACCGTAGGCA  780

Db   781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATGGAAGAATCTGCGCG  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATGGAAGAATCTGCGCG  840

Db   841 ATGTGATTATCCTGACCATGTTCTCCCGTCGGTTCGCGTTGCGGTCGCTCACGAGATCT  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 ATGTGATTATCCTGACCATGTTCTCCCGTCGGTTCGCGTTGCGGTCGCTCACGAGATCT  900

Db   901 ATATGGGGCGTGCTCACCGAGAAGTCATCAAGAAGTCCCGCTGGACGGTTCCTCGGGGCA  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 ATATGGGGCGTGCTCACCGAGAAGTCATCAAGAAGTCCCGCTGGACGGTTCCTCGGGGCA  960

Db   961 ATCTGACCGACGAGAACTGGGACTACACAATCGCAATAGCTCCAATTGGTATTCCGAGG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   961 ATCTGACCGACGAGAACTGGGACTACACAATCGCAATAGCTCCAATTGGTATTCCGAGG 1020

Db  1021 ACGAGGGCATCTCATTCCGTTGCCTGTATCCGTGCGGGGCAATATCCGTGCGGCGACGACG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1021 ACGAGGGCATCTCATTCCGTTGCCTGTATCCGTGCGGGGCAATATCCGTGCGGCGACGACG 1080

Db  1081 ATTACGTGCCTCGCAGGGGTTGGTCCGGCCTTCCGAATCGGAATTATGGCTACACCAGCTTCGATT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1081 ATTACGTGCCTCGCAGGGGTTGGTCCGGCCTTCCGAATCGGAATTATGGCTACACCAGCTTCGATT 1140

Db  1141 CGTTCGGATGGGCTTTCCTGTCCGCCTTCCGTGATGACACAGGACTTCTGGGAGGATC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1141 CGTTCGGATGGGCTTTCCTGTCCGCCTTCCGTGATGACACAGGACTTCTGGGAGGATC 1200

Db  1201 TGTACCAGCTGGTGTTGCGCGCCGCCGGACCATGGCACATGCTCGTTCTTTATAGTCATCA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1201 TGTACCAGCTGGTGTTGCGCGCCGCCGGACCATGGCACATGCTCGTTCTTTATAGTCATCA 1260

Db  1261 TCTTCCTAGGTTCATTCTATCTGTGAATTTGATTTTGGCCATTGTTGCCATGTCGTATG 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1261 TCTTCCTAGGTTCATTCTATCTGTGAATTTGATTTTGGCCATTGTTGCCATGTCGTATG 1320

Db  1321 ACGAATTGCAAAGGAAGGCCGAAGAGAGAGAGGCGTGCCCGAAGAGGAGGCGGATACGTGAAG 1380
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Qy  1321 ACGAATTGCAAAGGAAGGCCGAAGAGAGAGAGGCGTGCCCGAAGAGGAGGCGGATACGTGAAG 1380

Db  1381 CGGAAGAAGCTGCCGCGCCCAAGCTGGAGGACGCGGCCAAGCTGCCAGGCTC 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381 CGGAAGAAGCTGCCGCGCCCAAGCTGGAGGACGCGGCCAAGCTGCCAGGCTC 1440

Db  1441 AGGCAGCAGCGGATGCGGCGCTGCCGAAGAGGCTGCACTGCTGCCATCCGAAATGGCCAAGA 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441 AGGCAGCAGCGGATGCGGCGCTGCCGAAGAGGCTGCACTGCTGCCATCCGAAATGGCCAAGA 1500

Db  1501 GTCCGACGTATTCTTGCATCAGCTATGAGCTATTGTTGCGGCGAGAAGGGCAACGATG 1560
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Qy  1501 GTCCGACGTATTCTTGCATCAGCTATGAGCTATTGTTGCGGCGAGAAGGGCAACGATG 1560

Db  1561 ACAACAACAAAGAAGATGTCCATTCGGAGCGTCGGAGCGTCGGAGTGCGTCGAGCG 1620
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Qy  1561 ACAACAACAAAGAAGATGTCCATTCGGAGCGTCGGAGCGTCGGAGTGCGTCGGAGCG 1620

Db  1621 TTATACAAAGACAACCAGCAACTACCAGCACCACCAGCAACCAAGTTCGTAAAGTGA 1680
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Qy  1621 TTATACAAAGACAACCAGCAACTACCAGCACCACCAGCAACCAAGTTCGTAAAGTGA 1680

Db  1681 GCACGACATCCTTATCCTTACCGTTCACCGTTTAACATACGCAGGGGATCACGTAGTT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681 GCACGACATCCTTATCCTTACCGTTCACCGTTTAACATACGCAGGGGATCACGTAGTT 1740

Db  1741 CTCACAAGTACACGATACCGGAACGACGACGTGGCCCGTTGGTATACCCGGTGTACTCGTA 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741 CTCACAAGTACACGATACCGGAACGACGACGTGGCCCGTTGGTATACCCGGTGTACTCGTA 1800

Db  1801 AGCCATTGGTATTGTCAACATCAGGATGCCCAGCACTTGCCCTATGCCGACGACT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801 AGCCATTGGTATTGTCAACATCAGGATGCCCAGCACTTGCCCTATGCCGACGACT 1860

Db  1861 CGAATGCGGTCACCCCGATGTCCGAAGAGATGGGGCCATCATAGTGCCCGTGTACTAGTG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861 CGAATGCGGTCACCCCGATGTCCGAAGAGATGGGGCCATCATAGTGCCCGTGTACTAGTG 1920

Db  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTGCGAATATCGTATACCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTGCGAATATCGTATACCT 1980

Db  1981 CACATGGCCGATCTACTCGGCGCATGGGCGTCAGCACAATGACCAAGGAGA 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 CACATGGCCGATCTACTCGGCGCATGGGCGTCAGCACAATGACCAAGGAGA 2040

Db  2041 GCAAATTGCGCAACCGCAACACACGCAATCAATCAGTGGCCGCCACCA 2100
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Qy  2041 GCAAATTGGCAACCGCAACACGCAATCAATCAGTGGGCCCACCAATGCGGCACCA 2100

Db  2101 CCTGTCTGGACACCAATCCACAGCTCGATCATCGACTACGGCGCCTGGAGTGCA 2160
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Qy  2101 CCTGTCTGGACACCAATCCACAGCTCGATCATCGACTACGGCGCCTGGAGTGCA 2160

Db  2161 CGGACGAGCTGGCAAGATTAAACATCACATGACAATCCTTTATCGAGCCCAGACAC 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161 CGGACGAGCTGGCAAGATTAAACATCACATGACAATCCTTTATCGAGCCCAGACAC 2220

Db  2221 AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCCGCTG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCCGCTG 2280

Db  2281 GTCGGCACAGTCGGGCAAGCGGATCGGCGTGTCCGTTACTATTCCCAACAGAGGACG 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281 GTCGGCACAGTCGGGCAAGCGGATCGGCGTGTCCGTTACTATTCCCAACAGAGGACG 2340

Db  2341 ATGACGAGGATGGGCCGACGTTCAAAGACACTTCGAAGTGATCCTCAAAGGCCATCG 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341 ATGACGAGGATGGGCCGACGTTCAAAGACACTTCGAAGTGATCCTCAAAGGCCATCG 2400

Db  2401 ATGTGTTTGTGTGTGGGACTGTTGCTCGGGTTTGGTTGGGTTGGTGAAATTTCAGGAGTGGTATCGC 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401 ATGTGTTTGTGTGTGGGACTGTTGCTCGGGTTTGGTTGGGTTGGTGAAATTTCAGGAGTGGTATCGC 2460

Db  2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCGTGTCATTGTGGTCAACACGA 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461 TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCGTGTCATTGTGGTCAACACGA 2520

Db  2521 TGTTCATGGCAATGGCAATGGATCACCACGATGAACAAGGAGAGGAACGGCGTGCTCAAGAGTG 2580
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Qy  2521 TGTTCATGGCAATGGCAATGGATCACCACGATGAACAAGGAGAGGAACGGCGTGCTCAAGAGTG 2580

Db  2581 GCAACTATTCTTCACCGCACCTTGCCTGCGAGGCCACCATGAAGCTAATGGCCATGA 2640
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Qy  2581 GCAACTATTCTTCACCGCACCTTGCCTGCGAGGCCACCATGAAGCTAATGGCCATGA 2640

Db  2641 GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGCCCTAT 2700
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Qy  2641 GCCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGCCCTAT 2700

Db  2701 CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTGTCCGATTGCGTCCTTTCGAT 2760
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Qy  2701 CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTCTGTCCGATTGCGTCCTTTCGAT 2760

Db  2761 TGTCGCGTGTATTCAAACTGGCCAAGTCTTGGCCCACAGTTGGTATTACTTCATTCGATTA 2820
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Db  2821 TGGGACGCCACCATGGCCACTTGGGTAATCGCAACTGTTACTTTGCATTATCATCTTCA 2880
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Db  2881 TCTTTTGCGGTGATGGGAATGCCGACTTGCCCGCGGAGAAGACCGGCTTCATGATCG 2940
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Qy  2881 TCTTTTGCGGTGATGGGAATGCCGACTTGCCCGCGGAGAAGACCGGCTTCATGATCG 2940

Db  2941 TTCCCGGATGGGCAATCGCAACTGCTCTTCGGCGGAGAATGGAACTTTATGGGGACTGGGCG 3000
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Qy  2941 TTCCCGGATGGGCAATCGCAACTGCTCTTCGGCGGAGAATGGAACTTTATGGGGACTGGGCG 3000

Db  3001 TGTTCCGGGTGCTGCAATCCCTTCTTCTTCGGCCACCGTGTCATGTGGGACTGTTACGTGGGCG 3060
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Qy  3001 TGTTCCGGGTGCTGCAATCCCTTCTTCTTCGGCCACCGTGTCATGTGGGACTGTTACGTGGGCG 3060

Db  3061 ATGTCCTGTGCAATCGCAATGGGCTCATCGGCAATCGGCCAATCTCGTGTGGTACTTA 3120
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Qy  3061 ATGTCCTGTGCAATCGCAATGGGCTCATCGGCAATCGGCCAATCTCGTGTGGTACTTA 3120

Db  3121 ACCTTTCTTAGCCTTGCTTTTGTCCAATTTGGCTCATCAGCTTATCAGCGCCGCACTG 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121 ACCTTTCTTAGCCTTGCTTTTGTCCAATTTGGCTCATCAGCTTATCAGCGCCGCACTG 3180
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Db  3181 CCGATAACGATACGAATACAAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT 3240
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Qy  3181 CCGATAACGATACGAATACAAATAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT 3240

Db  3241 GGGTTAAGCGTAATATGCTGATTGTTCAAGTTAATACGTAACAAATTGACAAAATCAAA 3300
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Qy  3241 GGGTTAAGCGTAATATGCTGATTGTTCAAGTTAATACGTAACAAATTGACAAAATCAAA 3300

Db  3301 TAAGTGATCAACCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTGGAGCGGAAGAGC 3360
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Qy  3301 TAAGTGATCAACCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTGGAGCGGAAGAGC 3360

Db  3361 ATGGTGACAACGAACTGGAGCTGGCCACACGACGAGATCCTCGCCCGACGCGACCTCATCAAGA 3420
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Qy  3361 ATGGTGACAACGAACTGGAGCTGGCCACACGACGAGATCCTCGCCCGACGCGACCTCATCAAGA 3420

Db  3421 AGGGGATCAAGGAGCAGCAACTGGAGTGGCCAACTGGAGTGGATCGGGGATCGGGGATCGGAATTCACGA 3480
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Qy  3421 AGGGGATCAAGGAGCAGCAACTGGAGTGGCCAACTGGAGTGGATCGGGGATCGGGGATCGGAATTCACGA 3480

Db  3481 TACACGGCGACATGATGAAGAACAACAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
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Qy  3481 TACACGGCGACATGATGAAGAACAACAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540

Db  3541 TGATTGCAACTCAATTAACCACCAAGAACAATAGACTGGAACACGAGCTAAACCATAGAG 3600
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Qy  3541 TGATTGCAACTCAATTAACCACCAAGAACAATAGACTGGAACACGAGCTAAACCATAGAG 3600

Db  3601 GTTTGTCCTTACAGGACGACACTGCCAGCACTGCCAGCATCATATGGTAGCCATATAAGAATC 3660
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Qy  3601 GTTTGTCCTTACAGGACGACACTGCCAGCACTGCCAGCATCATATGGTAGCCATATAAGAATC 3660

Db  3661 GACCATTCAAGACGCAGAGCCACAGGGCAGCGCCGAGACGATGAGGGCGAGGAGAGC 3720
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Qy  3661 GACCATTCAAGACGCAGAGCCACAGGGCAGCGCCGAGACGATGAGGGCGAGGAGAGC 3720

Db  3721 GCGACGCCAGCAAGGAGGAGATTTAGGTCTCGACGAGGAACTGGACGAGGGCGAATGCG 3780
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Qy  3721 GCGACGCCAGCAAGGAGGAGATTTAGGTCTCGACGAGGAACTGGACGAGGGCGAATGCG 3780

Db  3781 AGGAGGGCCCGCTCGACGGTGATATCATTATTCATCGCACACGACGAGGATACTCGATG 3840
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Qy  3781 AGGAGGGCCCGCTCGACGGTGATATCATTATTCATCGCACACGACGAGGATACTCGATG 3840

Db  3841 AATATCCAGCTGATTGCTGCCCCGATTCGTACTATCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900
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Qy  3841 AATATCCAGCTGATTGCTGCCCCGATTCGTACTATCGTACTATAAGAAATTTCCGATCTTAGCCGGTG 3900

Db  3901 ACGATGACTCGCCCGTTCTGCAAGGATGGGCAATTTACGACTGCAATTTACTATACTATA 3960
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Qy  3901 ACGATGACTCGCCCGTTCTGCAAGGATGGGCAATTTACGACTGCAATTTACTATACTATA 3960

Db  3961 TTGAAAATAAATATTTACGGTTATATTCTCTTGAAACAGCTGTTATCACTATGATTTTAATGAGTTAGCTT 4020
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Qy  3961 TTGAAAATAAATATTTACGGTTATATTCTCTTGAAACAGCTGTTATCACTATGATTTTAATGAGTTAGCTT 4020

Db  4021 TGGCATTAGAAGATGTACATCTGCCACAAAAGACCCATACTGCAGGATATTTATACTATA 4080
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Qy  4021 TGGCATTAGAAGATGTACATCTGCCACAAAAGACCCATACTGCAGGATATTTATACTATA 4080

Db  4081 TGGACAGAATATTACGGTTAATCACTGTTATCACTATCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
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Qy  4081 TGGACAGAATATTACGGTTAATCACTGTTATCACTATCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140

Db  4141 GCTTCAAAGTGTACTTCACCGACTTGGCTCGATTTCGTGATTCCGATTCGATTGTCATGGTAT 4200
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Qy  4141 GCTTCAAAGTGTACTTCACCGACTTGGCTCGATTTCGTGATTCCGATTCGATTGTCATGGTAT 4200

Db  4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGCTTGGGTGGTATTCAAGCCTTCAAGAGACTA 4260
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGCTTGGGTGGTATTCAAGCCTTCAAGAGACTA 4260
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Db  4261 TCCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGAGGGCATGAGGG  4320
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Qy  4261 TCCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGAGGGCATGAGGG  4320

Db  4321 TCGTCGTTAATGCGGCTGCTGTACAAGCTATACCGTCCATCTTCAAGACTTCAATGGTGTGTC  4380
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Qy  4321 TCGTCGTTAATGCGGCTGCTGTACAAGCTATACCGTCCATCTTCAAGACTTCAATGGTGTGTC  4380

Db  4381 TAATATTTTGGCTAATTTTGCCATAATGGTGTACAGCTTTTTGCTCGGAAAATATTTTA  4440
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Qy  4381 TAATATTTTGGCTAATTTTGCCATAATGGTGTACAGCTTTTTGCTCGGAAAATATTTTA  4440

Db  4441 AGTGCGAGGACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATCGCAATGCCT  4500
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Qy  4441 AGTGCGAGGACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATCGCAATGCCT  4500

Db  4501 GCGAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG  4560
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Qy  4501 GCGAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTCGATCATGTAGGTAACG  4560

Db  4561 CGTATCTGTGCCTTTCCAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG  4620
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Qy  4561 CGTATCTGTGCCTTTCCAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG  4620

Db  4621 CTATCGATTCACGAGAGTGGACAAGCAACCAATTCGTTGAAACATCTACATGTATT  4680
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Qy  4621 CTATCGATTCACGAGAGTGGACAAGCAACCAATTCGTTGAAACATCTACATGTATT  4680

Db  4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG  4740
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Qy  4681 TATATTTCGTATTCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG  4740

Db  4741 TTATCATTGATAATTTAATGAGCAAAAAGAGGTGGATCATTAGAAATGTTCA  4800
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Qy  4741 TTATCATTGATAATTTAATGAGCAAAAAGAGGTGGATCATTAGAAATGTTCA  4800

Db  4801 TGACAGAGATCAGAAAAGTACTATAATGCTATAATGGGCTCTAAAAAACCAT  4860
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Qy  4801 TGACAGAGATCAGAAAAGTACTATAATGCTATAATGGGCTCTAAAAAACCAT  4860

Db  4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTAACCG  4920
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Qy  4861 TAAAAGCCATTCCAAGACCAAGGTGGCGACCACCAAGCAATAGTCTTTGAAATAGTAACCG  4920

Db  4921 ATAAGAAATTCGATATAATCATTATGTCTATTATTCATTGATAGTAGTGTTCACCATGACCC  4980
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Qy  4921 ATAAGAAATTCGATATAATCATTATGTCTATTATTCATTGATAGTAGTGTTCACCATGACCC  4980

Db  4981 TCGATCGTTACGATGCGTCGGACACGTATAACGGGTCCTAGACTATCTCAATGCGATAT  5040
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Qy  4981 TCGATCGTTACGATGCGTCGGACACGTATAACGGGTCCTAGACTATCTCAATGCGATAT  5040

Db  5041 TCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATT  5100
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Qy  5041 TCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATT  5100

Db  5101 TTATTGAGCCATGGAATTTATTTGATGTAGTAGTGTTCATTTTATCCATCTTAGGTCTTG  5160
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Qy  5101 TTATTGAGCCATGGAATTTATTTGATGTAGTAGTGTTCATTTTATCCATCTTAGGTCTTG  5160

Db  5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCGCCGACCCTGCTCCGAGTGGTGCGTG  5220
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Qy  5161 TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCGCCGACCCTGCTCCGAGTGGTGCGTG  5220

Db  5221 TGGCGAAAGTAGTGGGCCGTGTCCGACTGGTCCTTCGACATTCGGAAGGGAGCCAAGGGAGCCATTCGGACACTGC  5280
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Qy  5221 TGGCGAAAGTAGTGGGCCGTGTCCGACTGGTCCTTCGACATTCGGAAGGGAGCCAAGGGAGCCATTCGGACACTGC  5280

Db  5281 TCTTCGCGTTGGCCATGTCGCTGCCGGCCCTGTTCAACATCTGCCTGCTCGTGTTCCTGG  5340
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Qy  5281 TCTTCGCGTTGGCCATGTCGCTGCCGGCCCTGTTCAACATCTGCCTGCTCGTGTTCCTGG  5340

Db  5341 TCATGTTCATCTTTGCCATTTTCGGCATTGTCGTTCTTCTTCATGCACGTGAAGGAGAAGAGCG  5400
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Qy  5341 TCATGTTCATCTTTGCCATTTTCGGCATTGTCGTTCTTCTTCATGCACGTGAAGGAGAAGAGCG  5400

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Qy  5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGAGCATGATGATCCTGCTCTTTCAGA  5460

Db  5461 TGTCGACGTCAGCCGGTTGGGATGGTGTACTGACGACGCGCCATTATCAATGAGGAAGCATGCG  5520
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Qy  5461 TGTCGACGTCAGCCGGTTGGGATGGTGTACTGACGACGCGCCATTATCAATGAGGAAGCATGCG  5520

Db  5521 ATCCACCCGACAGCGACAAAGGCTATCCGGCAATTGGTTCAGCGCAATTGGTTCAGCGACCGTTGGAATAA  5580
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Db  5581 CGTTTCTCTCTCATACCTAGTTATAAGCTTTTTGATAGTATTATTAATATGTACATTGCTG  5640
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Qy  5581 CGTTTCTCTCTCATACCTAGTTATAAGCTTTTTGATAGTATTATTAATATGTACATTGCTG  5640

Db  5641 TCATTCTGAGAACTATAGTCAGGCCACCAGAGACGTGCAAGAGGGTCTAACCGACGACG  5700
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Qy  5641 TCATTCTGAGAACTATAGTCAGGCCACCAGAGACGTGCAAGAGGGTCTAACCGACGACG  5700

Db  5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCGGAGGCACCCAGTACATAC  5760
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Qy  5701 ACTACGACATGTACTATGAGATCTGGCAGCAATTCGATCGGAGGCACCCAGTACATAC  5760

Db  5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCGCTCGAGATCCACAAAC  5820
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Qy  5761 GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCGCTCGAGATCCACAAAC  5820

Db  5821 CGAACAAGTACAAGATCATATCGATGACATATCGATGATAGAGATAGGCGCCCCGTGTCCGGTGACCTCATGTACT  5880
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Qy  5821 CGAACAAGTACAAGATCATATCGATGACATATCGATGATAGAGATAGGCGCCCCGTGTCCGGTGACCTCATGTACT  5880

Db  5881 GCGTCGACATCCTGACGCCCTTACGACGCCCTTACGAGGGCAATCCGATAG  5940
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Qy  5881 GCGTCGACATCCTGACGCCCTTACGACGCCCTTACGAGGGCAATCCGATAG  5940

Db  5941 AGGAGACGGGTGAGATTGGTGAGATAGGCGGCCCGGCCCGGGTACGAGCCCG  6000
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Qy  5941 AGGAGACGGGTGAGATTGGTGAGATAGGCGGCCCGGCCCGGGTACGAGCCCG  6000

Db  6001 TCTCATCAACGCGTGTGGGCGTCAGCGTGAGGAGTACTGCGCCCGCTAATCCAGCCACGCCT  6060
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Qy  6001 TCTCATCAACGCGTGTGGGCGTCAGCGTGAGGAGTACTGCGCCCGCTAATCCAGCCACGCCT  6060

Db  6061 GGCGAAAGCACAAGGCGCGCGGCCAGGGAGGTGGCTGCAGCGCGCGCGGATCATG  6120
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Qy  6061 GGCGAAAGCACAAGGCGCGCGGCCAGGGAGGTGGCTGCAGCGCGCGCGGATCATG  6120

Db  6121 GCGATGGCGGTGATCCGGATCCGGCGCGGCCCGGGACCAACGGACGGCGATG  6180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  6121 GCGATGGCGGTGATCCGGATCCGGCGCGGCCCGGGACCAACGGACGGCGATG  6180

Db  6181 CGCCCGCTGGTGGAGATGGTAGTGTTAACGGTGTTAACGGTTCTCGACGAAGGAGCTGCCGAGGAGCTGCCGATGCCGATG  6240
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Qy  6181 CGCCCGCTGGTGGAGATGGTAGTGTTAACGGTGTTAACGGTTCTCGACGAAGGAGCTGCCGAGGAGCTGCCGATGCCGATG  6240

Db  6241 AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCGCGCGCAGCAGCGCCAGCAGCAG  6300
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Qy  6241 AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCGCGCGCAGCAGCGCCAGCAGCAG  6300

Db  6301 CGGCGGCGGCGGCGGCGGCGGCCACGACGACGGGCCGGAGCGGCCGGTAGCGCCGGACAGA  6360
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Qy  6301 CGGCGGCGGCGGCGGCGGCGGCCACGACGACGGGCCGGAGCGGCCGGTAGCGCCGGACAGA  6360

Db  6361 CCGGCCGTTCGTGGAGACGGCACGACGGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC  6420
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Qy  6361 CCGGCCGTTCGTGGAGACGGCACGACGGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC  6420

Db  6421 ACTGCGATCGCCCAGCATCGCCCACGTCGCCGCAGCGGATGTCTGAGCCACGCCTCGGCCCCC  6480
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Qy   6421 ACTCGGCGATCCCGAGCGACATCACGTCGCGCACGGCGATGTCTGAGCGAGGCCTCGCCCCC 6480

Db   6481 CCCTCCAAGATGCACGCGAGTGATTAGCTCTAGA 6513
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RESULT      3
LOCUS       I25433        6513 bp    DNA                      PAT      03-SEP-1996
DEFINITION  Sequence 7 from patent US 5550049.
ACCESSION   I25433
NID         g1605303
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.

REFERENCE   1  (bases 1 to 6513)
AUTHORS     Van Der Ploeg,L.H.T. and Warmke,J.W.
TITLE       Process for identifying para cation channel modulators
JOURNAL     Patent: US 5550049-A 7 27-AUG-1996;
FEATURES             Location/Qualifiers
     source          1..6513
                     /organism="unknown"
BASE COUNT     1681 a   1548 c   1702 g   1582 t
ORIGIN

Query Match        100.0%;   Score 6513;   DB 18;   Length 6513;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 6513;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db      1 TCTAGACGTTGGCCGCATAGACAATGACAGAGATTCCGACTCGATATCTGAGGAAGAAC 60
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Qy      1 TCTAGACGTTGGCCGCATAGACAATGACAGAGATTCCGACTCGATATCTGAGGAAGAAC 60

Db     61 GCAGTTGTTCCGTCCCTTTACCCGCCGGAATCATTGGTCGAACAACGCATTGCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 GCAGTTGTTCCGTCCCTTTACCCGCCGGAATCATTGGTCGAACAACGCATTGCCG 120

Db    121 CTGAACATGAAAAGCAGAGAGAGCTGGAAAGAAAGAGAGCCGAGGAGAGTGCCGCGAT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 CTGAACATGAAAAGCAGAGAGAGCTGGAAAGAAAGAGAGCCGAGGAGAGTGCCGCGAT 180

Db    181 ATGGTCGCAAGAAAAACAAAAGAAAATCCGATATGATGACGAGGACGAGGATGAAGGTC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 ATGGTCGCAAGAAAAACAAAAGAAAATCCGATATGATGACGAGGACGAGGATGAAGGTC 240

Db    241 CACAACCGGATCCTCACTTGAACACTGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 CACAACCGGATCCTCACTTGAACACTGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT 300

Db    301 TCCCCGCCGGAATTGGCCTCCACTCGTGTGGCCATTTACATTTCGCTTTTCTGCATTACAATTACACATTTGAT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 TCCCCGCCGGAATTGGCCTCCACTCGTGTGGCCATTTACATTTCGCTTTTCTGCATTACAATTACACATTTGAT 360

Db    361 TGACATTCGTAGTTGTAAGCAAAGAAAAGATATATTTTCGCTTTTCTGCATCAGCAATGTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361 TGACATTCGTAGTTGTAAGCAAAGAAAAGATATATTTTCGCTTTTCTGCATCAGCAATGTAC 420

Db    421 TGTGGATGCTCGATCCATTCATTCATTCATCATCATCTCGTCGTGTGGCCATTTACATTTACACATTTGATAATGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    421 TGTGGATGCTCGATCCATTCATTCATTCATCATCATCTCGTCGTGTGGCCATTTACACATTTGATAATGC 480

Db    481 CATTATTTTCCCTATTCATCATCATCCTACCACCACAAATTCTCGTCAACTGCATCGATGATAATGC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    481 CATTATTTTCCCTATTCATCATCATCCTACCACCACAAATTCTCGTCAACTGCATCGATGATAATGC 540

Db    541 CGACAACGCCCCACGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACACATTTGAAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    541 CGACAACGCCCCACGTTGAGTCCACTGAGGTGATATTCACCGGAATCTACACACATTTGAAT 600

Db    601 CAGCTGTTAAAGTGATGATGGCACGAGGTTTCATTTTTATGCCCGTTTACGTATCTTAGAGATG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601 CAGCTGTTAAAGTGATGATGGCACGAGGTTTCATTTTTATGCCCGTTTACGTATCTTAGAGATG 660

Db    661 CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    661 CATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 720

Db    721 TAGGTAATCTAGCAGCCGTTAGGGTGCTGCGAGCGTTAAAACCGTAGCCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721 TAGGTAATCTAGCAGCCGTTAGGGTGCTGCGAGCGTTAAAACCGTAGCCA 780

Db    781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGGTGAGAATCTGCCG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781 TTGTGCCAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGGTGAGAATCTGCCG 840

Db    841 ATGTGATTATCCTGACCATGTTCTCCCGTGTTCGCGTTGTCGGTTGATGGCCTACAGATCT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841 ATGTGATTATCCTGACCATGTTCTCCCGTGTTCGCGTTGTCGGTTGATGGCCTACAGATCT 900

Db    901 ATATGGGCGTGCTCACCGAGAGTGCATCAAGAAGTTCCCGCTGACGGTTCCTCGGGGCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901 ATATGGGCGTGCTCACCGAGAGTGCATCAAGAAGTTCCCGCTGACGGTTCCTCGGGGCA 960

Db    961 ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATATCACAATAGCTCCAATTGGTATTCCGAGG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961 ATCTGACCGACGAGAACTGGGACTATCACAATCGCAATATCACAATAGCTCCAATTGGTATTCCGAGG 1020

Db   1021 ACGAGGGCATCTCATTTCCGTTATGCGGCAATATATCCGGTGCGGGGCAATGCGACGACG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021 ACGAGGGCATCTCATTTCCGTTATGCGGCAATATATCCGGTGCGGGGCAATGCGACGACG 1080

Db   1081 ATTACGTGCCTCGCAGGGGTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081 ATTACGTGCCTCGCAGGGGTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT 1140

Db   1141 CGTTCCGATGGGCTTTCCTGTCCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGGATC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 CGTTCCGATGGGCTTTCCTGTCCGCCCTTCCGGCTGATGACACAGGACTTCTGGGAGGATC 1200

Db   1201 TGTACCAGCTGGTGTTGCGCGGCCGGACCATGCGACACATGCGCACATGCGCACAGTGTCTTATAGTCATCA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201 TGTACCAGCTGGTGTTGCGCGGCCGGACCATGCGACACATGCGCACAGTGTCTTATAGTCATCA 1260

Db   1261 TCTTCCTAGGTTCATTCTATCTTGTGAATTTGATTTTGCCATTGTGCCATGTCGTATG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261 TCTTCCTAGGTTCATTCTATCTTGTGAATTTGATTTTGCCATTGTGCCATGTCGTATG 1320

Db   1321 ACGAATTGCAAAGGAAGCCGCGCCGCCCAAAGCGGCCAATGCGCAGGCGATACGTGAAG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321 ACGAATTGCAAAGGAAGCCGCGCCGCCCAAAGCGGCCAATGCGCAGGCGATACGTGAAG 1380

Db   1381 CGGAAGAAGCTGCGCCGCCCAAAGCGGCCGAAGAGGAGGCGGCCAATGCGCAGGCTC 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381 CGGAAGAAGCTGCGCCGCCCAAAGCGGCCGAAGAGGAGGCGGCCAATGCGCAGGCTC 1440

Db   1441 AGGCAGCAGCGGATGCGGCGGCCGCCGCCCAAGAGAGGCGCACTGCACTATTGTTGGCGGCAACGATG 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441 AGGCAGCAGCGGATGCGGCGGCCGCCGCCCAAGAGAGGCGCACTATTGTTGGCGGCAACGATG 1500

Db   1501 GTCCGACGTATTCTTGCATCAGCGATATGAGCTATTCGGAGGCGTCGGAGTGGAGCG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501 GTCCGACGTATTCTTGCATCAGCGATATGAGCTATTCGGAGGCGTCGGAGTGGAGCG 1560

Db   1561 ACAACAACAAAGAAGAAGATGTCCATTCCGTCAACTGCATCTGATGATAATGC 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1561 ACAACAACAAAGAAGAAGATGTCCATTCCGTCAACTGCATCTGATGATAATGC 1620

Db   1621 TTATACAAAGACAACAACAGCAGCACTACCAAGTACGGGGATCACAATTGAAT 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1621 TTATACAAAGACAACAACAGCAGCACTACCAAGTACGGGGATCACAATTGAAT 1680

Db   1681 GCACGACATCCTTATCCTGTTCACCGGTTCACCGGGATCACGGGGATCACGTAGTT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1681 GCACGACATCCTTATCCTGTTCACCGGTTCACCGGGATCACGTAGTT 1740
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Db  1741 CTCACAAGTACACGATACGGAACGGACGTGGCCGCTTGGTATACCCGGTAGCGATCGTA 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741 CTCACAAGTACACGATACGGAACGGACGTGGCCGCTTGGTATACCCGGTAGCGATCGTA 1800

Db  1801 AGCCATTGGTATTGTCAACATATCAGGATGCCCAGCAGCACTTGCCCATGCCGACGACT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801 AGCCATTGGTATTGTCAACATATCAGGATGCCCAGCAGCACTTGCCCATGCCGACGACT 1860

Db  1861 CGAATGCCGTCACCCGATGTCCGAAGAGAATGGGCCATCATAGTGCCCGTGTACTATG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861 CGAATGCCGTCACCCGATGTCCGAAGAGAATGGGCCATCATAGTGCCCGTGTACTATG 1920

Db  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT 1980

Db  1981 CACATGGCCGATCTACTCGGCGGCATGGCCCGTCAATCAATCCGCCACCA 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 CACATGGGCCGATCTACTCGGCGGCATGGGCCGTCAATCAATGGCCGGCACCA 2040

Db  2041 GCAAATTGCGCAACCGCAACACACGCCAACAATCAATCAGTGGCGCCCACCA 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041 GCAAATTGCGCAACCGCAACACACGCCAACAATCAATCAGTGGCGCCCACCA 2100

Db  2101 CCTGTCTGACACACCAATCACAAGCTCGATCATCGCGACTACGGAAATTGGCCTGAGTGCA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2101 CCTGTCTGGACACACCAATCACAAGCTCGATCATCGCGACTACGGAAATTGGCCTGGAGTGCA 2160

Db  2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC 2220

Db  2221 AAACGGTGGTTGATATGAAAGATGTGATGTCCTGAATGCATCATCGAACAGGCCGCTG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 AAACGGTGGTTGATAATGAAAGATGTGATGTCCTGAATGCATCATCGAACAGGCCGCTG 2280

Db  2281 GTCGGCACAGTCGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGGAGGACG 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281 GTCGGCACAGTCGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGGAGGACG 2340

Db  2341 ATGACGAGGATGGGCCGACGTTCAAAGACAAGGCACTCGAAGTCGATCCTCAAAGGCATCG 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341 ATGACGAGGATGGGCCGACGTTCAAAGACAAGGCACTCGAAGTCGATCCTCAAAGGCATCG 2400

Db  2401 ATGTGTTTTGTGTGGGACTGTGTTGGGTTGTTCAGGAGTGGTATCGC 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401 ATGTGTTTTGTGTGGGACTGTGTTGGGTTGTTCAGGAGTGGTATCGC 2460

Db  2461 TCATCGTCTTCGATCCCTTCGTCGCAGCTCTTCATCACGCGTGTGGCATTGTGGTCAACACGA 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461 TCATCGTCTTCGATCCCTTCGTCGCAGCTCTTCATCACGCGTGTGGCATTGTGGTCAACACGA 2520

Db  2521 TGTTCATGGCAATGCAATGGAACGCGTGCTGTCCAAGAGTG 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521 TGTTCATGGCAATGCAATGGAACGCGTGCTGTCCAAGAGTG 2580

Db  2581 GCAACTATTCTTCACCGCCACCTTGCCCATGAGCGTAATGGCCATGA 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581 GCAACTATTCTTCACCGCCACCTTGCCCATGAGCGTAATGGCCATGA 2640

Db  2641 GCCCCAAGTACTATTTCGCAGGAGGGCTGAAACATCTTCGACTTCATTATCGTGGCCCTAT 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2641 GCCCCAAGTACTATTTCGCAGGAGGGCTGAAACATCTTCGACTTCATTATCGTGGCCCTAT 2700

Db  2701 CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTGTCCGGTTGCCTTTCGTTCCTTTTCGAT 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701 CGCTATTGGAACTGGGACTCGAGGGTGTCCAGGGTGTCCGGTTGCCTTTCGTTCCTTTTCGAT 2760

Db  2761 TGCTCGTGTATTCAAACTGCCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTA 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2761 TGCTCGTGTATTCAAACTGGCGTATTCAAACTGGCCCACACTTAATTTACTCATTTCGATTA 2820

Db  2821 TGGGACGCACCATGGCCGCTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA 2880
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Db  2821 TGGGACGCACCATGGGCGCTTTGGGTAATCTGACATTTGCATTATCATCTTCA 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821 TGGGACGCACCATGGGCGCTTTGGGTAATCTGACATTTGCATTATCATCTTCA 2880

Db  2881 TCTTTGCGGTGATGGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCT 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881 TCTTTGCGGTGATGGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCT 2940

Db  2941 TTCCGGATGGCGACCTGCCGCGCTGGAACTTCACCGACTTTATGCAGCTTCATGATCG 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941 TTCCGGATGGCGACCTGCCGCGCTGGAACTTCACCGACTTTATGCAGCTTCATGATCG 3000

Db  3001 TGTTCCGGGTGCTCTGCGGAGAATGGATCAGTCCATGTGGACTGCATGTGACTGTGGGCG 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001 TGTTCCGGGTGCTCTGCGGAGAATGGATCAGTCCATGTGGACTGCATGTGACTGTGGGCG 3060

Db  3061 ATGTCGTGCATCCCTTCTTCCTTCTTCCTTCTGGTAATCTGGCAATCTTGTGGTACTTA 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061 ATGTCGTGCATCCCTTCTTCCTTCTTCCTTCTGGTCATCGGCAATCTTGTGGTACTTA 3120

Db  3121 ACCTTTCTTAGCCTTGTCTTTTGTCTTCCCAATTTGGCTCTATCGCTATCAGCCGCCGACTG 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121 ACCTTTCTTAGCCTTGTCTTTTGTCTTCCCAATTTGGCTCTATCGCTATCAGCCGCCGACTG 3180

Db  3181 CCGATAACGATACGGAATAAAATAGCCGAGGCCTTCAATCGAATTGCCGATTTAAAAGTT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181 CCGATAACGATACGGAATAAAATAGCCGAGGCCTTCAATCGAATTGCCGATTTAAAAGTT 3240

Db  3241 GGGTTAAGCGTAATATTGCTGATTGTTCAAGTTAATACGTAATACGTAACAAATCAAA 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241 GGGTTAAGCGTAATATTGCTGATTGTTCAAGTTAATACGTAATACGTAACAAATCAAA 3300

Db  3301 TAAGTGATCAACCATCAGTGAGACCAACCAGCAGTCAGTTGGATTTGGAGCGGAAGAGC 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301 TAAGTGATCAACCATCAGTGAGACCAACCAGCAGTCAGTTGGATTTGGAGCGGAAGAGC 3360

Db  3361 ATGGTGACAACGAACTGGAGCTGGGCCACGCGAGACTCCTGCGCCGACGAGTCCTCATCAAGA 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361 ATGGTGACAACGAACTGGAGCTGGGCCACGCGAGACTCCTGCGCCGACGAGTCCTCATCAAGA 3420

Db  3421 AGGGGATCAAGGAGGAGCGACGACGCAACTGGAGGTGGCCATCGGGGATCGGATGAATTCACGA 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421 AGGGGATCAAGGAGGAGCGACGACGCAACTGGAGGTGGCCATCGGGGATCGGATGAATTCACGA 3480

Db  3481 TACACGGCGACATGGAAGTGAGAGAACAACAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481 TACACGGCGACATGGAAGTGAGAGAACAACAGCCGAAGAAATCCAAATATCTAAATAACGCAACGA 3540

Db  3541 TGATTGGCAACTCAATTAACCACCAAGAGAACAATAGACTGGAACACCAAGAGCTAAACCATAGAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3541 TGATTGGCAACTCAATTAACCACCAAGAGAACAATAGACTGGAACACCAAGAGCTAAACCATAGAG 3600

Db  3601 GTTTGTTCCTTACAGGACGACGACGCCCAGCATTAACTCATTATTCACACGACGACGAGGAATC 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601 GTTTGTTCCTTACAGGACGACGACGCCCAGCATTAACTCATTATTCACACGACGACGAGGAATC 3660

Db  3661 GACCATTCAAGGACCAGCAGCCCGAGAGGGCGGATGGGAAGCGAGGAGGCGGAAGAGC 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3661 GACCATTCAAGGACCAGCAGCCCGAGAGGGCGGATGGGAAGCGAGGAGGCGGAAGAGC 3720

Db  3721 GCGACGCCAGCAAGGACGGATTTAGGTCTCGACGAGGACGTGGACTGGAGCGGCGAATGCG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3721 GCGACGCCAGCAAGGACGGATTTAGGTCTCGACGAGGAACTGGACTGGAGCGGCGAATGCG 3780

Db  3781 AGGAGGGCCGCTCAACGCGTGATATCATTATTCATTGCACACGACGACGGAATACTCGATG 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3781 AGGAGGGCCCCGCTCACGGTGTATATCATTATTCATTATCGACACGAGGATATACTCGATG 3840

Db  3841 AATATCCAGCTGACGACGAGGAGGATTTCGTGCTACTATAAGAAATTCCGATCTTAGCGGTG 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3841 AATATCCAGCTGACGACGAGGAGGATTTCGTGCTACTATAAGAAATTCCGATCTTAGCGGTG 3900

Db  3901 ACGATGACTCGCCGTTCTGCGGACGATGGGCAAGTTACGACTGAAAACTTTCAATTAA 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3901 ACGATGACTCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAACTTTCAATTAA 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TTGAAAATAAATATTTGAAACAGTCGTTATCCACTACTGATTTAATGAGTAGCTTAGCTT 4020

Qy   3961 TTGAAAATAAATATTTGAAACAGTCGTTATCCACTACTGATTTAATGAGTAGCTTAGCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCGAGGATATTTATACTATA 4080

Qy   4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCGAGGATATTTATACTATA 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140

Qy   4081 TGGACAGAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        GCTTCAAAGTGTACTTCACCAACGCGTCGTGTTGGCTCGATTTCGATTTCGATTGTCATGGTAT 4200

Qy   4141 GCTTCAAAGTGTACTTCACCAACGCGTCGTGTTGGCTCGATTTCGATTGTCATGGTAT 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTGTATTCAAGCCTTCAAGACTA 4260

Qy   4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTGTATTCAAGCCTTCAAGACTA 4260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TGGGAACGTTAAGAGCACTGAGACCTACGTGCCATGTCCCGTATGCAGGGCATGAGGG 4320

Qy   4261 TGGGAACGTTAAGAGCACTGAGACCTACGTGCCATGTCCCGTATGCAGGGCATGAGGG 4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TCGTCGTTAATGCGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380

Qy   4321 TCGTCGTTAATGCGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTC 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TAATATTTTGGCTAATTTTTGCCATAATGGTGTACAGCTTTTTCTGGAAAATATTTTA 4440

Qy   4381 TAATATTTTGGCTAATTTTTGCCATAATGGTGTACAGCTTTTTCTGGAAAATATTTTA 4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        AGTGCGGAGGACATGAGAATGGCACGAGAGCTCAGCCACCACCAGATCATACCAAATCGCAATGCCT 4500

Qy   4441 AGTGCGGAGGACATGAGAATGGCACGAGAGCTCAGCCACCACCAGATCATACCAAATCGCAATGCCT 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTATATGTACATTGCTG 4560

Qy   4501 CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTATATGTACATTGCTG 4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        TCATTCTCGAGAACTATAGTCAGGCAGTCGGTCTCAACGATG 4620

Qy   4561 TCATTCTCGAGAACTATAGTCAGGCAGTCGGTCTCAACGATG 4620
          ||||||||||||||||||||||||||||||||||||||||||
Db        ACTACGACATGTACTATGAGATCGATCGAATTCGAACGATG 4680

Qy   4621 ACTACGACATGTACTATGAGATCGATCGAATTCGAACGATG 4680
          |||||||||||||||||||||||||||||||||||||||||
Db        GCTATGATCAGCTGTCGCGAATTCCTGGACGTGAGATACG 4740

Qy   4681 GCTATGATCAGCTGTCGCGAATTCCTGGACGTGAGATACG 4740
          ||||||||||||||||||||||||||||||||||||||||
Db        CGAACAAGTACAAGATCATATCGATGGACATATCGATACAC 4800

Qy   4741 CGAACAAGTACAAGATCATATCGATGGACATATCGATACAC 4800
          |||||||||||||||||||||||||||||||||||||||||
Db        GCGTCGCACATCCTCACGCGCCCGGCAAGGGCTACGAGCCCC 4860

Qy   4801 GCGTCGCACATCCTCACGCGCCCGGCAAGGGCTACGAGCCCC 4860
          ||||||||||||||||||||||||||||||||||||||||||
Db        AGGAGACGGGTGAGATTGGTGCGTCAGCGTGAGATAGCGG 4920

Qy   4861 AGGAGACGGGTGAGATTGGTGCGTCAGCGTGAGATAGCGG 4920
          ||||||||||||||||||||||||||||||||||||||||
Db        TCTCATCAACGCGTCGTGTGCGCGAGGAGGTGGTCCTTTGAGCCGATACGGATCATG 4980

Qy   4921 TCTCATCAACGCGTCGTGTGCGCGAGGAGGTGGTCCTTTGAGCCGATACGGATCATG 4980
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Db        TCGATCGTTACGATCGCGGTCCGGACACGTATAACGCGGTATAACGCGCTAGAGACTATCTCAAGTCGATAT 5040

Qy   4981 TCGATCGTTACGATCGCGGTCCGGACACGTATAACGCGGTATAACGCGCTAGAGACTATCTCAAGTCGATAT 5040
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Db   5041 TCGTAGTTATTTCAGTTCCGAATGTCTCATTAAAAATATTCGCTTTACGACTACACTAA 5100
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Qy   5041 TCGTAGTTATTTCAGTTCCGAATGTCTCATTAAAAATATTCGCTTTACGACTACACTAA 5100

Db   5101 TTATTGAGCCATGGAATTATTTGATGTAGTAGTGTCATTTGTCATTTATCCATCTTAGGTCTTG 5160
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Qy   5101 TTATTGAGCCATGGAATTATTTGATGTAGTAGTGTCATTTGTCATTTATCCATCTTAGGTCTTG 5160

Db   5161 TACTTAGCGATATTATCGAGAAGTACTTCGTCGTCGCGACCCTGCCTCCGAGTGTGTGCGTG 5220
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Qy   5161 TACTTAGCGATATTATCGAGAAGTACTTCGTCGTCGCGACCCTGCCTCCGAGTGTGTGCGTG 5220

Db   5221 TGGCGAAAGTGGGCCCGTGTCCTTCGACTGGTGTGAAGGGAGCCAAGGCAATCGGACACTGC 5280
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Qy   5221 TGGCGAAAGTGGGCCCGTGTCCTTCGACTGGTGTGAAGGGAGCCAAGGCAATCGGACACTGC 5280

Db   5281 TCTTCGCGTTGGCCATGTCGCGCCGCGCCCGCGCCCGTGTTCAACATCTGCCTCGTCGTTCCTGG 5340
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Qy   5281 TCTTCGCGTTGGCCATGTCGCGCCGCGCCCGCGCCCGTGTTCAACATCTGCCTCGTCGTTCCTGG 5340

Db   5341 TCATGTTCATCTTGCCATTTTCGGCACTTCAAGACCTTTGGGCAGCATGGATCAGGAGACGCG 5400
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Qy   5341 TCATGTTCATCTTGCCATTTTCGGCACTTCAAGACCTTTGGGCAGCATGGATCAGGAGACGCG 5400

Db   5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGGGGTCTGTAGGCCATTATCAATGAGAAGCATGCG 5460
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Qy   5401 GCATTAACGACGTCTACAACTTCAAGACCTTTGGGGTCTGTAGGCCATTATCAATGAGAAGCATGCG 5460

Db   5461 TGTCGACGTCAGCGCGGTTGGGGATGGTGTACTGGACGGCCATTATCAATGAGAGCATGCG 5520
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Db   5521 ATCCACCCGACAGCGACAAAGGCTATCCGGTTCAGGTGGTTCAGCGACCGGTTGGAATAA 5580
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Db   5581 CGTTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTATATGTACATTGCTG 5640
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Db   5701 ACTACGACATGTACTATGAGATCGATCGAATTCGATCGGCAGCAATTCGATCGATCTACTATAC 5760
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Db   5761 GCTATGATCAGCTGTCGCGAATTCCTGGAGCCCGCGCGGATACGGCTCACAAAC 5820
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Db   5881 GCGTCGCACATCCTCACGCGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAG 5940
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Qy   5881 GCGTCGCACATCCTCACGCGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAG 5940

Db   5941 AGGAGACGGGTGAGATTGGTGCGTCAGCGTGAGATAGCGGTAATCAGTAGTAACCG 6000
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Qy   6001 TCTCATCAACGCGTCGTGTGCGCGAGGAGGTGGTCCTTTGAGCCGTAATCCAGCACGCCT 6060

Db   6061 GGCGAAAGCACAAGGCGCCGCGGCGCGAGGAGGCGGTGGTCCTTTGAGCCGGATACGGATCATG 6120
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Qy   6061 GGCGAAAGCACAAGGCGCCGCGGCGCGAGGAGGCGGTGGTCCTTTGAGCCGGATACGGATCATG 6120
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Db   6121 GCGATGGGCGGTGATCCGGATGCCGGGGACCCGGCGCGCCCGATGAAGCAACGGACGGCGATG 6180
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Db   6241 AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCGGCCGCGGCAGCAGCAGCAGCAG 6300
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Db   6301 CGGCGGCCGCGGGCGACGACGACGACGCGGGAAGTCCCGGAGCCGGTAGCGCCGGGCGACAGA 6360
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Db   6361 CCGCCGGTTCTCGTGGAGAGCGACGCGGTTCGTGACGAAGAACGGCCACAAGGTCGTCATCC 6420
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Db   6421 ACTCGGATCGCCCAGCATCACGTCGCGCACGCGCGATCGTCTGAGCCAGGCCCTCGCCCCC 6480
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RESULT   4
LOCUS      DROSODCHA      6883 bp      mRNA             INV       28-SEP-1993
DEFINITION Drosophila melanogaster para locus, sodium channel alpha subunit
           mRNA, complete cds.
ACCESSION  M32078 M24285 M32079 M32080
NID        g403441
KEYWORDS   alternative splicing; opa repetitive sequence; sodium channel alpha
           subunit.
SOURCE     D.melanogaster (strain para-hd2), cDNA to mRNA, clone ZS10.3.
  ORGANISM Drosophila melanogaster
           Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;
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           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1  (bases 1 to 6883)
  AUTHORS  Loughney,K., Kreber,R. and Ganetzky,B.
  TITLE    Molecular analysis of the para locus, a sodium channel gene in
           Drosophila
  JOURNAL  Cell 58, 1143-1154 (1989)
  MEDLINE  89376565
REFERENCE  2  (sites)
  AUTHORS  Ramaswami,M. and Tanouye,M.A.
  TITLE    Two sodium channel genes in Drosophila: Implications for channel
           diversity
  JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 86, 2079-2082 (1989)
  MEDLINE  89184571
REFERENCE  3  (sites)
  AUTHORS  Thackeray,J.R. and Ganetzky,B.
  TITLE    Developmentally regulated alternative splicing generates a complex
           array of Drosophila para sodium channel isoforms
  JOURNAL  Unpublished (1993)
COMMENT    Draft entry and computer-readable sequence for [Proc. Natl. Acad.
           Sci. U.S.A. 58, 1143-1154 (1989)] kindly submitted by B.Ganetzky,
           25-APR-1989.
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Note: remainder of annotations omitted.

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Query Match         92.0%;  Score 5992;  DB 15;  Length 6883;
Best Local Similarity 97.8%;  Pred. No. 0.00e+00;
Matches 6359;  Conservative  0;  Mismatches 97;  Indels 45;  Gaps 28;
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Db   255 CGTTGGCCGCATAGACAATGACAGAAGAATTCCGACTCGATATCTGAGGAAGAACGCAGTT 314
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Qy     7 CGTTGGCCGCATAGACAATGACAGAAGAATTCCGACTCGATATCTGAGGAAGAACGCAGTT 66

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Qy   127 ATGAAAAGCAGAAGGAGCTGGAAAGAAAGAGAAATCCGAGGAGGAGGAGGTCGCCGATATGGTC 186

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Qy   667 ATTGGCTGGACTTCGTAGTAATAGCTTAGCTTATGTATGTGACCATGGTATAGATTTAGGTA 726

Db   975 ATCTAGCAGCCCTGCCGAACGTTAGGGTGCTGCGAGCGCTTAAAACCGTAGCCATTGTGC 1034
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Db  1035 CAGGCTTGAAGACCATCGTCGGCGCCGTCATCGAATCGGTGAAGAATCTGCGCGATGTGA 1094
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Db  4830 ATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTGATTTATATT 4889

Qy  4627 ATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATTTATATT 4686
         ||||||||||||||||||||||||||||||||||||||||||||||||||    |||||
Db  4890 TCGTATTCTTCATCATATTTGGATCATTTTCACACTCAATCTGTTCATTGGTGTTATCA 4949

Qy  4687 TCGTATTCTTCATCATATTTGGATCATTTTCACACTCAATCCTTCATTGGTGTTATCA 4746
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Qy  4747 TTGATAATTTTAATGAGCAAAAGAAAAAAGCAGGTGGATACAAAATCATGAACAGCAGGTG 4806
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Db  5010 AAGATCAGAAAAGTACTATAGTGCTATGAAAAGATGGGCTCTAAAAAACCATTAAAAG 5069

Qy  4807 AAGATCAGAAAAGTACTATAGTGCTATGAAAAGATGGGCTCTAAAAAACCATTAAAAG 4866
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Db  5070 CCATTCCAAGACCAAGGTGGCGACCACAAGAGCAATAGTCTTTGAAATAGTAACCGATAAGA 5129

Qy  4867 CCATTCCAAGACCAAGGTGGCGACCACAAGAGCAATAGTCTTTGAAATAGTAACCGATAAGA 4926
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Db  5130 AATTCGATATAATCATTCATTATGTGTCTGCTGAACAGTGTCACCATGCGGATCGTCGATC 5189

Qy  4927 AATTCGATATAATCATTCATTATGTGTCTGCTGAACAGTGTCACCATGCGGATCGATC 4986
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Db  5190 GTTACGATGCGTCCGACACGTAGCGTTCAATTATCTCGAATTCTCCAGACTAGTCGTAG 5249

Qy  4987 GTTACGATGCGTCCGACACGTAGCGTTCAATTATCTCGATTCTCCAGACTAGATCGTAG 5046
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Db  5250 TTAATTGAATTCGATATAATGAGTAGTGATTTTATTCGATGTTCGTCAATAATACTATTTATTG 5309

Qy  5047 TTAATTTCGATATAATGAGTAGTGATTTTAATATTCGATGTTCGTCAATAATACTATTTATTG 5106
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Db  5310 AGCCATGGAATTAATTGATGTAGTAGTTGTCGCCGGACCCTCCGAGTGGTGCGTGGTGGCGA 5359

Qy  5107 AGCCATGGAATTAATTGATGTAGTAGTTGTCATCTTAGGCTTGTCATTTTATCCATCTTAGGCTTGTACTTA 5166
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Qy  5167 GCGATTATTCGAGAAGTAATCAAGTGGTTGGCGCTCGGCTTCA 5226
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Qy  6307 CGGCGGGCACGACGACGCGGGAGTCCCGGACGCGGGTAGCGCCGGGCGGGGCAGCAGACCGCCG 6366

Db  6570 TTCTCCTGGAGACGCACGGTTCGTGACGAAGAACGACCCACAAGGTGGTCATCCACTCGC 6629
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Qy  6367 TTCTCCTGGAGACGCACGGTTCGTGACGAAGAACGACCCACAAGGTGGTCATCCACTCGC 6426

Db  6630 GATCGCCGAGCATCACGTCGCGCACGCCGGATGTCTGAGCCAGGCCTCGAGCCAGGCCATTA 6689
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Qy  6427 GATCGCCGAGCATCACGTCGCGCACGCCGGATGTCTGAGCCAGGCCTCGAGCCAGGCCATTA 6486

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Qy  6487 AAGATGCACGCGAGTATTAGC 6507
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RESULT      5
LOCUS       MDU38813      6318 bp     mRNA            INV       19-FEB-1997
DEFINITION  Musca domestica insecticide-susceptible strain voltage-sensitive
            sodium channel mRNA, complete cds.
ACCESSION   U38813
NID         g1783372
KEYWORDS    .
SOURCE      house fly.
  ORGANISM  Musca domestica
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
            Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
            Muscomorpha; Muscoidea; Muscidae; Musca.
REFERENCE   1  (bases 1 to 6318)
  AUTHORS   Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.
  TITLE     Tight genetic linkage between the kdr insecticide resistance trait
            and a voltage-sensitive sodium channel gene in the house fly
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)
  MEDLINE   94195766
REFERENCE   2  (bases 1 to 6318)
  AUTHORS   Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
  TITLE     Characterization of voltage-sensitive sodium channel gene coding
            sequences from insecticide-susceptible and knockdown-resistant
            house fly strains
  JOURNAL   Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)
  MEDLINE   96245434
REFERENCE   3  (bases 1 to 6318)
  AUTHORS   Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York
            State Agricultural Experiment Station, Cornell University, Castle
            Street, Geneva, NY 14456, USA
REFERENCE   4  (bases 1 to 6318)
  AUTHORS   Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York
            State Agricultural Experiment Station, Cornell University, Castle
            Street, Geneva, NY 14456, USA
REMARK      Nucleotide and protein update by submitter
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                     /chromosome="3"
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                     TFVVISKGDIFRFSASKAMWLLDPFNPIRRVAYIYLVHPLFSLFIITTILTNCILMI
                     MPTTPTVESTEVIFTGIYTFESAVKVMARGFIICPFTYLRDAWNWLDFVVIALAYVTM
                     GIDLGNLAALRTFRVLRALKTVAIVPGLKTIVGAVIESVKNLRDVIILTMFSLSVFAL
                     MGLQIYMGVLTQKCIKRFPLDGSWGNLTDENWFLHNSNSSNWFTENDGESYPVCGNVS
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Db  5430 AAGTGGGCCGTGTCCTTCGACTGGTGAAGGGCATTCGGACACTGCTCTTCG 5489
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Qy  5227 AAGTGGGCCGTGTCCTTCGACTGGTGAAGGGCATTCGGACACTGCTCTTCG 5286

Db  5490 CGTTGGCCATGTCCTGCGGCCCTGTCAACATCTGCCTGTTCCTGGTCATGT 5549
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Qy  5287 CGTTGGCCATGTCCTGCGGCCCTGTCAACATCTGCCTGTTCCTGGTCATGT 5346

Db  5550 TCATCTTTGCCATTTCGGCATGTCGTCTTCATGCACGTGAAGGAGAGCGGCATTA 5609
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Db  5610 ACCAGCGTCTACAACTTCAAGACCTTTGCCAGAGCCATGATCCGCTCTTCAGATGTCGA 5669
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Qy  5407 ACGACGTCTACAACTTCAAGACCTTTGCCCAGAGCCATGATGATCCTGCTCTTTCAGATGTCGA 5466

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Qy  5467 CGTCAGCCGGTTGGGATGGTGTACTGGACGCGCCATTATCAATGAGGAAGCATGCGGATCCAC 5526

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Db  5790 TCCCTCATACCTAGTTATAAGCTTTTTTGATAGTTATTAATATGTACATTGCTGTCATTC 5849
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Qy  5587 TCCCTCATACCTAGTTATAAGCTTTTTTGATAGTTATTAATATGTACATTGCTGTCATTC 5646

Db  5850 TCGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACTACG 5909
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Qy  5647 TCGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACTACG 5706

Db  5910 ACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCCACCCAGTACATACGCTATG 5969
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Qy  5707 ACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCCACCCAGTACATACGCTATG 5766

Db  5970 ATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCCTGCGCAGATCCACAAACCGAACA 6029
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Qy  5767 ATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCCTGCGCAGATCCACAAACCGAACA 5826

Db  6030 AGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACTGCGTCG 6089
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5827 AGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACTGCGTCG 5886

Db  6090 ACATCCTCGACGCGCCTTACGAAAGACTTCTTTGCGCGGCAATCCGATAGAGGAGA 6149
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5887 ACATCCTCGACGCGCCTTACGAAAGACTTCTTTGCGCGGCAATCCGATAGAGGAGA 5946

Db  6150 CGGGTGAGATTGGTGAGATAGCGGCCCCGGATACGGCGGGCCTACGAGCCCGTCTCAT 6209
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Qy  5947 CGGGTGAGATTGGTGAGATAGCGGCCCCGGATACGGCGGGCCTACGAGCCCGTCTCAT 6006

Db  6210 CAACGCTGTGCGTCAGCGTGAGGAGTACTGCGCCGGCTAATCCAGCACGCGCCTGGCGAA 6269
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Qy  6007 CAACGCTGTGCGTCAGCGTGAGGAGTACTGCGCCGGCTAATCCAGCACGCGCCTGGCGAA 6066

Db  6270 AGCACAAGGCCGCGCGGAGGAGTGGGTCCTTGACCCGGATACGGATCATGGCGATG 6329
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Qy  6067 AGCACAAGGCCGCGCGGAGGAGTGGGTCCTTGACCCGGATACGGATCATGGCGATG 6126

Db  6330 GCGGGATCCGGATGCCGGGGGACCCCGGCCCCGGCGACGGCGGATGCGCCCG 6389
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Qy  6127 GCGGGATCCGGATGCCGGGGGACCCCGGCCCCGGCGACGGCGGATGCGCCCG 6186

Db  6390 CTGGTGGAGATGGTAGTGTTAACCGTACTGCAGAAGGAGCTGCCGATGCCGATGAGAGTA 6449
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Qy  6187 CTGGTGGAGATGGTAGTGTTAACCGTACTGCAGAAGGAGCTGCCGATGCCGATGAGAGTA 6246

Db  6450 ATGTAAATAGTCCGGGTGAGGATGCCAGCGGCGCGGCGGCGGCAGCAGCAGGGG 6509
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Qy  6247 ATGTAAATAGTCCGGGTGAGGATGCCAGCGGCGCGGCGGCGGCAGCAGCAGCGCGG 6306
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Db  691  TTTAGGGTACTGCGAGCTCTGAAAACCGTAGCCAATGTGCCAGTGTCTAAAAACCATTGTC  750
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Qy  747  TTTAGGGTGCTGCGAGCCTCTAAAAACCGTAGCCAATGTGCCAGGCTTGAAGACCATCGTC  806

Db  751  GGTGCTGTCATTGAATCGTAAAAAATCTACGCGATGTGATGATAATTTGACAATGTTTCC  810
              || | ||||||  |  ||  ||   |  |||||||||||||||| || | |||
Qy  807  GGCGCCGTCAATCCGGTCAGAATCTGCGGCGATGGCGCGGATGTCGACCATGTTCTCC  866

Db  811  CTGTCGGTGTTCGCGCTGATGGGCTACAAAATCTATATGGTGTTCTAACACAAAAGTGC  870
              || || ||||| || ||||||||| || ||||||| | || || |
Qy  867  CTGTCGGTGTTCCGCGTTGATGGGCCTACAGATCTATATGGGCGTCTCACCCGAGAAGTGC  926

Db  871  ATTAAACGATTCCCCCTGGACGGCAGTTGGGGCAATCTGACCGATGAAAAACTGGTTTCTA  930
              ||     |||   |||  ||| ||  ||  ||||  ||||  ||| || ||
Qy  927  ATCAAGAAGAGTTCCCGCTGCGCACGTTCCCGGGGCAATCTGACCGACGACGAACTGGGACTAT  986

Db  931  CACAATAGCAACAGTTCCAATTGGTTACGGAGAACATGGGCGAGTCATATCCGGTGTGC  990
              |||||  | |||||| |||||||  |||  ||  |||  ||| |||| ||| |
Qy  987  CACAATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGGGGCATCTCATTTCCGTTATGC  1046

Db  991  GGGAATGTATCCGGTGCGGGACAATGCGGCGGAGGATTACGTCTGCCTGCCGGCTTCCGC  1050
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Qy  1047  GGCAATATATCCGGTGCGGGGGCAATGCGACGACGACGATTACGTCTGCCTGCCGCAGGGGTTTGGT  1106

Db  1051  CCCAATCCCAACTACGACTACACCAGTTCGATTCATTCGGTTGGGCTTTCCTGTCGCG  1110
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Qy  1107  CCGAATCCGAATTATGGCTACAACCAGCTCGATTCGTTCGGATGGGCCTTCCTGTCGCCC  1166

Db  1111  TTTCGTCTCATGACCCAAGAATTCTCGGAGGAGTCGTATCACACCTCCTAGGTTCATTCATCTGTG  1170
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Qy  1167  TTCCGGCTGTGATGACACAGGACTTCTCGGAGGAGTCGTACCAGCTGGTTGTTGGCGCCGCC  1226

Db  1171  GGACCCTGCACAGTTGTTCTTTATAGTCATCATCATCCTAGGTTCATTCATCTGTG  1230
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Qy  1227  GGACCCATGGCACATGCTTTGGCCATGTCCATGTCCATGTCTTATAGCGAATTGCAAAAGGCCGAAGAA  1286

Db  1231  AATTTGATTTTGGCCATTTGGCCATTTGCTTTATGACGAATTGCAAAAGGCCGAAGAA  1290
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Qy  1287  AATTTGATTTTGGCCATTTGGCCATTTGCTTTATGACGAATTGCAAAAGGCCGAAGAA  1346

Db  1291  GAAGAGGCTGCCGAGGAGGAGGCGATACGAGAGGTCGAGAGGTCGAGAAGCTGAAGAGAGCG  1350
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Qy  1347  GAAGAGGCTGCCGAGGAGGAGGCGATACGTGAGGTCGAGAGGTCGAGAAGCTGCGCCCGCCAAAGCG  1406

Db  1351  GCCAAACTGGAGAGACGGGCGGGCCAATGTAGCAGCTCAAGCGGGTCAAGCGGCGATGCC  1410
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Qy  1407  GCCAAGCTGGAGAGACGGGCGGGCCAATGCGCAGCTCAGCGCAGCGGCGTGCGCCGC  1466

Db  1411  GCTGCGGCAGCTCTGCATCCCGACGATGGCGCAAAAGTCCCCACGTACTACTACCATCCG  1470
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Qy  1467  GAAGAGGCTGCACTGCATCCGACGAAGTCGCGGAAAGTCCGACGTATTCTTGCATCAGCTAT  1526

Db  1471  GAACTGTTTGTTGGGCGGCGAAGGGCAACGATGACAACAACAAAGAGAAGATGTCCATA  1530
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Qy  1527  GAGCTGTTTGTTGGGCGGCGAAGGGCAACGATGACAACAACAAAGAGAAGATGTCCATT  1586

Db  1531  CGGCAGCGTCGAAGTGGAATCGGAGTCGGTGGAGTCGGTGAAAGTCCGACCACCACCA  1590
              || |||| ||||||| |||||||| |||||||||| || ||||||||||||||||||
Qy  1587  CGGACCGTCGAAGTCGGAGTCGGTGGAGTCGGTGAGTCGGTGTATCAAAAGAACCAGCAACCACC  1646

Db  1591  ACAGCGAC-CC--GCTTACTAAAAGTCCGTAAAGTCGTAAAGTCCTAAAGTCGCACCTGGT  1647
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Qy  1647  ACAGCGACCACCAAGCTACCACCAAGTTCGTAAAGTCGCACCATCCTTATCCTTACCTGGT  1706

Db  1648  TCACCATTTAACCTACCGCCGGGAATCAGCATGGATGGACTTCGTAGTA  1707
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Qy  1707  TCACCCGTTTAACCGGGATCAGCGGGATCAGCGGGAGCTTCGTAGTA  1766

Db  1708  CGTTGGACGTTTGGTATACCGGGTACTGGTTACTGGTACTTTGAGAACA  1767
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Qy  1767  CGTTGGACGTTTGGTATACCGGGTAGCGATCGTAAGCTGTAACAATATCAG  1826

Db  1768  GATGGCCCAGCAGCATTTGCCCTATGCCTATGCCGATGACTCAGCAGCCCTGCGAACG  1827
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BASE COUNT     1713 a    1341 c    1597 g    1667 t
ORIGIN

Query Match        56.48;
Best Local Similarity    84.9%;    Score 3676;    DB 15;    Length 6318;
Matches 4986;    Conservative    0;    Mismatches 806;    Pred. No. 0.00e+00;    Indels 84;    Gaps 21;

Db  151  ATACGATGATGACGAGGAGCAAGAGGAGCGTGAGAGGTCCACAGCCGGATCCCACACTTGAACAG  210
              || ||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||
Qy  207  ATCCGATGATGACGAGGAGCAAGAGGAGCGTGAGAGGTCCACAACCGGATCCTACACTTGAACAG  266

Db  211  GGTGTGCCTATACCTGTTCGAATGCAGGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT  270
              |||||||||||||||||||||| |||||||||||||||||||||||||||| |||||||
Qy  267  GGTGTGCCAATACCTGTTCGATTGCAGGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT  326

Db  271  CTCGAGGATAATCGATCCCTTCTACAGTAATGTACTGACATTTGTAGTAATAAGTAAAGGA  330
              |||||||||||||||| ||||||||||||||||||||||||| |||||||||||||||||
Qy  327  CTCGAGGATAATCGATCCTACTACACAGTAATGTACTGACAGTTCGTAGTTGTTGTAAGCAAAGGA  386

Db  331  AAGGATATTTTTCGTTTTTCTGCCTCAAAAGCCACACGCCCACACGCCCAATCCG  390
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Qy  387  AAAGATATTTTTCGCTTTTCTGCATCAAAAGCCACATGTGGATCTCGATCCATTCAATCCG  446

Db  391  ATACGTCGTGTAGCCATTTATATTTTAGTGCATCCCTTGTTTTCGTTATTCATTATCACC  450
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Qy  447  ATACGTCGTGTGGCCATTTATATTTTAGTGCATCCTTTGTTTCCCTATTCTTATTCATCATCACC  506

Db  451  ACTATTCTCAACTGAATAATGTATTTAATGATAATGCCCGACAACGCCCACGGTCGAATCCAA  510
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Qy  507  ACAATTCTCGTCAACTGCATAATGTCATTGAATCAGCTGCTGCGCTGCTCGATCCGATCCAATCCG  566

Db  511  GAGGTGAATTCACCGGAATCTACACATTGAATCAGCTGGCATGGATGGCGCACGAGGT  570
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Qy  567  GAGGTGATATTCACCGGAATCTACACATTGAATCAGCTGGCATGGATGGCGCACGAGGT  626

Db  571  TTCATTTTATGCCCGTTTACGTATCTTAGAGATGCAGAAGGCTGAATTGGCGACTTCGTAGTA  630
              || |||||||||||||||||||||||||||||||| |||||||| |||||||| |||||
Qy  627  TTCATTTTATGCCCGTTTACGTATCTTAGAGATGCAGAAGGCTGAATTGGCGACTTCGTAGTA  686

Db  631  ATAGCTTTAGCTTATGGCCATGGGCATAGATTTAGTAATCTGCAGCTTTGAGAACA  690
              |||||||||||||||||||||| ||||||||||||| |||||||| |||||||
Qy  687  ATAGCTTTAGCTTATGTTGGCCATGGGCATAGATTTAGTAATCTAGCAGCTTTGTCAACATATCAG  746
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           |||||||||||||| |||||||||||||| |||||||||||||| || || |||||||||
Qy    1827 GATGCCCAGCAGCACTTGCCCTATGCCGACGACTCGAATGCCGTCACCCCGATGTCCGAA 1886

Db    1828 GAGAATGGTGCCATTATAGTACCAGCCTACTATTGTAATTTAGGTTCTAGACATTCTTCA 1887
           |||||||| ||||| ||||| || |  |||||| | ||| |||| ||  |||| || ||
Qy    1887 GAGAATGGGGCCATCATAGTGCCCGTGTACTATGGCAATCTAGGCTCCCGACACTCATCG 1946

Db    1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCACATGGTGATTTATTGGGTGGCATG 1947
           |||||||||||||| ||  |||| |||||||| |||||||| ||| || | || ||||||
Qy    1947 TATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGGCGGCATG 2006

Db    1948 GCGGCCATGGGTGCCAGCACAATGACCAAAGAGAGCAAATTGCGCAGTCGCAACACACGC 2007
           || | |||||| | ||||||||||||||| ||||||||||||||||  ||||||||||||
Qy    2007 GCCGTCATGGGCGTCAGCACAATGACCAAGGAGAGCAAATTGCGCAACCGCAACACACGC 2066

Db    2008 AATCAATCAATCGGTGCTGCAACCAATGGTGGCAGTAGTACGGCTGGTGGTGGCTATCCC 2067
           ||||||||| | || || || |||||||| ||||  |   |  ||| |  |||  |  ||
Qy    2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGGCACCA---C--CTG-TC-TGGACA--CC 2114

Db    2068 GATGCCAATCACAAGGAACAAAGGGATTATGAAATGGGTCAGGATTATACAGACGAAGCT 2127
            ||  ||| | |   || ||  | || || ||||| || | ||| |  || |||||||||
Qy    2115 AATCACAAGCTC---GATCATCGCGACTACGAAATTGGCCTGGAGTGCACGGACGAAGCT 2171

Db    2128 GGCAAAATAAAACACCACGACAATCCTTTTATCGAGCCCGTCCAAACTCAAACAGTGGTA 2187
           ||||| || ||||| || |||||||||||||||||||||||||| || ||||| |||||
Qy    2172 GGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCCGTCCAGACACAAACGGTGGTT 2231

Db    2188 GACATGAAAGATGTTATGGTCTTAAATGATATCATTGAACAAGCCGCTGGTCGGCATAGT 2247
           || ||||||||||| |||||| | ||||| ||||| ||||| |||||||||||||| |||
Qy    2232 GATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTGGTCGGCACAGT 2291

Db    2248 CGTGCTAGTGAACGAGGTG------------------------AGGACGATGACGAAGAT 2283
           || || || || || ||||                        ||||||||||||| |||
Qy    2292 CGGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGGACGATGACGAGGAT 2351

Db    2284 GGTCCCACATTCAAGGACATCGCCCTCGAATACATCCTAAAAGGCATCGAAATCTTTTGT 2343
           || || || ||||| ||||  || ||||||   ||||| |||||||||||  | ||||||
Qy    2352 GGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTGTTTTGT 2411

Db    2344 GTATGGGACTGTTGTTGGGTGTGGTTAAAATTTCAGGAATGGGTGTCCTTTATTGTGTTC 2403
           || ||||||||||| ||||| ||||| ||||||||||| ||||| ||  | || || |||
Qy    2412 GTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTCAGGAGTGGGTATCGCTCATCGTCTTC 2471

Db    2404 GATCCATTCGTGGAGCTCTTCATTACCCTGTGTATTGTGGTCAATACGATGTTTATGGCC 2463
           ||||| ||||| ||||||||||| || ||||| ||||||||||| |||||||| |||||
Qy    2472 GATCCCTTCGTCGAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGATGTTCATGGCA 2531

Db    2464 ATGGATCATCACGACATGAATCCGGAATTAGAGAAGGTGCTGAAAAGTGGTAACTATTTC 2523
           |||||||| ||||| |||||   |||  | ||    ||||| || ||||| |||||||||
Qy    2532 ATGGATCACCACGATATGAACAAGGAGATGGAACGCGTGCTCAAGAGTGGCAACTATTTC 2591

Db    2524 TTCACGGCCACTTTTGCAATTGAAGCCAGCATGAAACTGATGGCCATGAGCCCGAAGTAC 2583
           ||||| ||||| ||||| || || |||| |||||| || |||||||||||||| ||||||
Qy    2592 TTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCAAGTAC 2651

Db    2584 TACTTCCAGGAAGGCTGGAACATTTTCGATTTCATTATTGTGGCCTTGTCTCTGCTGGAA 2643
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Qy    2652 TATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATCGCTATTGGAA 2711

Db    2644 TTGGGCCTGGAGGGTGTCCAGGGCCTGTCGGTGTTGAGAAGTTTTCGTTTGCTTCGTGTA 2703
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Qy    2712 CTGGGACTCGAGGGTGTCCAGGGTCTGTCCGTATTGCGTTCCTTTCGATTGCTGCGTGTA 2771

Db    2704 TTCAAATTGGCAAAATCATGGCCCACACTCAATTTACTCATTTCGATTATGGGCCGGACA 2763
           |||||| |||| || || ||||||||||| ||||||||||||||||||||||| || ||
Qy    2772 TTCAAACTGGCCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTATGGGACGCACC 2831

Db    2764 ATGGGTGCATTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTTGCCGTG 2823
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Qy    2832 ATGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTTGCGGTG 2891

Db    2824 ATGGGAATGCAACTTTTCGGAAAGAACTATATTGACCACAAGGATCGCTTCAAGGACCAT 2883
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Qy    2892 ATGGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGGC 2951

Db    2884 GAATTACCGCGCTGGAACTTCACCGACTTCATGCACAGCTTCATGATTGTGTTCCGAGTG 2943
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Qy    2952 GACCTGCCGCGCTGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTGTTCCGGGTG 3011

Db    2944 CTGTGCGGAGAGTGGATCGAGTCCATGTGGGACTGCATGTATGTGGGCGATGTCAGCTGT 3003
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Qy    3012 CTCTGCGGAGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCTCGTGC 3071

Db    3004 ATACCCTTCTTCTTGGCCACGGTCGTGATAGGCAATCTTGTGGTTCTTAATCTTTTCTTA 3063
           || ||||||||||||||||| || || || |||||||||||||| ||||| |||||||||
Qy    3072 ATTCCCTTCTTCTTGGCCACCGTTGTCATCGGCAATCTTGTGGTACTTAACCTTTTCTTA 3131

Db    3064 GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTTATCAGCCCCGACTGCCGACAATGAT 3123
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Qy    3132 GCCTTGCTTTTGTCCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGAT 3191

Db    3124 ACCAATAAAATAGCAGAGGCCTTCAATCGTATTGCTCGTTTTAAGAACTGGGTGAAACGT 3183
           || ||||||||||| |||||||||||||| ||||  || ||||| |  ||||| || |||
Qy    3192 ACGAATAAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTTGGGTTAAGCGT 3251

Db    3184 AATATTGCCGATTGTTTTAAGTTAATTCGAAATAAATTGACAAATCAAATAAGTGACCAA 3243
           |||||||| |||||||| |||||||| || || ||||||||||||||||||||||| |||
Qy    3252 AATATTGCTGATTGTTTCAAGTTAATACGTAACAAATTGACAAATCAAATAAGTGATCAA 3311

Db    3244 CCATCAG---------------A-A-CA--------TGG--CGAT-A--ATG-------- 3265
           |||||||               | | ||        |||  |||  |  |||
Qy    3312 CCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTTGGAGCGAAGAGCATGGTGACAAC 3371

Db    3266 -AACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTTGATCAAAAAGGGTATGAAG 3324
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Qy    3372 GAACTGGAGCTGGGCCACGACGAGATCCTCGCCGACGGCCTCATCAAGAAGGGGATCAAG 3431

Db    3325 GGCGAGACCCAGCTGGAGGTGGCCATTGGCGATGGCATGGAGTTCACGATACATGGCGAT 3384
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Qy    3432 GAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGATACACGGCGAC 3491

Db    3385 ATGAAAAACAACAAGCCGAAGAAATCAAAATTCATGAACAACACAACGATGATTGGAAAC 3444
           ||||| |||||||||||||||||||| ||||   | || ||| ||||||||||||| |||
Qy    3492 ATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCAAC 3551

Db    3445 TCAATAAACCACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGGTTTGTCCATA 3504
           ||||| |||||||||||||||||||||||||| |||||||||||||||||||||||| ||
Qy    3552 TCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCCTTA 3611

Db    3505 CAGGACGATGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG 3564
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Qy    3612 CAGGACGACGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG 3671

Db    3565 GACGAGAGCCACAAGGGCAGCGCCGAGACCATCGAGGGCGAGGAGAAACGCGACGTCAGC 3624
           ||||||||||||||||||||||||||||| || |||||||||||||| ||||||| ||||
Qy    3672 GACGAGAGCCACAAGGGCAGCGCCGAGACGATGGAGGGCGAGGAGAAGCGCGACGCCAGC 3731

Db    3625 AAAGAGGACCTCGGCCTCGACGAGGAACTGGACGAGGAGGCCGAGGGCGATGAGGGCCAG 3684
           || |||||  | || ||||||||||||||||||||||||| |||  |||| ||||||| |
Qy    3732 AAGGAGGATTTAGGTCTCGACGAGGAACTGGACGAGGAGGGCGAATGCGAGGAGGGCCCG 3791

Db    3685 CTGGATGGTGACATTATCATTCATGCGCAAAACGACGACGAGATAATCGACGACTATCCG 3744
           || || ||||| || || |||||||| ||   |||||| || ||| |||| || |||||
Qy    3792 CTCGACGGTGATATCATTATTCATGCACA---CGACGAGGATATACTCGATGAATATCCA 3848

Db    3745 GCCGACTGTTTCCCCGACTCGTACTACAAGAAGTTTCCGATCTTGGCCGGCGACGAGGAC 3804
           || || || | |||||| |||||||| ||||| ||||||||||| ||||| ||||| |||
Qy    3849 GCTGATTGCTGCCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGAC 3908

Db    3805 TCGCCGTTCTGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCAATTAATTGAAAAT 3864
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3909 TCGCCGTTCTGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCAATTAATTGAAAAT 3968

Db    3865 AAATATTTTGAAACCGCAGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCCTTA 3924
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Qy    3969 AAATATTTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTA 4028
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Db  3925 GAAGATGTTCATTTACCCGATGACCTGTCAGGATATACTGTACTACACATGGACAGG 3984
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Qy  4029 GAAGATGTACATCTGCCCACAAAGACCCACTCAGCCGGATAATTTTATACTATATGGACAGA 4088

Db  3985 ATATTACCGGTGATATTCTTTTTGGAGATGTTGATCAAATGGTTGGCCTGGCCTTAAG 4044
              | |  ||| |||| |||||||| ||||  |||| ||||  ||| ||| |||||||
Qy  4089 ATATTACCGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCCTCCGGCTTCAAA 4148

Db  4045 GTTTACTTCACCAATGCGCGGTCCGTGGTGGCTGGATTTCGTGATTGCATCGCTATCGCTTATA 4104
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Qy  4149 GTGTACTTCACCAACGCCGGTGGTGTTGGCCTCGGATTCGTGATTGCATCGCTATCGCTTATC 4208

Db  4105 AATTTGGTTGCCCTTTTGTCGGGCTAAATGATAATAGCCGTGTTTAGATCAATGCGCACA 4164
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Qy  4209 AACTTCGTTGCTTGCTTCACTTGTTGCTGTGTCTCTGGTATTCAAGACTATGCGAACG 4268

Db  4165 CTCGCCGCGCCCTAAGGCCATTGCGTGCTGTCTCTAGATGCGGAGGGTATGAAAGTTGTCGTG 4224
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Qy  4269 TTAAGAGCACTGAGACCACTACGTGCCATGTGCCCGTATGCCAGGGCATGAGGGTTCGTCGTT 4328

Db  4225 AATGCGCTGTTCAAGCTATACCGTCCATCTTCAATGTGTCTATTTGGTGTGTCTGATATTT 4284
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Qy  4329 AATGCGCTGTACAAGCTATACCGTCCATCTTCAATGTGTCTATTTGGTGTGTCTAATATTT 4388

Db  4285 TGGCTTATTTTTGCCATTATGGGAGTACAGCTTTTTGCTGTGGAAAATATTTTAAGTGTAAA 4344
           |||| ||||||||||||| |||| || || ||||||||||||||||||||||||||||||
Qy  4389 TGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTGCTGTGGAAAATATTTTAAGTGCGAG 4448

Db  4345 GATGGTAATGACACTGTCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT 4404
           | | |  ||||| || | ||  ||||  ||||| |||  |  ||| |||| ||  ||
Qy  4449 GACAGCGACAAAGGCTATCCGGAGCATCACCAAATCGCAATCGGCACCGCTGGTATAACGTTTTCTC 4508

Db  4405 GAAAACTACACCTGGGAAAAATTCGGCAATGAACTTCGATCATGTAGGTAATGCGTATCTC 4464
           ||  |||||| |||||||||||||||| ||| ||||||||| || || || ||||||||||
Qy  4509 GAGAACTACACGTGGGATGAATTCAGCAATGAACTTCAGATTCGATCATGTAGGTAACGCGTATCTG 4568

Db  4465 TGTCTATTTCAAGTGCCCACCTTTAAGGCTGGATCCAGATTATGAACGATGCCATTGAT 4524
           |||||||||||||||||||||| |||||||||||| ||| ||||| | ||||| ||||
Qy  4569 TGCCTTTTCCAAGTGCCCACCTTTCAAAGGCTGGATACAAATCATGAACGATGCTAICGAT 4628

Db  4525 TCACGAGAGGTGGACAAGCAGCAGGCCGATCCGAGAAAACCAATATCTACATGTATTATATTC 4584
           ||||||||| ||||||||||||| || || |  |||| |||| |||||| |||  ||||||||
Qy  4629 TCACGAGAGGTGGACAAGCAGCAGGCTGATCCGAGAAAAGCAATTCGTGAAATGTTCATTATTTC 4688

Db  4585 GTATTCTTCATTATATTGGATCATTTTCACACTCGTTCATTGGTGTTATCATT 4644
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Qy  4689 GTATTCTTCATCATATTTGGATCCTTTTCACACTCGTTCATTGGTGTTAICAIT 4748

Db  4645 GATAATTTTAATGAACAAAGAAGAAAGCTGGTGGATCATTCATCAGAAAATGTTCATGACAGA 4704
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Qy  4749 GATAATTTTAATGAGCAAAGAAGAAAGCAGTGGATGGATCATTCATCAGAAATGTTCATGACAGAA 4808

Db  4705 GATCAGAAAAAGCTACTATAAATGCTATGAAAAAAGATGGCTCTAAAAAAACCATTAAAAGCC 4764
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Qy  4809 GATCAGAAAAGTACTATAATGCTATGAAAAAGATGGCTCTAAAAAAACCATTAAAAGCC 4868

Db  4765 ATTCCAAGACCCAGGTGGCGACCACCAACCAATTCGTTGAAACATGTTTACCATGACCCTGATCGG 4824
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Db  4825 TTCGATAAATCATTATGTTGTTCATTGGCTTAAACATGTTTACCATGACCCTCGATCGG 4884
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Qy  4929 TTCGATAAATCATTATGTTTATTCATTGGTCTCAACGTGTCTGAACATCCCTCGATCGT 4988

Db  4885 TACGACGGCTCCGAACATGCTACAACAAACATGTCCTCGACAAACTTCAATGGATATTCGTAGTT 4944
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Qy  4989 TACGATGCGTCGGACACGTTCCTAGAACTTATCCGATATTCGTAGTT 5048

Db  4945 ATTTTCAGTGGCGAATGCTATTTAAAAATATTCGCTTAAGATATCACTATTTCAAAGAG 5004
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Qy  4989 ATTTTCAGTTCCGAATGTCTATTAITAAAAATATTCGCTTTACGATATCACTACTATTTATTGAG 5108
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Db  5005 CCATGGAATTTATTGATGTAGTAGTAGTTGTCATTTATCCATCTTAGGTCTTGTACTCAGC 5064
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Qy  5109 CCATGGAATTTATTTGATGTAGTAGTAGTTGTCATTTTATTCCATCTTAGTCTCTTGTACTTAGC 5168

Db  5065 GACATCATTGAGAAGTATTTCCGTACCGACACTGCTCCGTCGTGTGTGAGAGTTGGCCAAA 5124
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Qy  5169 GATATTATCGAGAAGTACTTCGTCGTCGCCGACCCTGCTCCGTCGTGTGCTGTGTGGCCAAA 5228

Db  5125 GTGGGTGTCGTCCGTCGTTAGTCAAGGTGCCAAGGTATCGGACGGTATCGGTTGCTGTTCGCG 5184
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Qy  5229 GTGGGCCGTGGTCCGTCCGACTGGTGAAGGGAGCCAAGGAGCATTCGGACACTGCTCTTCGCG 5288

Db  5185 TTAGCCATGTCGTTGCCTGCCTTATTCAACATTTGTCTGTTGCTGTTCTTGGTGATGTTC 5244
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Qy  5289 TTGGCCATGTCGTTGCCGCCGCCCGTTCAACATCTGCCTGCTGCTGCTGTTCCTGGTCATGTTC 5348

Db  5245 ATCTTTGCTATCTTGCATGTCATCTCCTTCTCATGCATGTCAAAGAGGAGGGGCATAAAT 5304
           |||||| | | || |||||||||||| ||||||||  ||| || ||||||| ||||||
Qy  5349 ATCTTTGCCATTTCGGCATGCTGTTCTTCATGCACGTGCACGACCTTCAGAGTCGAGTCGAACG 5408

Db  5305 GCTGTGTATAATTTAAGACATTGGCCAAAGTATGACATTTGTGTTTCAGATGTCTACC 5364
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Qy  5409 GACGTCTACAACTTCAAGACCTTTGGGCCAGCATGCATGCATCCTGCTCTTTCAGATGTCGACG 5468

Db  5365 TCAGCCCGGTTGGGATGGTGTGTTAGATGCCATTATCAATGAGGAAGATTGCCATCCACCCC 5424
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Qy  5469 TCAGCCGGTTGGGATGGTGTACTGACGCCATTATCAATGAGGAAGCATGCCGATCCACCCC 5528

Db  5425 GACAACGACAAGGGCTATCCGGCAATTGTGGTTCAGCGACACTGTTGGAATTACGTTTCTC 5484
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Qy  5529 GACAGCGACAAAGGCTATCCGGCAATTGTGGTTCAGCGACCCGTTGGAATAACGTTTTCTC 5588

Db  5485 CTTTCATATCTAGTTATAAGCTTTTTGATAGTGAGTATTAATAATGTCATTGCTGTCATTCTC 5544
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Qy  5589 CTCTCATACCTAGTTATAAGCTTTTTGATAGTGAGTATTAATAATGTACATTGCTGTCATTCTC 5648

Db  5545 GAGAACTATAGCCAGGCTACGAGGATGTACAGGAGGTCTCACCGACGACGATTACGAT 5604
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Qy  5649 GAGAACTATAGTCAGGCTACGAGGATGTACAGGAGGTCGCAAGAGACGTCTAACCGACGACTACGAC 5708

Db  5605 ATGTACTACGAGATTGGCAACAATTGCATACCCATCTGTCTGCGAGGGACGACGTACGACGTACGAC 5664
           |||||||||||| |  ||| |||| |||||| |||| | | |||||||| || |||||||||
Qy  5709 ATGTACTATGAGATCTGGCAGCAATTCGATCCGAGCCAGCCAGTACATACGCTATGAT 5768

Db  5665 CAGCTGTCCCGAGTTTCTGGACGTCGTGCAGATCCACAAGCCGAACAAG 5724
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Qy  5769 CAGCTGTCCGAATTCCTGGACGTCGTGCAGATCCACAAAACCGAACAAG 5828

Db  5725 TACAAAATCATATCGATGGACATGCCGATATGTCGGGGGCGACATGATGATGTACTGTGTGGAT 5784
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Qy  5829 TACAAGATCATATCGATGGACATACCGGGTGACCTCATGTGACCTCATCGTACTGCCGTCGAC 5888

Db  5785 ATATTGGATCGCCCTGACCAAGGACTTCTTTGCGCGTCAAGGGTAATCCACGTGAGGAGACG 5844
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Qy  5889 ATCCTTCGACGCCCTTACGACAAAGACTTCTTTGCGCGGCAATCGATAGAGAGAGACG 5948

Db  5845 GGTGAAATTGGTGCGGCCACGGGGTCATGCGCCCAAGCCTATGATCCGGTGTCGTCA 5904
           |||||| |||| |  ||| | || ||| |||||||| ||||||||||||||| ||||
Qy  5949 GGTGAGATTGGTGAGATAGCGGCCCCCGGATACGAGGGTACGAGCCGGTGTCGTCA 6008

Db  5905 ACACTGTGGCGGCCAGCGTGAGGAGTACTGCGCGCAAGCGTGATACGAGAATGCGTGGCG 5960
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Qy  6009 ACGCTGTGGCCGCTCAGCGTGAGGAGTACTGCGCGCAAGCGTAATCCAGCACGCGCCTGGCG 6064
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RESULT     6
LOCUS      MDPARA        6899 bp    RNA             INV       17-SEP-1996
DEFINITION M.domestica mRNA for voltage-sensitive sodium channel, complete
           CDS.
ACCESSION  X96668
NID        g1550780
KEYWORDS   voltage-sensitive sodium channel.
SOURCE     house fly.
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ORGANISM  Musca domestica
          Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
          Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
          Muscomorpha; Muscoidea; Muscidae; Musca.
REFERENCE  1 (bases 1 to 6899)
AUTHORS    Williamson,M.S., Martinez-Torres,D., Hick,C.A. and Devonshire,A.L.
TITLE      Identification of mutations in the housefly para-type sodium
           channel gene associated with knockdown resistance (kdr) to
           pyrethroid insecticides
JOURNAL    Mol. Gen. Genet. 252 (1-2), 51-60 (1996)
MEDLINE    9397509
REFERENCE  2 (bases 1 to 6899)
AUTHORS    Williamson,M.S.
TITLE      Direct Submission
JOURNAL    Submitted (15-MAR-1996) M.S. Williamson, IACR-Rothamsted,
           Department of Biological & Ecological Chemistry, Harpenden,
           Hertfordshire, AL5 2JQ, UK
FEATURES   Location/Qualifiers
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           /strain="Cooper"
           /db_xref="taxon:7370"
           /chromosome="autosome III, short arm"
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CDS        14..6340
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           WHMLFFIVIIFLGSFYLVNLILAIVAMSYDELQKKAEEEEAAEEEAIREAEEEAAAKA
           AKLEERANVAAQAQOADADAAAALHPEMAKSPTYSCISYELFVGGEKGNDDNNKEKM
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           GNSINHQDNRLEHELNHRGLSIQDDTASINSYGSHKNRPFKDESHKGSAETIEGEEK
           RDVSKEDLGLDEEELDEEAEGDEGQLDGDIIIHAQNDDEIDDYPADCFPDSYYKKFPI
           LAGDEDSPFWQGWGNLRLKTFQLIENKYFETAVITMILMSSLALALEDVHLPDRPVMQ
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           DTEGYDPVSSTLWRQREEYCAKLIQNAWRRYKNGPPQEGDEGRAAGGEDGAEEGEGEG
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           TAVLVESGFVTKNGHKVHSRSPSITSRTADV"
BASE COUNT    1965 a   1445 c   1660 g   1829 t
ORIGIN

Best Local Similarity 84.9%;   Pred. NO. 0.00e+00;
Matches 4986;   Conservative 0;   Mismatches 806;   Indels 84;   Gaps 22;

Db   164  ATACGATATGATGACGAGGACGAAGATGAAGGTCCACAGCCGGATCCACACTTGAACAG  223
          || |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Qy   207  ATCCGATATGATGACGAGGACGAGGATGAAGGTCCAACCGGATCCTACACTTGAACAG  266

Db   224  GGTGTGCCTATACCTGTTCGAATGCAGAGGGCAGCTTCCCGCCCGAATTGGCCTCCACTCCT  283
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   267  GGTGTGCCAATACCTGTTCGATTGCAGAGGGCAGCTTCCCGCCCGAATTGGCCTCCACTCCT  326

Db   284  CTCGAGGATATCGATCCTTCTACAGTAATGTACTGACATTTGTAGTAATAAGTAAAGGA  343
          |||||||||||||||||| |||||| |||||||||||| ||||| |||| ||||||||||
Qy   327  CTCGAGGATATCGATCCCTACTACAGCAATGTACTGACATTCGTAGTTGTAAGCAAAGGA  386

Db   344  AAGGATATTTTTCGTTTTCTGCCTCAAAAGCAATGGCCTGCTCGATCCATTCAATCCG  403
          |||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   387  AAAGATATTTTTCGCTTTCTGCATCAAAAGCAATGGCCTGCTCGATCCATTCAATCCG  446

Db   404  ATACGTCGTGTAGCCATTTATATTTAGTGCATCCCTTGTTTCGTTATTCATTATCACC  463
          |||||||||||||| ||||||||| ||| |||||||| || |||||||||| ||||||
Qy   447  ATACGTCGTGTGGCCATTTACATTCAGTGCATCATCATTTCCCTATTCATCATCACC  506

Db   464  ACTATTCTAACTAATTGTATTTTAATGATATATGCCGACAACGCCCACGGTCGAATCCACA  523
          || ||||  | ||||||  ||||||  ||  |||||||||||||||||| ||||| ||||||
Qy   507  ACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCCACGGTTGAGTCCACT  566

Db   524  GAGGTGATATTCACCGGAATCTACACATTTGAATCACGTGTTAAAGTGATGGCACGAGGT  583
          |||||||||||||||||||||||||||||| ||||| |||||||||||||||||||||||
Qy   567  GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTGTAAAGTGATGGCACGAGGT  626

Db   584  TTCATTTTATGCCCGTTACGTATCTTAGAGATGATGGAATTGGCTGGACTTCGTAGTA  643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   627  TTCATTTTATGCCCGTTACGTATCTTAGAGATGATGGAATTGGCTGGACTTCGTAGTA  686

Db   644  ATAGCTTTAGCTTATGATGACCATGGCATAGATTTAGGTAATCTCGCAGCTTTGAGAACA  703
          ||||||||||||||||||||||||||||||||||||||||||||||| |||| | |||
Qy   687  ATAGCTTTAGCTTATGATGACCATGGCTATAGATTTAGGTAATCTAGCAGCCCCTGCGAACG  746

Db   704  TTTAGGGTACTGCGAGCTCTGAAAACCGTAGCCATTGTGCCAGGTCTAAAAACCATTGTC  763
          ||||||| |||||||||||||||||||||||||||||| ||| | |||||| |||||||
Qy   747  TTTAGGGTGCTGCGAGCGCTTAAAACCGTAGCCATTGTGCCAGGTCTGAAGACCATCGTC  806

Db   764  GGTGCTGTCATTGAATCTGTAAAAAATCTACACGCATCGATGATAATTTGACAATGTTTCC  823
          || || |||||| ||||| |||||||||| |||| ||||| ||| |||| ||||| |||||
Qy   807  GGCGCCGTCATCGAATCGGTGAAGAATCTGCGCGATGTGATTATCCTGACCATGTTCTCC  866

Db   824  CTGTCCGTGTTCGCGCTGATGGGCCTGACAAATCTATATGGGTGTTCAACACAAAAGTGC  883
          ||||||||||||| ||||||||||||| || ||||| |||||  ||| |||| |||
Qy   867  CTGTCCGTGTTCGCGCTGATGGGCCTGACAGATGAGAATTGGGGCGTCTCACCGGAGAAGTGC  926

Db   884  ATTAAACGAATCCCCCTGGGACGGCAGTTGGGGTCAATCTGACCGATGAAAACTGGTTTCTA  943
          || |  |||||||||| ||||||||||||| |||||||||| ||||||||| |||| |
Qy   927  ATCAACGAAGTCCCCGCGGAGCGGTTCCGGGCAATCTGACCGACGAGAACTGGGACTAT  986

Db   944  CACAATAGCAACAGTTCCAATTGGTTACGGAGGAACGATGGCGAGTCATATCCGGTGTGC  1003
          ||||| ||| || ||||||||||| || ||| |||||||||| |||| ||||||| |||
Qy   987  CACAATCGCAATAGCTCCAATTGGTATTCCGAGGACGAGGGCATCTCATTTCCGTTATGC  1046

Db   1004 GGGAATGTATCCGGTGCGGGAACATGCGGCGAAGATTACGTCGCCCTGCAGGGCTTCGGC  1063
          | ||| |||||||||| ||||| ||||||||||||||||||| |||||||||||||||||
Qy   1047 GGCAATATATCCGGTGCGGGCAATGCGACGACGATTACGTCTGCCCTGCAGGGGTTTGGT  1106

Db   1064 CCCAATCCCAACTACGATTACCAGTTCGATTCATTCGGTTTGGGCTTCTGTCTGGCCG  1123
          || ||||| |||| ||| |||||||| |||| ||| |||| |||| |||| |||| ||
Qy   1107 CCGAATCCGAATTATGCTAATCAGCTTCGTTCGGATGGGTTTCCGTCGCCC  1166

Db   1124 TTTCGTCTCATGACCCAAGATTTCTGGGAGGATCTCGGAGGATCTGTATCAGCAGCT  1183
          || || |||||||||||||||||||||||||||||||||||| |||||||||||||
Qy   1167 TTCCGGCTGATGACACAGGACTTCTGGGAGGATCTGTACCAGCTGGTGTTGCGGCGCCC  1226

Db   1184 GGACCCTGCACATGTTGTTCTTATAGTCATCATCTTCCTAGTTCATCATCTTGTG  1243
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Db  2297  GGTCCCACATTCAAGGACATCGCCCTCGAATATATCCTCGAATATCCTAAAAGGCATCGAAATCTTTTGT  2356
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Qy  2352  GGCCGCGACGTTCAAAGACAAGGCACTCGAGTGATCCTCGAGTGATCCTCGAAAGGCATCGATGTGTTTTTGT  2411

Db  2357  GTATGGGACTGTTGGTGGTGCTGGGTTTGGTTGAAATTTCAGGAATGGTGTCTTCATTGTGTTC  2416
          || ||||||||||||||||||||||||||||||||||||||||| ||| || | | |||| | |||
Qy  2412  GTGTGGGACTGTTGGTGGTGCTGGGTTTGGTTGAAATTTCAGGAGTGGTATCGTCATCGTCTTC  2471

Db  2417  GATCCATTCGTGGAGCTCTTCATTACCCTGTGTATTGGTGTCAATACAAATGTTCATCGACC  2476
          |||||  |||||  ||||||||    | |||||| |||  ||||   ||||||||||||||||
Qy  2472  GATCCCTTCGTGCGAGCTCTTCACACGCGTGTGTCAACACGATGTTCATCGACA  2531

Db  2477  ATGGATCATCACGACACATCCGGAATTGGACGAGAAGTGCTGAAAAGTGGTAACTATTTC  2536
          |||||||| ||||| |   |  |||| || ||||| ||| || || |||||||||||||||
Qy  2532  ATGGATCACCACGATATGCAACAAGGAGATGGAACGCGTCGTCAAGAGTGGCAACTATTTC  2591

Db  2537  TTCACGGCCACTTTGCAATTGAGGCCAGCATGAAACATGATGGCCATGAGCCCGAAGTAC  2596
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Qy  2592  TTCACGGCCACCTTTGCCATCGAGCCCATCATGAATGGCCATGAGCCCCAAGTAC  2651

Db  2597  TACTTCCAGGAAGGCTGGAACATTTCATTTCATTATTGTGGCCTTGCTCTGTCTGGAA  2656
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Qy  2652  TATTTCCAGGAGGGCTGGAACATCTTCGACTTCATTGTGTACTCGTGGAA  2711

Db  2657  TTGGGCTCGGAGGGTGTCCAGGCCGTCGGGTTGGTCCGAATTGCGTTGTCGTGTA  2716
          |||| |||||||||||||||||| |||| |   |  |||||||||| ||| |||||
Qy  2712  CTGGGACTCGGAGGGTGTCCAGGGTCTGTCCAGGGTCTGCGTATTGCTGCGTGTA  2771

Db  2717  TTCAAATTGCAAAATCATGGCCCACACTGAATTCACTCATTTCGATTATGGGCCGGACA  2776
          |||||| ||||  | |||||||||| || |||| |||| ||||||| |  ||||| ||
Qy  2772  TTCAAACTGGCCAAGTCTTGGCCCCAAGTCTTGGCCCCACACTTAATTACTCATTCGATTCGTCGTCCGGGTG  2831

Db  2777  ATGGTGCATTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTTGCCGTG  2836
          ||||  || |||||||||||||||||||||||||||||||||| |||||||||||| |||
Qy  2832  ATGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCATCATCTTTGCGGTG  2891

Db  2837  ATGGGAATGCAACTTTCCGGAAAGAACTATATTGACCACCAGAGATCGCTTCAAGGACCAT  2896
          ||||||||||||||| |||||||||| |||| | |||||| || || ||||| ||| |
Qy  2892  ATGGGAATGCAACTGTTCCGGAAAGAATTATCATGATCACAAGGACCGCTTCCCGGATGGC  2951

Db  2897  GAATTACCGCCGCTCGAAATTCACCGACTTCATGTGGGACTGCAGTCCATGTATGTGGGACTGCTG  2956
          ||  | ||| ||| | || ||||||||||| |||| ||| |||||||||||||| ||||||||||
Qy  2952  GACCTGCCGCGCGCGCTGGAACTTCACCGACTTTATGCAGACGCTGCAGTCCATGTATGTGGGACTGCTG  3011

Db  2957  CTGTGCCGGAGAGTGGATGGATCGAGTCCATGTCATGTATGTGGGACTGCAGTCAGCTGT  3016
          || ||| ||||| ||||| ||||||||||||||||||   ||| || ||| | | |||
Qy  3012  CTCTGCGGGAGAAATGGATCGAGTCCATGTCATGTGGGACGTGGGCCGATGTCCGTGCTC  3071

Db  3017  ATACCCTTCTTCTTGCTTGGCATGGGCGCCGTGATCGGCAATTCGGCAATTCGTATTAATCTTTTCTTA  3076
          || |||||||||||| |||||| ||| |||| || ||||||||||  |   |||| | ||||||||||
Qy  3072  ATTCCCTTCTTCTTGGCTTGGCCACCGGTTGTCATCGGCAATTCGTTGGTACTTAACCTTTTCTTA  3131

Db  3077  GCTTTGCTTTTGTGTCCAAACTCGGTTCATCGAGTTTAAGTTAATTGAAATAAATGACGACCAA  3136
          || ||||||||||||||||  | || ||  | |  |||||||   |  | ||| |   ||||
Qy  3132  GCCTTGCTTTTGTGTCCAATTTTGGCTCTAGCTTTCAAGCTGCGACTAGCTTTATCAGCCGACGATACGAT  3191

Db  3137  ACCAATAAAATAGCAGAGCCTTCAATCGTATTGCTGTATTGGTGAACTGGTGAAACGT  3196
          || ||||||||||| ||| |||||||||  |||| |||| | | |||| |||| |||||
Qy  3192  ACGAATAAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTTGGGTTAAGCGT  3251

Db  3197  AATATTGCCGATTGTTTTAAGTAATTGAAATAAATGACAAAATCAAATAAAGTGACCAA  3256
          |||||||| |||||||| |||||| ||| || |   |   || ||  |    | |||||
Qy  3252  AATATTGCTGATTGTTTCAAGTAACTGAGCTGTTATCAGGCTTGATCAGATGGAGCATCAA  3311

Db  3257  CCATACAG------------------------A-A-CA------TGG--CGAT-A--ATG--------  3278
          |||| |                          | | ||      |||   |       |
Qy  3312  CCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTTGGAGCGAAGAGCATCGGTGCAAC  3371

Db  3279  -AACTGGAGTTGGGTCATGAGGAAATCATAGGGCGGGATCCTCGCCGCGACGATGAAATCAA  3337
           |||||||| |||   |||||| | ||||| |||||||||||||||||||||||||  ||||
Qy  3372  GAACTGGAGCTGGAAGCCCACGATGAGGACGATGACGAGAT  3431


Qy  1227  GGACCATGGCACATGCTGTCTTGTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTG  1286

Db  1244  AATTTGATTTGGCCATTGTTGGCCATGTGTGCCATGTGACGAGAAGGCCGAAGAA  1303
          ||||||||||||||||||||||||  |||| |||||||||||||||||||||||
Qy  1287  AATTTGATTTGGCCATTGTTGGCCGCATGTGACGAGAAGGCCGAAGAA  1346

Db  1304  GAAGAGGCTGCCGAGGAGGAGGCCGATACGAGAAGCTGAAGAGAGCGGCAGCCAAGGCG  1363
          ||||||||||||||||||||||||||||| |||||||| |   | |||  |||||||||
Qy  1347  GAAGAGGCTGCCGAGGAGGAGGCCGATACGGAGAAGCTGCCCCGCCAAAGCG  1406

Db  1364  GCCAAAACTGGAGGACGGCGGCCAATGTAGCAGCTCAAGCCGGCTCAGGATGCAGGGGATGCC  1423
          |||||  ||||||||||  |||||||  |  | |||| | || ||||| | |||| | ||||
Qy  1407  GCCAAGCTGGAGGACGCGGCCAATGCCAGGCTCAGGCAGCAGCGGCTCGGGCTGCCCGCC  1466

Db  1424  GCTGCGGCAGCTCGCATCCCGAGATGGCCAAAGAGTCCCACGTACTCTTGCATTAGCTAT  1483
          |   |  |||| | |||||| | ||||||||||||||| ||||| | ||||||| ||||
Qy  1467  GAAGAGGCTGCACTGCATCCGGAAATGGCCAAGAGTCCGACGTATTCTTGCATCAGCTAT  1526

Db  1484  GAACTGTTGTTGGCGGCGAGGAGGCAACGATGACAACAACAACAGAGAGATGTCCATA  1543
          || |||| ||||||||||||||||||||||||||||||||||||||| | |||||||
Qy  1527  GAGCTATTTGTTGGCGGCGAGGAGGCAACGATGACAACAACAACAGAGAAGATGTCCATT  1586

Db  1544  CGCAGCGTCGAAGTGGAATGGGAGTCGGTGAGCGTTATACAAGACAACCAGCACCTACC  1603
          || ||||||||| ||||  ||||| |||||||||||||||||||||||||||||||||
Qy  1587  CGGAGCGTCGAGGTGGAGTCGGTGGTCGGTGAGCGTTATACAAAGACAACCAGCACCTACC  1646

Db  1604  ACAGCAC-CC--GCTACTAAGTCCGTAAAGTTCGTAAAGAGTTCCTTATCCTTACCTGGT  1660
          ||||||| ||   |||||||||||||||||| |||||||| || ||||||||||||||||
Qy  1647  ACAGCACCACCAAGTACCAAAGTTCGTAAAGTTGACCACGACATCCTTATCCTTACCTGGT  1706

Db  1661  TCACCATTAACCTACGCCGGGGATCACGTTAGTTCACACAATACGAAAATGGG  1720
          ||||| |||||| |||||| |||||||| | | |||||| ||||| | ||| |
Qy  1707  TCACCGTTTAACATACGCCAGGGGATCACGTTCACAAGTTCTCACAGTACGGAACGGA  1766

Db  1721  CGTGGACGTTTTGGTATACCAGAGTAGCGATCGGCAAGCCATTGGTACTGCAAACATATCAG  1780
          ||||||||||| |||||||| || || |||  ||  | |||||||| | |||||||||||
Qy  1767  CGTGGACGTTTGGTATACCCGTGGTATTGGTATTGTCAACATATCAG  1826

Db  1781  GATGCCCAGCAGCATTGCCCTATGCCGATGACTCGAATGCCGTAACACCCATGTCCGAA  1840
          ||||||||||||| |||||| | |||||| | |    ||| | |||| ||||||||||
Qy  1827  GATGCCCAGCAGCACTGCCCTGCCCTATGCCGACTCGTCACCCCGATGTCCGAA  1886

Db  1841  GAGAATGGTGCCCATTATAGTAGCCAGCCTACTATTGTAATTTAGGTTCTAGACATTCTTCA  1900
          |||||||| |||||| || ||  || | ||||| |||  | |  |||| | |  || | | |
Qy  1887  GAGAATGGGCGCCCATCATCAGTGACCCGTGTACTATCTAGGCGCTCCCGACCACTCATCG  1946

Db  1901  TATACCTTCGCATCAAGAATCTCGTATCATCAAGAATCGTATACATGGTTCGATTTGATTGAT  1960
          ||||| | |||||||  | ||  | |  ||  |  |  |||| | |||  || | |
Qy  1947  TATACCTCGCATCAGTGCCGATATCGTGTATATCCTCACATGGCGGCCATG  2006

Db  1961  GCGGCCATGGGTGCCAGCAGGTCGCAGCAATTGCGCAGTCGGCAATTGCCGCAACACGC  2020
          ||  ||||||| ||||||| |  ||||||||||||| | ||||||| |||||||||| ||
Qy  2007  GCCGTCATGGGCCGTCAGCGACTCAGCAAATTGCCGCCAACACCGC  2066

Db  2021  AATCCAATCAATCGACACAGACAATCCTTTATCGCGACAATCCTTTATCGAGACTGTA  2080
          |||| |||||||||||| | || ||||||| ||| |||||||| |||  |||  |||||
Qy  2067  AATCAATCAATCGACAACAATCCTTTTATCGAGCCGTCAAACTCAGACAACAAACGGTGTT  2115

Db  2081  GATGCCAATCACAAGGATTATGGTCTTAAATGATATCATTGAAATAGCCGGATGAAGCT  2140
             |  |||||||| | | | | ||| |||| | || |  ||| |  |  |  ||||||||
Qy  2116  -ATCACAAGCTC---GATCATCGGCACAATCTTTATGCTGCCCTGTCGGACGGAAGCT  2171

Db  2141  GGCAAAGTAAAACACCGACAATCCTTTATCGACACAATCCTTTATCGAGCCGTCAAACTCA  2200
          ||||| | |||||||  |||| ||||| |||  |||||| ||||  |||||||||  |||
Qy  2172  GGCAAGATTAAAACATCAATGACAAATCCTTTTATCGAGCCGTCCAGCTGTGTA  2231

Db  2201  GACATGAAAGATGTTATGGTCTTGAAATGATATCATTGAAATGACGATGAAGCT  2260
          || |||||||||||  ||||||| |||||| | |||  |||  || |||||||| |
Qy  2232  GATATGAAAGATGTGATGGTCCTGAAATGACATCATCGAACGACGCCACAGT  2291

Db  2261  CGTGCTAGTGAACGAGGTG------------------AGGACGGACGAGAGAT  2296
          || ||  ||||  || | |                   |||| ||||| |||
Qy  2292  CGGGCCAAGCCGATCGGCCGGTGTCTCCGTTACTATTCCCAACGAGGACGATGACGAGGAT  2351
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Db  3338  GGGCAGGACCCAGCTGGAGGTGGCCGATGGCCATTGCGATGGCATGGAGTTCACGGATACATGGCGAT  3397
              |||  ||| |||||||||||||||||||||| ||  ||||||||||||||||||||||||
Qy  3432  GAGCAGGACGCAACTGGAGGTGGCCGATCGGGGATGGGATGGAATTCACGGATGGCACGGCGAC       3491

Db  3398  ATGAAAAACAACAGCCCAAGAAATTCATAAACAACGAAATTCATAAACAACGATGATTGGAAAC       3457
              ||||||| |||||||||||||    |||||  || ||||||||||||||||||||||| ||||
Qy  3492  ATGAAGAACAACAGCCCAGAAGAAATCCAAATATCTAAATAACTAAACGATGATTGGCAAC        3551

Db  3458  TCAATAAACCACCACCAAGAACATGGAACATGAGCTAAACCATAGAGGTTTGTCCATA          3517
          |||||| |||||||||||||||||| |||||||||||||||||||||||||||||| ||
Qy  3552  TCAATTAACCAAGACACCACCAAGAACTGGAACACGAGCTAAACCATAGAGGTTTGTCCTTA       3611

Db  3518  CAGGACGATGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG        3577
          ||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3612  CAGGACGACGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG        3671

Db  3578  GACGAGGAGGCCACAAGGGCAGCGGCCGAGACCATCGAGGGGCGAGGAGAAACCGACGTCAGC     3637
          ||||||||| |||||||||||||| |||||| | |||||||| || | |||||| |||||||
Qy  3672  GACGAGGAGCCACAAGGGCAGCGATGGGGCCGAGGAGGCCGAGGAGAAGCCGCACGCCCAGC     3731

Db  3638  AAAGAGGACCTCGGCCTCGACGAGGAACTGGACGAGGCCGAGGGCCGATGAGGGCCAG        3697
          || | |||| || |||||||| || || ||||  ||||||||| ||| |||||||||||
Qy  3732  AAGGAGGATTAGGTCTCGACGAGGAACTGGACGAGGCCGAGGGCCGATGCGGACGAGGAGGGGCCCG  3791

Db  3698  CTGGATGTGACATCATCATTCATGCGCAAAGACGACGAGATAATCGACGACTATCCG        3757
          |||||||||| |||| || ||||| ||||||||  ||||||||||||||||||| | |
Qy  3792  CTCGACGCGTGTATATCATTCATTCATGAATATACTCGATGAATATCCA                 3848

Db  3758  GCCCACTCGTTCCCCGACTCGTACTACAGAGAAGTTCCGATCTGGCCGGCGGCCGACGAGGAC     3817
          | |||||||| ||||||||| |||||||||||||||||  |||||||||||||||||||| |||
Qy  3849  GCTGATTGCTGCCCGATTCGTACTATAGAAGAAATTCCGATCTAGCCGGCGGCGGTGACGATGAC   3908

Db  3818  TCGCCGTTCTGGCAAGGATGGGCAATTGGGCCAATTTTCAATTAATTGAAAAT         3877
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy  3909  TCGCCGTTCTGGCAAGGATGGGCAATTGGGCCAATTTTCAATTAATTGAAAAT         3968

Db  3878  AAATATTTTGAAACCGCAGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCCTTA       3937
          |||||||||||| ||  ||| |||||||||| |||||||||||| |||| |||||||||||
Qy  3969  AAATATTTTGAAAACGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTA       4028

Db  3938  GAAGATGTTCATTCGCTTACCCGATCGACCTGTCATGCGAGGATAATACTGTACTACACATGGACACAGG  3997
          |||||||||||| ||||||||| ||| | | | ||||| ||||||||||| |||||||||||||||||||
Qy  4029  GAAGATGTACATCTGCCACAAGACCCATACTGGCATATATTTATACATACAGATGGACACAGA         4088

Db  3998  ATATTTACCGTGATATTCTTTTGGAGATGTTGATCAAATGGTTGGCCCCGGGCTTTAAG      4057
          |||||| || | |||| ||||||| ||||| |   |||| |||  |  ||||  ||| | |
Qy  4089  ATATTTACCGTTATATTCTTTGGAAATGTTAATCAAGTGGTTGGTCGGTTATCAAGTGGTTAATCAAGTG 4148

Db  4058  GTTTACTTCACCAATGCCTGGTGTTGGTCGGATTGTCATGCTATCGGCTTATA        4117
              ||| || ||||||||||||||||||  |||||||||||||||||||||||
Qy  4149  GTGTACTTCACCAACGCGTGGTGTGTTCGGTATTGTCATGGTATCGGCTTATC        4208

Db  4118  AATTGGTTGCCGTTTGGTCGGGCTTAAATGATAGAGCCGTTAGATCAATGCCACA        4177
          |||||| |||||| || || || | ||||||||||||||  |||||||||||| |
Qy  4209  AACTTCGTTGCTTCACTGTTGGAGCGTGGTATTCAAGCCTTCAAGACTATGCGAACG       4268

Db  4178  CTGCCGCGCCCTAAGCCATTGGGTCGTGTCTCTAGATGGGAGGGTATGAAAGTTGTCGTG     4237
          | | ||| |||   |||||||| ||||||||||||||||||| |||||||||||||||||
Qy  4269  TTAAGAGCACTGAGACAGTATGGGGTGTTCTCTAGATGTCCTATGCGGGAAAATATTTTTT   4328

Db  4238  TGGCTTATTTTGCCATTATGGGGCTATACCGTCCATCTTCAAATGTGCTAATGTCCTTGATATT   4297
          ||||||||||| |||||| ||| ||||||||||||||||| ||||||||||||||||||
Qy  4329  AATCGGCTGGTTCAAGACTTTCGGCCATTATCCATGTCCATTGGTGTGTCTAATATTT         4388

Db  4298  TGGCTTATTTTGCCATTATGGGGCTATACCGTCCTTTTTGCTGGAAATATTTTAAGCTGTAAA     4357
          |||||||||||| |||  ||||| ||||||||| |||| |||||||| |||||  ||||| |||
Qy  4389  TGGCTAATTTTGCCATAATGGGGTGTACAGCTTTTTGCTGTGGAAATATTTTAAGTGCCGAG     4448

Db  4358  GATGGTAATGACACTGTCTGAGCCATGAAATCATTACCGAATCGTAATCGTAAGCCTGCAAAAGT 4417
          |  |||| |||||||| ||||||||||   || |||||||||||||||||||||| |||||| |
Qy  4449  GACAGCGACGACAAGGCTATCCGGGCATCACCACAAGTGGCAATGCCTGCGAGAGC         4508

Db  4418  GAAAACTACACCTCGGGAAAAATTCGGCAATGAACTTCGATCATGCGCAATAGCGTAATCTC     4477
          | |||||||||||  ||||  ||| | ||| |  | ||| |  ||| ||| ||  |||||||
Qy  4509  GAGAACTACACGTGGGTGAATTCAGCAGCAATGAATTCGATCATGCGGTAACGCGTATCTG     4568
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Qy  4509  GAGAACTACACGTGGGTGAATTCAGCAGCAATGAATTCGATCATGCGGTAACGCGTATCTG     4568
          | |||||||||    |||   ||||| ||||||
Db  4478  TGTCTATTCAAGTGGCACCTTTAAGGCTCTTGGATCCGGATTCCAGATTATGAACGATGCCATTGAT   4537
           |||| |||||||||||||  || ||||||||||||||||||||||||||||||||||| |
Qy  4569  TGCCCTTTCCAAGTGCCACTTTCAAGGCTGGATACAAATCATGACGATGCTATCGAT        4628

Db  4538  TCACGAGAGGTGGACAAGCAGCCGATCCGAGAAACCAATATCTACACGCATGATTATATTC       4597
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy  4629  TCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACACGATGATTATATTC       4688

Db  4598  GTATTCTTCATTATATTGGATCATTTTCACACTCGTCGTTCATTGGTGTTATCATT          4657
          |||| |||||||||||||||||| ||||||||||||||||||||||||||||||||
Qy  4689  GTATTCTTCATTATCATTGGATCCTTTTCACACTCGTCGTTCATTGGTGTTATCATT          4748

Db  4658  GATAATTTAATGAACAAAAGAAGAAAGCAGGTGATCATTAGAAATGTTCATGACAGAA         4717
          |||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Qy  4749  GATAATTTTAATGAGCAAAAGAAAAGCAGGTGGATCATTAGAAATGTTCATGACAGAA         4808

Db  4718  GATCAGAAAAAGTACTATAATGCTATGAAAAAAGATGGCCTAAAAAACCATTAAAAGCC        4777
          ||||||||||||||||||||||||||||| |||||||| | |||||||||||||||||||
Qy  4809  GATCAGAAAAAGTACTATAATGCTATGAATGAAAAAGATGGCTCAAAAAACCATTAAAAGCC      4868

Db  4778  ATTCCAAGACCGAGGTGGCGACCACAAGCAATAGTATTCGAAATAGTTACAGATAAAAAA       4837
          ||||||||||| ||||||||||||||||| |||| ||||||||||| || ||||||| ||
Qy  4869  ATTCCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAAATAGTAACCGATAAGAAA       4928

Db  4838  TTCGATATAATCATTATGTGTTCATTGGCTTAAACATGTTACCATGACCCTCGATCGG        4897
          || |||||||||| ||| ||||||||| ||||||||||||| ||||||||||||||||
Qy  4929  TTCGATATAATCATTATGTGTTCATTTGTGTCGAACATGTTCACCATGACCCTCGATCGT       4988

Db  4898  TACGACGCCTCCGAGGGTACAACAATGTCCTCGACAAACTCGACAAAACTCAATGGGATATTCGTAGTT 4957
          |||||||||| | | || ||||| |||| ||||||||||||| ||||||||| | |||||||||||||||
Qy  4989  TACGACGCTGCGGCACCGGTCTCGGACTATCCTGAGACTATCAATGGCGTATTCGTAGTT      5048

Db  4958  ATTTTCAGTGCGAATGTCTATTAAAAAATATTCGCTTACGATATCACTATTTCAAAGAG        5017
          ||||||||| || || ||| | |   |||||||||||| |||||||| ||||||||| |||
Qy  5049  ATTTTCAGTTCCGAATGTCTATTAATGAGTCTATTACGATATCACTATTTTATTGAG        5108

Db  5018  CCATGGAATTTATTTGATGTAGTACTGTGCATTTTATCCATCTTAGGTCTTGCTACTCAGC       5077
          |||| ||||| | || || ||| |||||||||||| ||||| |||||||||||| |||||||
Qy  5109  CCATGGAATTTATTTGATGTAGTAGTGTCATTTTATCCATCTTAGGTCTTCTGTACTTAGC      5168

Db  5078  GACAATCATTGAGAAGAGTATTCGTATCGCCGCACACTGCTCCCGTGTGTGGAGTGGCCAAA      5137
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Qy  5169  GATATTATCGAGAAGAGTACTTCGTCGTCGCCGCACCCTGCTCCCGAGTGGTGCGTGTGGCGAAA  5228

Db  5138  GTGGGTCGTGTCCTCGCGTTTAGTCAAGGGTATCCAAGGGTATCCGGACTTGCTGTTCGCG     5197
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Qy  5229  GTGGGCCGTGTCCTTCGACGGTGAAGGGAGCCAAGGGCCAAGGGAGCAGTCATTGCTGTTTATC   5288

Db  5198  TTAGCCATGTCGTTCGCTCCTGCCCGCTTAAATGATAGCCGTTAGATCAATCAATCGCCACA     5257
          ||||||||| ||||| |||||||||| || ||| |||||||||||||||||||||| ||| ||
Qy  5289  TTGGCCATGTCGTTCGCTCCTGCCCCGTGTTAAATCATCGTTCGTCCTGTCGTCTGTGCATGTTC     5348

Db  5258  ATCTTTGCTATCTTTGGCTTCCATCTTCAAGCATGTCATGTGGCAAAAGAGAGAGCGGCATAAAT  5317
          ||||||||| ||||| || || ||  || ||||||| |||||||||||| | || |||||||||
Qy  5349  ATCTTTGCCATTTTCGGCATTGTTCGTCGTGTACGACGCCATTATCAATGAAGAGCGGCATTAAC      5408

Db  5318  GCTTGTGTATAATTTTAAGACATTTGGTTGTCAGATGTGCTTAATGCCTGAATGTCGTGAATTGCTTACC  5377
          ||| |||  ||||||  |||||| |||||| |||||| |  |||| ||| ||| ||| ||| || ||||
Qy  5409  GACGTCTACAACTTCAAGAACCTTTGGTTGTGTTACTGTCGTCCATTATCAATGAGATGTTCAGATGTCGACG 5468

Db  5378  TGGCTTATTTTGCCATTATGGGGTACAGCAGCTATTGCTGCTTTTTTGCTGGAAATATTTTAAGCTGTAAA  5437
          ||||||  ||||| ||| || ||| || |||  || |||||| ||||||||||| |||||||  |||||||
Qy  5469  TCAGCCCGGTTGGGATGGTGGTGACTAGCTACTATTGCCATGGCCATTATCAATGAAGAGCGGCATTAAC     5528

Db  5438  GATGGTAATGACAACGACAAGGCTATCCGGGCAATCATTACCGAATCACGAGATCATCGCTACCGAG     5497
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Qy  5529  GACAGCGACAAAGGCTATCCGGGCATCATTGTTGTTCAGCGACCGGTTGGAATAACGTTTCTC        5588

Db  5498  GAAAACTACACCTCGGGAAAAATTCGGCAATGAACTTCGATCATGCGCAATAGCGTAATCTC     5557
          || ||||| | |  ||||| |||  ||||||| ||||| |||||||||||| | |  |||| |
Qy  5498  CTTCATATCTAGTTATAAGGCTTTTTGATAGTATTAATAATGTACATTCGTGTCATTCTC      5557
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Qy    5589  CTCTCATACCTAGTTATAAGCTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTC  5648
                  |||||||||||||||||| ||||| |||||||||||||||||||||||||||||| ||
Db    5558  GAGAACTATAGCCAGGCTACGGAGGATGTACACAGGAGGGTCTCACCGACGACGATTACGAT  5617
                  |||||| |||||| |||||||||||| |||||||||||||||||||||||||| ||||||
Qy    5649  GAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGAGGGTCTCAACCGACGACGACTACGAC  5708

Db    5618  ATGTACTACGAGATTGGCAACAATTCGATCCGAGAGGCACCCAGTACATAAGATACGAC     5677
                  ||||||| ||||| ||| ||| |||||||||||||||||||| |||||| || ||
Qy    5709  ATGTACTATGAGATCGGCAGCAGCAATTCGATCCGAGAGGCACCCAGTACATACCCTATGAT  5768

Db    5678  CAGCTGTCCGAGTTTCTGGACGTGCTGCTGGAGCCCGGCCGTGCCAGATCCGCCAAGCCGAACAAG  5737
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Qy    5769  CAGCTGTCCGAATTCCTGGACGTACTGGGGAGCCCCCCGCTGCAGATCCCACAAACCGAACAAG  5828

Db    5738  TACAAAATCATATCATGGACGATCGGGGACATGTCGGGGCAGATGAGTACTGTGTGAT     5797
                  ||||| |||| |||| ||| |||||| || | |||||||||||||| ||||||||||
Qy    5829  TACAAGATCATATCGATGGACAATACCCATCTGTCGCGGTGAGCCTCATGTACTGCGTCGAC  5888

Db    5798  ATATTGGATGCCCTGACCAAGGACTTCTTTGCCGCGTAATCCGAGGTAATCCGATCGAGGAGACG  5857
                  || ||| |||||||| || | |||||||||||||||||||| |||||||||||||||||||
Qy    5889  ATCCTCGACGCCCTTACGAAAGACTTCTTTGCCGCGGAAGGGCAATCCGATAGAGGAGACG  5948

Db    5858  GGTGAAATTGGTGAGATTGGCGGCGCCGGACACCGAGGGCTATGATCCGGTTCGTCG     5917
                  |||||||| |||||||| |||||||||||| |||||||| || |||||||||||||||
Qy    5949  GGTGAGATTGGTGAGATAGGGGCGCCCCCGCGATACGGAGGGCTACGAGCCCGTCTCATCA  6008

Db    5918  ACACTGTGGCCGCCAGCGTGAGGAGTACTGCGCCCAAGCTGACATACAGAATGCGTGCCG     5973
                  |||||||||||||||||||||||||||||||||||  ||| |||||||||||||||||||
Qy    6009  ACGCTGTGGGCGTGGGCGTGAGGAGTACTGCGCCCGCCCGCTAATCCAGCACCCCTGCGCG  6064
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RESULT  7
LOCUS        MDU38814      6315 bp    mRNA              INV      19-FEB-1997
DEFINITION   Musca domestica insecticide-resistant strain voltage-sensitive
             sodium channel mRNA, complete cds.
ACCESSION    U38814
NID          g1842213
KEYWORDS     .
SOURCE       house fly.
ORGANISM     Musca domestica
             Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;
             Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
             Muscomorpha; Muscoidea; Muscidae; Musca.
REFERENCE    1  (bases 1 to 6315)
AUTHORS      Knipple,D.C., Doyle,K.E., Marsella-Herrick,P.A. and Soderlund,D.M.
TITLE        Tight genetic linkage between the kdr insecticide resistance trait
             and a voltage-sensitive sodium channel gene in the house fly
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)
MEDLINE      94195766
REFERENCE    2  (bases 1 to 6315)
AUTHORS      Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
TITLE        Characterization of voltage-sensitive sodium channel gene coding
             sequences from insecticide-susceptible and knockdown-resistant
             house fly strains
JOURNAL      Insect Biochem. Mol. Biol. 26 (4), 319-326 (1996)
MEDLINE      96245434
REFERENCE    3  (bases 1 to 6315)
AUTHORS      Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
TITLE        Direct Submission
JOURNAL      Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York
             State Agricultural Experiment Station, Cornell University, Castle
             Street, Geneva, NY 14456, USA
REFERENCE    4  (bases 1 to 6315)
AUTHORS      Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.
TITLE        Direct Submission
JOURNAL      Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York
             State Agricultural Experiment Station, Cornell University, Castle
             Street, Geneva, NY 14456, USA
REMARK       Nucleotide and protein update by submitter
FEATURES             Location/Qualifiers
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                     /strain="Kdr"
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                     /note="insecticide-resistant reference strain"
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                     /chromosome="3"
     CDS             1..6315
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                     /product="voltage-sensitive sodium channel"
                     /db_xref="PID:g1842214"
                     /translation="MTEDSSDSIEEERSLRPFTRESLLQIEQRIAEHEKQKELERKR
                     AAEGEQIRYDDEDEDEGPQPDPTLEQGVIPVRMGSFPPELASPLEDIDPFYSNVL
                     TFVVISKGKDIFRFSASKAMWLLDPFNPIRRVAIYILVHPLFSLFIITTILTNCILMI
                     MPTTPTVESTEVIFTGIYTFESAVKVMARGFILCPFTYLRDAWNWLDFVVIALAVTM
                     GIDLGNLAALRTFRVLRALKTVAIVPGLKTVGAVESVKNLRDVIILTMFSLSVFAL
                     MGLQIYMGVLTQKCIKRFPLDGSWGNLTDENWFLHNSSNWFTENDGESYPVCGNVS
                     GAGQCEDYVCLQGFGPNPNYDYTSFDSFGWAFLSAFRLMTQDFWEDLYQHVLQAAGP
                     WHMLFFIVIIFLGSFYLVNLLLAIVAMSYDELQKKAEEEAEEEAIREAEEAAAAKA
                     AKLEERANVAAQAAQDAADAAAAAALHPEMAKSPTYSCISYELFVGGEKGNDDNNKEKM
                     SIRSVEVSESSVSVIQRQPAPTTAPAIKVRKVSTTSLSLPGSPFNLRRGSRSSHKYTI
                     RNGRGRFGIPGSDRKPLVLQTYQDAQHDIALEYILKGIEIFCWDCCWVLKFQEWVSF
                     SRHSSYTSHQSRISVTSHGDLLGWAAMGASTMTKESKLRSRNTRNQSIGAATNGGSS
                     TAGGGIPDANHKEQRDYEMGQDYTDEAGKIKHHDNPFIEPVQTQVVDMKDVMVLNDI
                     IEQAAGHSRASERGEDDDEDGPTFKDIALEYILKGIEIFCWDCCWVLKFQEWVSF
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                     GNSINHQDNRLEHELNHRGLSIQDDTASINSYGSHKNRPFKDESHKGSAETIEGEEK
                     RDVSKEDIGLDEELDEEAEGDEGQLDGDIIHAQNDEIIDDYPADCFPDSYYKKFPI
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                     PWNLFDVVVVILSILGLVLSDIIEKYVSPTILRVVRVAKVGRVLRVLKVKGAKGIRTLL
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                     LQIHKPNKYKIISMDMPICRGDMMYCVDILDALTKDFFARKGNPIEETGEIGEIAARP
                     DTEGYDPVSSTLWRQREEYCAKLIQNAWRRKYNGPPQEGDEGEAAGEDAEGGEGEG
                     GSGGGGDDDGSATAAGATSPTDPDAGEADGASAGNGGGPLSPGCVSGSSNGRQTAVL
                     VESDGFVTKNGHKVVIHSRSPSTSRTADV"
BASE COUNT   1711 a   1344 c   1595 g   1665 t
ORIGIN

Query Match          56.3%;  Score 3664;  DB 15;  Length 6315;
Best Local Similarity 84.88;  Pred. No. 0.00e+00;
Matches 4980;  Conservative     0; Mismatches 812;  Indels 84;  Gaps 21;
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Db     151  ATACGATATGATGACGAGGACGAAGATGAAGGTCCACAGCCGGATCCCACACTTGAACAG  210
                  |||||||||| ||||| |||||||||||| ||||||||||||||||||||||||||||
Qy     207  ATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGAACAG  266

Db     211  GGTGTGCCTATACCGTTCGAATGCAGGAGGCAGCTTCCCGGAATTGGCCTCCACTCCT   270
                  |||||||||||||||||||| |||||||||||||||||| |||||||||||||||||
Qy     267  GGTGTGCCAATACCGTTCGATTGCAGGAGGCAGCTTCCCGGGAATTGGCCTCCACTCCT  326

Db     271  CTCGAGGATATCGATCCCTTCTACAGTAATGTACTGACATTGTAGTAATAAGTAAAGGA  330
                  |||||||||||||||| ||||||||||||| |||||||||||||||||| |||||||
Qy     327  CTCGAGGATATCGATCCCTTACTACAGCAATGTACTGACAATTGTACATTCGTAAGCAAAGGA  386

Db     331  AAGGATATATTTTCGTTTTCTGCCTCAAAAGCAATGTGGCTGCTGCTCAAATCCAG  390
                  ||| |||||||||| ||||||||||| |||||||||||||||||||||| |||||
Qy     387  AAAGATATTTTTCGGCTTTTCGCATCAAAAGCAAATGTGGATGCTCGATCCATTCAATCCG  446

Db     391  ATACGTCGTGTAGCCATTATATTTTAGTGCATCCCCTTGTTTTCGTTATTCATTATCACC  450
                  |||||||||||||||||||||| || ||||||||||||||||||| ||||| ||||||||
Qy     447  ATACGTCGTGTGGCCATTTTACCATTCTAGTGCATCCATTACATTTCCCTATTTCATCATCACC  506

Db     451  ACTATTCTAACTAATTGTATTTTAATGATAATGCCGACAACGCCCACGGTCGAATCCACA  510
                  || |||| ||   |   ||  |  |||||||||| ||||||||||||||||||||||
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Left column (continued in right column):

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Qy   507 ACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCCACGGTTGAGTCCACT  566
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Db   511 GAGGTGATATTCACCGGAATCACACCGGAATCACCGGAATCAGCTGTTAAAGTGATGGCACGAGGT  570

Qy   567 GAGGTGAATTCACCGGAATCTTACGTATCTTAGAGATGCATGGAATTGGCTGACTTCGTAGTA  626
             ||||||||||||||| ||||||||||||||||||
Db   571 TTCATTTATGCCCGTTACGTATCTTAGAGATCTTAGAGATGCATGGAATTGGCTGACTTCGTAGTA  630

Qy   627 TTCATTTTTATGCCCGTTACGTATCTTAGAGATCATGGAATTGGCTGACTTCGTAGTA  686
             ||||||||| |||||||||||
Db   631 ATAGCTTTAGCTTATGTGACCATGGCATAGATTAGGTAATCTCGCAGCTTCGGACCTTTGAGAACA  690

Qy   687 ATAGCTTTAGCTTATGTGACCATGGCATAGATTAGGTAATCTCGCAGCTTCGGACCTTTGAGAACA  746
             |||||||||||| ||
Db   691 TTTAGGGTACTGCGAGCTCTGAAAACCGTAGCCATTGTGCCAGGTCTAAAAACCATTGTC  750

Qy   747 TTTAGGGTGCTGCGAGCGCTTAAAAACCGTAGCCATTGTGCCAGGCTTGAAGACCATCGTC  806
             |||||||||||||||| || |
Db   751 GGTGCTGTGTCATTGAATCTACGCGATGTGATAATTTGACAATGTTTTCC  810

Qy   807 GGCGCCGTCGAATCGGTGAAGAAATCGGTGATTATCCTGACCATGTTCTCC  866
             || ||||| ||||
Db   811 CTGTCGGTTGTTCGCCTGATGGGCCTACAAATCTATATGGTGTTCTAACACAAAAGTGC  870

Qy   867 CTGTCGGTTGTTCGCCGTTCGGGCCTACAGAATCTATATGGGCCTGCTCACCGGAGAAGTGC  926
             |||||||||| |||||||||||||||||||||||
Db   871 ATTAAACGATTCCCCCTGGACGGCAGTTGGGCCAATCTGACCGATGAAAAACTGTTTCTA  930

Qy   927 ATCAGAAGTTCCCGCTGGACCGGTTCCTGGGGCAATCTGACCGAGAACTGGGACTAT  986
             ||| || ||| |||||||||||||||
Db   931 CACAATAGCAAACAGTTCCAATTGGTTTACGGAGAACGATGGCCAGTCATATCCGGTGTGC  990

Qy   987 CACAATCGCGAATAGTCCAATTGGTATTCCGAGGACGAGGCATCCATTTCCGTTATCG  1046

Db   991 GGGAATGTATCCGGTGCGGACAATGCGGCGAAGATTACGTTCTGCCTGCAGGGGCTTCGGC  1050

Qy  1047 GGCAATATATCCGGTGCGGACGACGGATTACGTGTCTGCCGGACGGGGTTTGGT  1106

Db  1051 CCCAATCCCAACTACGACCCAGTTCGACTCATTCGGTTGGCTTCTGTCGGGG  1110

Qy  1107 CCGAATCCGAATTGCGGCCATGGTGCCATGTCGTTCGATTCGTTCGATGGGCTTCCGTGTCCGCC  1166

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Qy  1167 TTTCCGGCTGATGACGACAGGACTTCTGGGAGGGATCTGTAGCCTGTGTTGTACCAGCCGCC  1226

Db  1171 GGACCCTGGCACATGTTGTCTTTATAGTCATCATCATCTTCCTAGGTTCATTCTATCTTGTG  1230

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Qy  1287 AATTTGATTTGGCCCATGTTGGCCACTGCATGTCGTATGGACGAATTGCAAAAGGAAGGCCGAAGAA  1346

Db  1291 GAAGAGGCTGCCGAGGAGCCGGCGATCCGAGAAGCTGAAGAACGCAGCAGCCAAGGCG  1350

Qy  1347 GAAGAGGCTGCCGAGGAGCCGGCGTACGTGAAGGCTGCCGCCAAGAAGGCCGAAGAA  1406

Db  1351 GCCAAACTCGAGCTGAGGAGCGGCCAATGCGGCGGCCAGTCCAAGGCGCTCAGGATGCAGCAGAGCC  1410

Qy  1407 GCCAAGCTGGACGCGGCGGCCAATGCGCCAGGCGCTCAGGCAGCACGAGGATGCGCCGCC  1466

Db  1411 GCTGCGGCAGCTCTGCATCCGAGATGGCCATGTCGATTCCTTGCATTAGCTAT  1470

Qy  1467 GCTGCGGCAGCGCTGCACTGCATCCGAGAAATGGCCAGTCGTATTCTTGCATCAGCTAT  1526

Db  1471 GAACTGTTTGTTGGCCGAGTCGGTGAGTCGGATCGGTGAATCGCAATGAAGATGTCGATA  1530

Qy  1527 GAGCTGTATTTTGTTGGCCGAGTCGGTGAGTCGGATCGGTGCAACAACAAAGATGTCCATT  1586

Db  1531 CGCAGGCGTCGAAGTGGAAGTCGGTGAGTCGGATCGGTGAATCTGTATACAACAACCAGCACCTACC  1590

Qy  1587 CGGAGGCGTCGAGTCGGATCGGTGAGTCGGTGCGTTATACAACAAAGACAACCAGCACCTACC  1646
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Right column (continuation):

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Db  1591 ACAGCAC-CC--GCTACTAAAGTCCGTAAAGTTAGCACGACTTCCTTCTTTATCCTTACCTGGT  1647
             |||||||    |   ||||||||| |||||||||||  |||||||  |||||||||||||
Qy  1647 ACAGCACCACCAAGCTACCACAAAGTTCGTAAAGTGAGCACGACCACATCCTTATCCTTACCTGGT  1706

Db  1648 TCACCATTAACCTACGCCGGGATCACGTAGTTCACAGATCACACAGTTCACACAACATGAAATGGG  1707
             ||||||||||||  |||||||||||| |||| ||||  ||||||||
Qy  1707 TCACCGTTAACATACGCAGGGATCACGTAGTTCACAAGTACGTAGTTCACAAGTACGGAACGGA  1766

Db  1708 CGTTGGACGTTTTGTATACCAGGTAGCGATCGCCAAGCCATTGGTACTGCAAAACATATCAG  1767
             || ||| || |||||||||||  ||||| ||||||||||||||||  |
Qy  1767 CGTTGGCGCTTGGTATACCCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG  1826

Db  1768 GATGCCCAGCAGCGATGTTGCCCTATGCCGGATGACGACTCGGATGAATGCCGTAACACCAATGTCCGAA  1827
             ||||||||||||||||||| |||||||||| ||||| |||||||| |||| ||||||||||||||
Qy  1827 GATGCCCAGCACCAGCACTTGCCCTATGCCGACGACTCGGATGAATGCCGTCACCCGATGTCCGAA  1886

Db  1828 GAGAATGGTGCCATTATAGTACCAGCTACTATTGTAATTGTAATTGTAATTCTAGACATTCTTCA  1887
             ||||||||||| |||||||||| ||||||||| ||| ||||||||||||||||||||||
Qy  1887 GAGAATGGGGCCATCATAGTGCCCGTACTAGTGCAATCTAGGCTCCCGACACTCATCG  1946

Db  1888 TATACCTCGCATCAATCAAGAATCTCGTATACATCACATGGTGATTATTGGGTGGCATG  1947
             ||||||||||||| |||||||||||||||| || |||||||||||||||||||||
Qy  1947 TATACCTCCGATCAGTCCGGAATATCGTATACCTCACATGGCGATCTACTGGCGCATG  2006

Db  1948 GCGGCCATGGTGCCAGCACGCAGCACAAATTGCGCAGTGCCAGTCCAACAACACACGC  2007
             ||||||||||||||||||||  |||||||||  ||||||||||||||||||||||||||
Qy  2007 GCCGTCATGGGCGTCAGCAGCACAAATTGCGCAATTGCGCAACCGCAACAACACACGC  2066

Db  2008 AATCAATCAATCGGTGCTGCAACCAATGGTGTGCGCAGTAGTACGGGCCGTGGTGCTATCGC  2067
             ||||||||||| |||||   || ||||   ||   |   ||  |  |  |||| ||
Qy  2067 AATCAATCAGT-GG-GC-GCCACCAATGGCGCACCAC--CTGTC--TGGA--C-A--CC  2114

Db  2068 GATGCCAATCACAAGGAACAAAGGATTATGAAATGGTCAGGATTATACAGACGAAGCT  2127
             |||||||||||||| |||||||||||||||| |||||||||||||||||||
Qy  2115 AATCACAAGCTC---GATCATCGGCGACTACGAAATTGCCTGGAGTGCACGGACGCAGAAGCT  2171

Db  2128 GGCAAAATAAAAACACCGACAACATCCTTTTATCGAGCCCGTCCAAACTCAAACAGTGGTA  2187
             |||||| ||||| |||||||||| |||||||| |||||||||||||||||||||||||
Qy  2172 GGCAAGATTAAAACATCATGACAATCCTTTATCGAGCCCGTCCAGCACAACAAACGGTGGTT  2231

Db  2188 GACATGAAAGATGTATGGTCTTAAATGATATCATTGACAACAAGGCCGTCGGGCATAGT  2247
             ||    ||| || ||||| |||   |||  | || ||  |  ||||||| |||||
Qy  2232 GATATGAAAGATGTGATGGTCCTGAATGAACATCGACAACAAGGCCGTGGGTCGGCACAGT  2291

Db  2248 CGTGCTAGTGAACGAGGTG----------------AGGACGATGACGAAGAT  2283
             |||   ||| ||   |||                ||||||| |||| |||||
Qy  2292 CGGGCAAGCCGATCGCGGTGTCTCCGTTCTCCGTTTACTATTTCCAACAGAGGACGATGAGGAGGAT  2351

Db  2284 GGTCCCACATTCAAGGACATGGACGAAATCCGGAATATATCCGAGAATATATCGAAATCTTTGT  2343
             || |||||||| ||||||||||||  ||   |  |||||  |||||||||||||||||||
Qy  2352 GGGCCGACGTTCAAAGAACAACAAGGCACTCGAAGTGATCCTCGAAGTGATCGATGTGTTTTGT  2411

Db  2344 GTATGGACTGTTGTTGGGTGGTTAAAATTTCAGGAATGGTTCTCCTTTATTGTGTTC  2403
             ||  |||| ||||| ||||| |||   |||   ||||| ||| | ||||| ||| ||
Qy  2412 GTGTGGGACTGTTGTTGCTGGGTTTGGTTGAAATTCAGGAGTGGTTCAGGAGTATCGCTCATCGTCTTC  2471

Db  2404 GATCCATTCGTGGAGCTCTTCATTACCCGTGTATTGTGTGTTCAATGTTCATGGCC  2463
             |||||  || |||| |||||| || ||    ||   ||  ||    ||||||||||
Qy  2472 GATCCCTTCGTCGAGCTCTTCGAGCTGTCGCATCACGCGTGTCAACACGATGTTCATGGCA  2531

Db  2464 ATGGATCATCACGACGAATCCGGAATTGGAGAGAGTGCTGAAAAGTGTAACTATTC  2523
             ||| ||||||||||| |  |  ||||| ||  |||| ||||||||| |||| || ||
Qy  2532 ATGGATCACCACGATGAACAAGGACGTCGAAGTGATCGAAGTGATCCGCAGTATTC  2591

Db  2524 TTCACGGCCACTTTTGCAATTGAGGCCGCATGGAAGCTGATGGCTCCTTTATTGTGTTC  2583
             ||||| ||| ||||| |||| ||||| || ||||||  ||||| ||||  |||| ||||
Qy  2592 TTCAGCGCCACCTTTGCCATCGAGGCCCACCATGGCCATGGCCCCCAGTAC  2651

Db  2584 TACTTCCAGGAAGGCTGGAACATTTTCGATTCATTATTGTGGCCTTGTCCTATTGGAA  2643
             ||||||||||||| ||||||||||||||| |||| ||| |||||| ||||||| ||||
Qy  2652 TATTTCCAGGAGGGGCTGGAACATCTTCGACTTCATTAGTCGTGGCCCTATCGCTATTGGAA  2711
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Qy   2644 TTGGGCCTGGAGGGTGTCCAGGGCCTGTCTGGTCGTGTTGAGAAGTTTCCGTTTGCTTCGTGTA 2703
          |||| ||| ||||||||||||||| ||||  ||||| || | || | |||||||||||||||||
Db   2712 CTGGGACTCGAGGGTGTCCAGGGCTGTCTGTTCCTTCGCGTTCGTATTGCGTTCGATCGTGTA 2771

Qy   2704 TTCAAATTGGCAAAATCATGGCCCACACTGAATTACTCATTTCGATTCATTTCGATTCGGGTG 2763
          || ||||| || |||  |||  | |||||  |||| || ||  |||| ||| |||||||| |||
Db   2772 TTCAAACTGGCCACAGTGGCCCACACTTACTCATTTCATTTCGCATTACTCATTTCGATCGGGTG 2831

Qy   2764 ATGGGTGCATTGGGTAATCTGACACTTGTACTTTGCATTGCATTATCATCTTGCATCTTTGCCGTG 2823
          |||  | |||   |||  ||| |||  ||  |||  ||||  |||||||  | | || |||||||||
Db   2832 ATGGGCGCTTTGGGTAATCTGACATCTTGCATTGCATTATCATCTTGCATCTTTGCCGTG 2891

Qy   2824 ATGGAATGCAACTTTCCGGAAAGAACTATATTGCACCACAAGGATCGCTTCAAGGACCAT 2883
          |||  | |||||    |||| ||  |||||  || | |||   ||| ||||  ||||| ||
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Qy   2884 GAATTACCGCGCCTGGAATTCACCGACTTCATGCACAGCTTCATGATTGTTCCGAGTG 2943
          ||    | ||  ||| ||||||||| | |||| |||   || ||||| ||  | |||||
Db   2952 GACCTGCGCCCGCCTGGAACTTCACCGACTTCATGTATGTGTTCATGTATGTGTTCGGGGTG 3011
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Qy   4869  ATTCCAAGACCAAGGTGCCGACCACAAGCAATAGTCTTCTTGAAATAGTAACCGATAAGAAA  4928
           ||||||||||||||||||||||||||||||||||||||||||| ||| ||||| ||||||||
Dd   5905  ACACTGTGCGCCGCCAGCGTGCGTGAGGAGTACTCGCGCCAAGCTGATACAGAATGCTGGCG  5960
           || |||||| || ||||||||||||||||||||||||||||||||||| ||| |||| |||
Qy   6009  ACGCTGTGGCGTCAGCGTGCGTGAGGAGTACTGCGCCCGGCTAATCCAGCACGCCTGGCG   6064

RESULT     8
LOCUS      BGU73584       6096 bp     mRNA            INV       19-MAR-1997
DEFINITION Blattella germanica para sodium channel mRNA, complete cds.
ACCESSION  U73584
NID        g1657985
KEYWORDS   .
SOURCE     German cockroach.
  ORGANISM Blattella germanica
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
           Tracheata; Hexapoda; Insecta; Pterygota; Orthopteroidea; Blattaria;
           Blattodea; Blattellidae; Blattellinae; Blattella.
REFERENCE  1  (bases 1 to 6096)
  AUTHORS  Dong,K.
  TITLE    A single amino acid change in the para sodium channel protein is
           associated with knockdown-resistance (kdr) to pyrethroid
           insecticides in German cockroach
  JOURNAL  Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)
  MEDLINE  97218696
REFERENCE  2  (bases 1 to 6096)
  AUTHORS  Dong,K.
  TITLE    Direct Submission
  JOURNAL  Submitted (07-OCT-1996) Entomology, Michigan State University, East
           Lansing, MI 48824, USA
FEATURES             Location/Qualifiers
     source          1..6096
                     /organism="Blattella germanica"
                     /strain="Ectiban-R"
                     /note="pyrethroid insecticide-resistant strain"
                     /db_xref="taxon:6973"
     CDS             1..6096
                     /codon_start=1
                     /product="para sodium channel"
                     /db_xref="PID:g1657986"
                     /translation="MSDDSSSISEEERSLFRPFTRESLAAIEARIAEEYAKQELEKK
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                     FVVVSKGKDIFRFSATDAMWILDPFGNPIRRVAIYILVHPLFSLFITTILTNCIFMIM
                     PTTPTIESTEVIFTGIYTFESAVKVMARGFILQPFTYLRDAWNWLDFVVIALAYVTMG
                     IDLGNLAALRTFRVLRALKTVAIVPGLKTIVGAVIESVKNLRDVIILMFSLSVFALM
                     GLQIYMGVLTQKCIKNFPINGSWGELNDENWHAFCSNNTNWYFPEGAPEVPLCGNSSG
                     AGTCPPDYTCLQFGENPNYGYTSFDTFGWAFLSAFRLMTQDWENLYQLVLRSAGPW
                     HMLFFIVIFLGSFYLVNLILAIVAMSYDELQKKAEEEEAAEEEALREAEEAALAKEA
                     KKLRQADKLAAQELAAAQELAGANLAKSPSGSSSRSYELFINQKDGNNDNKREMSIR
                     SEGGDSISEHKGRVGANGTAIRKVSAASLSLPGSPFNHRRGSGSHHFTIRNGRGRFV
                     GPPGGDRKPLVLSTYLDAQEHLPYADDSNAVTPMSEENGAIVVPVYYASLGSRHSSYT
                     SHASRISYTSHGDLLGAGNKSQTKNQASRVNNPSQVPNSTPYMNASADSDGAV
                     KAKHTDNPFIEQMOQTTIVDMNDVMVLNDIIEQAGQQSRASEHGVSIYYFPTDEDDE
                     GPTVKEKVLAICMRGIDIFCVWDCCWLMLKFQEVALLVFDPFVELFITLCIVVNTLF
                     MALDHHDMNKDMDKALKSGNYFFTATFAIEATLKLIAMSPKYYYFQEGWNIFDFIVAL
                     SLELGLESGVQGLSVLRSFRLLRVFKLAKSWPTLNLLISIMGRTVGALGNLTFVLCII
                     IFIFAVMGMQLFGKNYEDNVERPPDGDMPRWNFTDFMHSFMIVFRVLCGEWIESWMDC
                     MLVGDWSCIPFFLATVVIGNFVVLNLFLALLLSNFGSSNLSAPTADNETNKIAGAFER
                     FSRFNWIKRSALNVAKMLRAKLTNQISDQTPAHERDTDLDLTADEILADGIYYRDK
                     KSPKEQTQLEVAIGDGMEFTIHGDLKNKLKKDKLMMNSTKVIGNSLNHKDNRIESGDY
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                     EGEGPLEEDMVLDAGTEDVMSEYPADCCPDHCYKRFPELAGDEDSPFWQGWGNLRLK
                     TFQLIENKFETAVITMILLSSLALALEDVHLPHRPIIQDILYMDRIFTVIFFIEML
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                     QSKQFSDVLDYLNMIFIVIFSSECLMKIFALRYHYFKEPWNLFDFVVVILSIGLVL
                     SDIIEKYFVSPTLLRVVRVAKVGRVLRLIVKGAKGIRTLLFALAMSLPALFNICLLLFL
                     VMEIFAIFGMSFMHVRDKGGLDDVYNFKTFGQSMILLFQMSTSAGWDGVLDGIMNEE
                     DCNKPNSEIGYPGDCGSATVGIAFLLSYLVISFLIVINMYIAVILENYSQATEDVQEG
                     LTDDYDMYYEIWQQFDPDGTQYIRYDQLSDFLDVLEPPLQINHPNKYKIVSMDIPIC
                     QY  5949  GGTGAGAGTTGGTGAGATAGCCGGCCCCCGGATACGGAGGGCTACGAGCGCCCGTCTCATCA  6008  KGDLMFCVDILDALTKDFFARKGNPIEESAELGEVQPGRPDEVGYEPVSSTLWRQREE
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                    YCARLIQNAWRKHKQQRQGAPGEDSDEAGDDPELQDRHQTAVLVESDGFVTKNGHRVV
                    IHSRSPSVTSRSTDV"

BASE COUNT     1615 a   1376 c   1531 g   1574 t
ORIGIN
Query Match      29.48%;  Score 1912;  DB 15;  Length 6096;
Best Local Similarity 71.28%;  Pred. No. 0.00e+00;
Matches  4180;  Conservative   0;  Mismatches 1578;  Indels 115;  Gaps 74;
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Db    151 CGTACGATGAGCAGGACGAAGAGATGAAGGCCCTCAGCCGGATGGCGACTCTGGAGCAAGGG 210
Qy    210 CGATATGATGACGAGCAGGATGAGGAAGGTCCACAACCGGATCCTACACTTGAACAGGGT   269

Db    211 GCGCCCATCCCTGCCGAATGCAAGGCCTTTTCCCTCCGAGCTCGCCTCTACCCCGCTC    270
Qy    270 GTGCCAATACCTGTTCGATTGCAGGGGAGCTTCCCGCGGAATTGGCCTCCACTCCTCTC   329

Db    271 GAGGACATGACGACCCCTTCTACCACCAGCAGGAACATTGTGGTGGTGAGCAAAGGAAAG  330
Qy    330 GAGGATATCGATCCCTACTACAGCAATGTACTGACATTCGTAGTTGTAAGCAAAGGAAAA  389

Db    331 GATATTTTCCGGTTCAGTGCGACAGATGCCATGTGATTTTGGACCCATTCAACCCGATT   390
Qy    390 GATATTTTTCGGCTTTTCTCGCAATCAAAAGCAATGTGGATGCTCAATCTCAATCCGATA  449

Db    391 CGACGGGTTGCCATCTACATTTTGGTTCACCCCTTGTTCTCACTCTTCATCATTACCACC  450
Qy    450 CGTCGTGTGGCCATTTACATTCTAGTGCATCCATTATTTCCCTATTCATCATCACCACA   509

Db    451 ATTTTAACCAACTGCCATCATGATCATGCCTACACACCCCACACAAGTCCACTGAA      510
Qy    510 ATTTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCACGGTTGAGTGGGAGAGGGTTC 569

Db    511 GTAATTTTACTGGCATCTACACACTCACACATTTGAATCGGCCGTTAAGGTGATGGCCGAGGGTTC 570
Qy    570 GTGATATTCACCGGAATCGAATCCACACATTTGAATCGATGGCACGAGGTTTC        629

Db    571 ATACTTCAGCCATTCACGTACCTTAGAGATGCATGGAACTGGCTGGACTTCGTAGTAATA  630
Qy    630 ATTTTATGCCCGTTTACGTTCATGGTATAGAGATGCATGGAATTGGCTGGACTTCGTAGTAATA 689

Db    631 GCTTTAGCTTACGTAACTATGGGATAGATCTAGGAAAACCTGGCCGCCCTTGCGAACGTTC 690
Qy    690 GCTTTAGCTTAGTATGTGACCATGGGTATAGATTTAGTAGTTAATCTAGCAGCCCTGCCGAACGTTT 749

Db    691 AGGGTGCTCCGAGCTTTGAAGACTGTGCGTATTGTGCCAGGTTTGAAGACCATTGTTGGC  750
Qy    750 AGGGTGTGGCCGGTGCTTAAAACCGTAGGCCATTGTGCCCAGGCTTGAAGACCATCGTCGGC 809

Db    751 GCTGTGATTGAATCTGTAAAGAACTGCGGCAATGCTCGCGGATGCAATCCTCACCATGTTC 810
Qy    810 GCCGTCATCGAATCGGTGAAGAAATCGCGGATGTGATTTACATGGGTATCCTCACCATGTTC 869

Db    811 TCCGTGTTTGCCTTAATGGGCTCCAGATTGTGTCCTCTCACGCAGAGTGCATC         870
Qy    870 TCGGTGTTTCGCGTTGATGGGCTCGATGGGCCGTACAGATCCCGAATAATGGGCTCTCACGGAAGTGCATC 929

Db    871 AAAAACTTCCCATAAATGTTCATGGGGGAATTGAATGAGAACTTGAGGCCATGCATTT    930
Qy    930 AAGAAGTTCCCGCGTGACGGGTCCTGGGCAATCGTCGACCGCGACGAACTGGGACTATCAC 989

Db    931 TGCAGTAACAACAGCTCCAATTGTATTTGTGTACTTTCCGGAAGGTCGCACCAGAGTTCCACTGTGTGGG 990
Qy    990 AATCGGCCAATAGCTCCAATTGTGTATCCATTTCCGTTATGCGGGC               1049

Db    991 AATTCATCAGGAGCTGTACATGTCCACCTGATTACACATGTCTCCCAGGGCTTTGGAGAA 1050
Qy   1050 AATCATCCGGTGCGGGGCAATGCCGACGACGATTACGTTGGTTGGCATTCCTTCCCAGGGGTTTGGTCCG 1109

Db   1051 AATCCCAACTAGGTTACACCAGTTTCGATACGTTTGGTTGGCATTCCTTGGGCTTCTCTCGGCCTTC   1110
Qy   1110 AATCCGAATTATGGCGTACACCAGCTTCGATTCGTTCGGATGGGCTTCGTTCCCGCCTTC  1169
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Db   1111 AGACTGATGACCCAGGATTATTGGGAGAACCTTTATCAGCTGGTTTGAGATCTGCTGGG   1170
Qy   1170 CGGCTGATGACACAGGACTTCTGGGAGGATCTGTTACCAGCTGGTGTTGCGCCGCCGGA    1229

Db   1171 CCCTGCCATATGCTGTCTTCATTGTCATCATCTCTTAGGCTCACTTCTATCTTGTGAAC   1230
Qy   1230 CCATGGCACATGCTGTCTGTCTTCTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTGAAT 1289

Db   1231 TTGATTTGGCCATTGTCGCCATGTCTACAGATGATGTTGGAGAAGAAAGCTGAGGAGGAA  1290
Qy   1290 TTGATTTGGCCATTGTGTCCATGTCTCGTATGACGAATTGCAAAGGAAGGCCGAAGAAGAA 1349

Db   1291 GAAGCAGCCGGAAGAAGAAGCGGTTGAGGGAGGCGGAAGAAGCAGCTCTTGCGAAAGAGGCG 1350
Qy   1350 GAGGCTGCCGGAAGACGGATACTGAAGCGGAAGAAGCTGCCGCGCCAAAGCGGCC        1409

Db   1351 AAAAAATTAAGACAAGCGGATAAAACTGGC--AG-CACAAGAATTAGCAGCAGCACAAGAA  1407
Qy   1410 AAGCTGGAGAGCGGAGAGGCAACAATGCGCAGGCTCAGCGCAGCACGCGGATGCGCCGCCGAA   1469

Db   1408 CTAGCTGCGCGAAATCTAGCAAAATCTCCCTCGG--GAAGT-TCGTCTCGT-AGTTATGAG  1464
Qy   1470 GAGGCTGCACTGCATCCCGAAAATGGCCAAGAGTCCGACGTATTCTTGCATCAGCTATGAG  1529

Db   1465 TTGTTTATAAATCAAAAGGACGGCAACAATGACACAAAAGGGAGAACATGAGACATCCGC  1524
Qy   1530 CTATTTGTTGGCGGCGAGAAGGCAACGATGCAGTCTTCACAAGTACACGATACGGAACGGACGT 1589

Db   1525 AGCGA---AGGCGG----GGACTCGATAAGGCA-ACACAAAGG-AAG-AGTGGGTGCAAAT 1575
Qy   1590 AGCGTCGAGGTGGAGTCGGTGAGCGTTATCAAAGACAACAGCAGCACTACCACA        1649

Db   1576 GGT-ACG--GCGATCA--G---G-AAGTGAGCGCGGCAAGTTGAGTCTACCAGGCTCA     1626
Qy   1650 GCACACCAAGCTACCACAAAGTTCGTAAAGTGAGCTGTCCTTATCCTTACCTGGTTCA    1709

Db   1627 CCTTTCAACCATCGCCGAGGTTCCCAGGTAGTCATCACTTTACAATTAGAAACGGACGT   1686
Qy   1710 CCGTTAACATACGCAGGGATCACGTAGTTCTCACAAGTACGATACGGAACGGACGT       1769

Db   1687 GGAAGGTTCGTGGCGCCACCTGTGGTGATCGAAAACCCCTAGTACTTTCTACGTACCTC   1746
Qy   1770 GGCCGCTT--ACCCGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG           1826

Db   1747 GATGCACAAGAACATCTTCCTTATGCAGATGACTCGAATGCAATGCAGTAACACCATGTGTCAGAG 1806
Qy   1827 GATGCCCCAGCCAGCACTTGCCCTATCCGCAAGTGCCGTCACCGGATGTCCGAA          1886

Db   1807 GAGAATGGAGCAATAGTTGTACCAGTTTATTACGCCAGGCCTCCTCCGGTTCCAGGCACTCATCC 1866
Qy   1887 GAGAATGGGGGCCATCATAGTGCCCGATATCCGAATATCGTAATCCACATGCCAGAGTCATCG 1946

Db   1867 TATACATCACACCGCATCCAGGATACCTCATGGGGAAGAGTGCATC                 1924
Qy   1947 TATACCTCCATCAGTCCGAATATCGTAATCGTTCACATGCCGGAGTCGGCGGCCATG      2006

Db   1925 GCAA-CAAAT-C-TCAGACCAA-GATCAATCA-A-C----TGCGAGTCGTTCAGTCGCGC  1974
Qy   2007 GCCGTCATGGGCGTCAGCAACGACCAAGGAGCAAATTGCCAACACGCAACACAGC       2066

Db   1975 AA-CAACCCTT------CAC--A-GGTG-C-CTAA-T-TCT--ACACCATAACAATGAATGC 2018
Qy   2067 AATCAATCAGTGGGCGCGCCAATGGCGGCCACCACCTGTCTGACACCACCAATCACAACAGCTC 2126

Db   2019 G-TCAGCA-GAC-A-GTGAT--GA-TGGAG----CGGT-GAAA---GCAA-AGCA--CA-   2059
Qy   2127 GATCATCGGCGACGACTACGAGGCCTGGGCAGAAGCTGGCACGGACGAAGCTGGCACGGACAAT 2186

Db   2060 C-TGACAATCCATTCATTGAACAAATGAACAAATGACACCGACAAATGGTGGTTGATGAATGATGTA 2118
Qy   2187 CATGACAATCCTTTTATCGAGCCCGTCTGGGCATTCCTTCCTCCGGGGTTTGGTCCG       2246

Db   2119 ATGGTGCTGAATGACATTATAGAACAAGCTGCTGGACGAGCAGCAGTAGGAGGAGCCAGTGAAACAT 2178
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Qy   2247  ...                                         ...  2306
Db   2179  ...                                         ...  2235
Qy   2307  ...                                         ...  2366
Db   2236  ...                                         ...  2295
Qy   2367  ...                                         ...  2426
Db   2296  ...                                         ...  2355
Qy   2427  ...                                         ...  2486
Db   2356  ...                                         ...  2415
Qy   2487  ...                                         ...  2546
Db   2416  ...                                         ...  2475
Qy   2547  ...                                         ...  2606
Db   2476  ...                                         ...  2535
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Db   2536  ...                                         ...  2595
Qy   2667  ...                                         ...  2726
Db   2596  ...                                         ...  2655
Qy   2727  ...                                         ...  2786
Db   2656  ...                                         ...  2715
Qy   2787  ...                                         ...  2846
Db   2716  ...                                         ...  2775
Qy   2847  ...                                         ...  2906
Db   2776  ...                                         ...  2835
Qy   2907  ...                                         ...  2966
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Qy   2967  ...                                         ...  3026
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Db   2956  ...                                         ...  3015
Qy   3087  ...                                         ...  3146
Db   3016  ...                                         ...  3075
Qy   3147  ...                                         ...  3206
Db   3076  ...                                         ...  3134
Qy   3207  ...                                         ...  3266
Db   3135  ...                                         ...  3193
Qy   3267  ...                                         ...  3325
Db   3194  ...                                         ...  3241

Qy   3326  GACCAACCAGATCAGTTGGATTTGGAGCGGAGAGAGCATGGTGACACGGAACTGGAGTCGGG  3385
Db   3242  ...                                                           3290
Qy   3386  CCACGACGAGATCCTCGCCGACGCGGAATGGAATCGATCAAGAGAGGGATCAAGAGCACGCAACT  3445
Db   3291  GGAGGTGGCGATAGGAGATGGAATGACATCCATGGAGTCTGAAAAACAAGCT  3350
Qy   3446  GGAGGTGGCCATCGGGGATCGGATGGAATTCACGATACACGCGACATGAGAACAACAA  3505
Db   3351  GAAGAAGGACAAGCTGATGATGAACAGCACGACGAAGGTGATCGGCAATTCTTTGAATCATAA  3410
Qy   3506  GCCGGAGAAATCCAAATATCCAAATAACGATGATTGGCAACTCAATTAACCACCA  3565
Db   3411  AGACAATCGGATAGA...  3464
Qy   3566  AGACAATAGACTGGAACACGAACCATAGAGGTTGTCCTTACAGGGTCACGGACAC  3625
Db   3465  TTTGAGCACAGGGTCATATGGAAGTCCATACAAGGATGACAGCGCCATAA  3524
Qy   3626  TGCCAGCATTAACTCATCATATGGTAGCCATAGAAGGACGAGCGCCACAA  3685
Db   3525  GGGAAGTGCGAGACTATGATGGAGGAGAAGATGCAAGCAAAGAAGAGATCTCGA  3584
Qy   3686  GGGCAGCGCCGAGACGATGGAAGCGCGAGGAGGCAAGCAAGAGGAGGATTTAGG  3745
Db   3585  TCAAGAGGAGGAGGTGAAGAAGATGGAGAGGTCTGAGGACCTCTGGAGGACGGACATGGT  3644
Qy   3746  TCTCGACGAGGAACTGGCAGCGATGCGAGGAGGGGCAATGCGACGGTGATAT  3805
Db   3645  ATTGGATGCAGGCACT...  3703
Qy   3806  CATT...ATTCACGACACGACGAGGATATACTTCAGCTGATGAATGGAAATCTGC  3864
Db   3704  ATCACTGCTATAAGCGCTTCCCTTCCTTCCTTCTCTTTCTGCCAAG  3763
Qy   3865  ATTCGTACTATAAGAGAAATTTCCGATCTTAGCCGTGACGATGACTCGCCGTTCTCGGCCAAG  3924
Db   3764  GCTGGGCAACCTCGACTGAAAACCTTCCAACTCATTGAGACAAATACTTTGAAACAG  3823
Qy   3925  GATGGGCAATTTAACGACTGAAAACTTTTCAATTAATTGAAAATAAAATATTTGAAACAG  3984
Db   3824  CTGTGATCACCATGATCCTGCTTAGCAGTCTCGCCACTGGGGATGTACATCTGC  3883
Qy   3985  CTGTTTATCACTATGATTTAATGAGTAGCTTAGCTTTGACATGAATCGACATCTGC  4044
Db   3884  CTCATCGACCAATTCTGCAGGACAATCTTATATACACTTCACTGTCATCT  3943
Qy   4045  CACAAAGCCCATACTGCAGGGGATATATTTATATAACTACTATATGGACATCTGC  4104
Db   3944  TCTTCATTGAGATGTGATCAAGTGGCTGGCCCTTCAAAAAATACTTCACAAATG  4003
Qy   4105  TCTTCTTGGAAATGTTAATCAAGTGCGTTGGCCGTTCCAAAGTGTACTTCACCAACG  4164
Db   4004  CTTGGTGCTGGTTGATTCATCATTGGTGTCATCATGGTATGCTGTTCGTGCTGTCTC  4063
Qy   4165  CGTGGTGTTGGCTCGATTTCGTGATTGCATGGTATCATCATGGTGTGTCTTCGTTGTCTCAC  4224
Db   4064  TGGTGGGCGGTTGGTGGTATTCATCATCAAGCCCTTAGGC  4123
Qy   4225  TTGTTGGAGCTGGTGGTATTCAAGACACTATCAAGAGCATTAAGAGCACTGAGAC  4284
Db   4124  CTCTTAGGGCTATGTCTATGTCTTAGAATGCAGGGATGCAGAGGGTGGTGAACGCTTTGGTGCAAG  4183
Qy   4285  CACTACGTGCCATGGGCATGAGGGTCGTCGTTAATGCGCTGGTACAAAG  4344
Db   4184  CCATCCCAGTATCTTCAATGTCTCCGTGTCATCTTCGCTCATCTTCTGGCTCATTTGCCA  4243
Qy   4345  CTATACCGTCCATCTTCAATGTCCTAATTTTCAATGTGTCTAATATTTTTGCCA  4404
Db   4244  TCAATGGTGTCGCTGTTTCTGCTGAAAATATCATAATGTGTGATTCCAACTCTACCA  4303
Qy   4405  TAATGGGTGTACAGCTTTTGCTGGTGAAAATATTTAAGTGCCGAGGACAATGGGCACGA  4464

```
4304 Db CTTTGAGCCACGAAATCATTCCTGACAGAAATGCTTGCATTGCTGACGAAAACTACACACATGGG 4363
         |||||| ||     |       ||         ||||| ||  ||||  ||  |||||||| ||||
4465 Qy AGCTCAGCCAGCGACAATCATCACCACATCCGAATCCGTGCTGCGAGAGCGAGAACTACACGTGGG 4524

4364 Db AGAACTCGGCCAATGAATTTGATCACGTCGGCAAAGCTTATCGCGTATCCTTCCAAGTGG 4423
         || || ||    |  |||| ||   ||   |  || || ||   ||||| |||||||||||
4525 Qy TGAATTCAGCAATGAATTTCGATCATGTTGGACGCATGCCTATAGACTCTAGAGAGTCCATA 4584

4424 Db CCACCTTCAAAGATGAGATTCAGATCAGTCATGACGCTATAGACTGCTATCAGAGCTCCATA 4483
         |||||||||||| |          |   |   ||  ||| ||||| || | ||  ||  ||
4585 Qy CCACCTTCAAAGCTGGATACAAATCATGAACGATGCCTATCCTTCTTGTGTCTTTTATCATCT 4644

4484 Db AGCAGCCAATCAGGGAAACGAACATCTACACATGTACCCTTCACTTGTGTCTTTTATCATCT 4543
         |||||| ||    || |  |||||||||  ||||  ||   | ||||||| |||||| |
4645 Qy AGCAACCAATTCGTGAAACGAACACATCACATGTATATTTCGTATTTTCGTATTCTCATCATAT 4704

4544 Db TTGGCTCATTTTCACTCTCAACCTATTCATTGTGTGATCATCGACAACTTTAATGAGC 4603
         || ||| ||||  |  |  | |  ||| ||||| |||| ||   | |||| |||||||
4705 Qy TTGGATCCTTTTGCACACTCAATCTGTTCATTGGTGTTTATCATTGATAATTTTAATGAGC 4764

4604 Db AAAGAAAAAGGCAGAGAGGTCGCTAGAGATGTTCATGACTGAAGATCAGAAGAAATACT 4663
         |||| |||||||||  ||||| | || | ||| || |   |  ||| ||  || ||||||
4765 Qy AAAAGAAAAAGCAGGTGGATCATTAGAAATGTTCATGACCAATCCTATAGAAGAGGCAAAGT 4824

4664 Db ACAATGCTATGAAGAAAATGGTTCGAAAAACCGTTAAAAGCCATCCCCAGGCCAAAGT 4723
         |  ||| |||||||   ||| | |  |||| || |||| ||| || |||||  ||||||
4825 Qy ATAATGTCATGAAAAGATGGGTCTCTAAAAAGCCATTCAAAGCCATTGAGTCCAAGAGT 4884

4724 Db GGAGACCCCAGGCCATTGTGTTGTGAAAATCTGCACAGACAAGAAATTTGACGATCATCA 4783
         ||   | ||  ||||| |  |  |||||||| | |   || ||||||| |||| ||||
4785 Qy TTGGATTCCTTTGCACACTCAATCTGTTCATTGGTGTTTATCATTGATAATTTTAATGAGC 4764

4724 Db GGAGACCCCAGGCCATTGTGTTGTGAAAATCTGCACAGACAAGAAATTTGACGATCATCA 4783
         ||  ||  | | ||  |||| ||||||||| | || ||| |||||||| ||  ||||||
4884 Qy ATAATGTCATGAAAAGATGGGTCTCTAAAAAGCCATTCAAAGCCATTGAGTCCAAGAGT 4884

4784 Db GGCGACCACAAGCAATCAGTCTTTGAAGAATAGTAACCGATAGAAATTCGATTATAATCATTA 4843
         |||| || |  | ||| |  ||| |||| | ||  |  |  | |  | ||| | ||  ||  |
4945 Qy GGCGAAGAAGAATATTGTGCGCGACTGATCAGCAGAATGCATGGGCCCAAGCCAAG 5916

4784 Db TGTTGTTCATTGGCTTTAACAGTTAACATGTAAACATGTTCACCATGACCCTCGAATCGTTACGAACATGCTGGACA 4843
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4945 Qy TGTTATTCATTGGTGTCTGAACATGTTGTTGCTGTTCACCATGACCCTCGGATCGTTACGAACATGCTGGACA 5004

4844 Db AGTTCAGCGACGTTCTTGATTACTTGACAGATGATCTTCATCGTCGTCATCTTCAGTTCCAGT 4903
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5005 Qy CGTATAACGCGGTCCTAGCATCTCAATGCGATATTCCAATTCGTAGTTATTTTCAGTTCCGAAT 5064

4904 Db GTCTGATGAAAGATATTGTCGCCCCCAGATACCACTACTCTTCAAGGAACCATGGAAGTCTTTG 4963
         | || ||| |||  | | | | |   ||| ||  |||| |  |  ||| ||| | |  |  |||
5065 Qy GTCTATTAAAAATATATTGTCGTTTACGGATATACTCAATTCATTTATTGTTGAAATTTTATTTG 5124

4964 Db ATTTCGTAGTGTCTCATCCTATCTATATTGGGTGCTGTATTGGTATGGTCTGAGTGAGTCAGCATCATTGAGAAAT 5023
         | ||||| |||||| |||  |||| |||| || ||||| ||||| |  | | ||  | | |  |||| |||||||||
5125 Qy ATGTAGTAGTTGTCATTATTCCATCTTAGGTCTTGGACTTGTTGTTTACGCTTAGGCGATTATTCGGATTATTCGAAGAGT 5184

5024 Db ACTTTGTGTCGCCTACACTGCTTCGAGTGGTGAGAGTGGTCGGGTGCGAAGGTGGCCGAGTCCTGC 5083
         |  ||| | | |  |||| || || | ||  |  ||| || | | |  |||| | ||  ||  | ||
5185 Qy ACTTCGTGTCGCCGACCCTGCTGCGTGTGGTGGCAAAGTGGGCGAAAGTGGGCCGTGTCCTTC 5244

5084 Db GTCGTGGTGAAAGTGCTAAGGGTATTCGGACATTGTGTTCCTTGGCTATGTCTTTGC 5143
         ||| | | ||||||  |   |  || | ||||| || || ||||| | |||||| |||
5245 Qy GACTGGTGAAGGTGGAGGCCAAGGGACCAAGTGTTGGCTTGGCCATGTCCTTGGGATG 5304

5144 Db CAGCGCTCTTCAATAATCGCCTACTACATGTTTATTGTCGATCATTGTGTAGTCATCCATCTTCG 5203
         | ||| ||||||    || || | ||||  ||  ||  | |  |||| | || || |||||  |||
5305 Qy CGGCCCTGTTCAACACTCTGCCCTGCTCCGTGTTGCCTGGGTGCTTGCCATTTTGCCATTTTCG 5364

5204 Db GCATGTCCTTCTTCATGCAGCGCACGTCCCGGATAAAGGTGGCCCTTGACGTGTACAATTTCA 5263
         ||||||||||||| |||||||||  || | | || ||||| | |  | | || || | |||||
5365 Qy GCATGTCGTTCTTCATGCAGCGCGCATTAACGACGTCTACAGCTTCACAACTTCA 5424

5264 Db AGAGCTTTGGGCAGTCCAGTCATGCCATGATGTCCCAGTTCAACATCACTAGTCTGCGGCCGATG 5323
         ||   ||| ||||| ||    || || ||  ||||| |||| | || |  || | |  ||||  |
5425 Qy AGAGCCTTTGGCCAGGCCATGGAATCGCAGGTCGACGTCAGCTCGGTTGGGATG 5484

5324 Db GTGTTTAGAATGGGATCCATGAATGAAGAGGACTGCAACAAACCAAAATAGGCCGAGATTGGCT 5383
         |||| || ||  ||  |||||  ||| |||| |||  ||| |     | |  |||| ||||| ||
5485 Qy GTGTACTGGACGCCCATTATCAATGGGAGCAGCATCCGATCCCACCCCGACGCAGCCGCAAAGGCT 5544
```

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5384 Db ACCCGGGAGACTGTGGATCAGCTACTGTCGCGGCATAGCTTTCTTGTGTGTCATACCTCGTCA 5443
         | |||||       ||| |  | |  |||| |  | | ||  ||| |  |||  |    |  ||
5545 Qy ATCCGGGCAATTGTGGTTCAGCCGACCCTGGTTCAGCGGAATAACGTTTCTCCCTCATACCTAGTTA 5604

5444 Db TCAGTTTCCTTATTGTTAATAACAGTGATCACGTTCATTAACATGTTGTACACGTTAAATGAGC 5503
         | ||||||  |  |||| || |  || ||   || ||    |  || || | || | |||||||
5605 Qy TAAGCTTTTGATAGTTATTATAACATGCTCATCTCGAGAACTCGTCATCTGTCATTTGAGTCAGG 5664

5504 Db CGACAGAGGATGTGCAGGAGGCTTGACGGATGATGACTACCGACGAGGTCGCAAGATCCACTAC 5563
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5665 Qy CCACCCGAGGACGTGCAAGAGGTCTCAACCGACGACGACTACGACGACTACATGAGATCT 5724

5564 Db GGCAGCAGTTGACCCAGATACGGACCAATATATTGCTCATGACCAGCGTGCTGGATTTCC 5623
         ||||| || || | |  | |   |||| |  | | ||    | ||| ||||||||| |||
5725 Qy GGCAGCAATTCGATCCCGAGGGGCACCCAGTTACACAAGGTACAAGATACCAGCTGTCGAATCC 5784

5624 Db TCGACGTGCTGAGAACCTCCGCTGCAGATACATACAAGTACGAACAGTAGTGTCGA 5683
         | | || |  || |  | || || |  |||  | ||||| |||| |||  ||| | |
5785 Qy TGGACGTACTGGAGCCCCCGCCGTGCAGATCGACAAAGTACAAGAATATCATATCGA 5844

5684 Db TGGACATTCGATCTGCAAGGGGACCTCAGTTCTCTGTGGGGACCATTTGGATGCTTTGA 5743
         |||| | || |  || ||||||  || || | | ||||||| || |  ||||| ||  |
5845 Qy TGGACATACCCATCCTGCAAGGGTGACCTCCATGTCATCCGACGCCCCCTTA 5904

5744 Db CGAAGGACTTCTTTGCAAGGAAAGCAATCCTATAGAAGAGAGTCTGCAGAGTTGGGTGAAG 5803
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5905 Qy CGAAAGACTTCTTTGCGCGCGGAAGGGCAATCCGGATAGCGATAGAAGGAGTGTGAGAT 5964

5804 Db TGCAACCAGGGCGGCCGGACGAAGTGGGCTATGGCCTGTGTCCTCTACGCTGTGGCGGC 5863
         ||  |||||||| | ||  ||| | || | || | |||||| ||| |  | || |||||
5965 Qy T---AGCGGCCCGCCGGATACCGGAGGGCTACGACGGCTGTGTCCTGTCTCATCAAGCCTGTGGCCTC 6021

5864 Db AGCGAGAAGAATATTGTGCGCGACTGATCAGCAGAATGCATGGGCCCAAGCCAAG 5916
         |||  ||||  |||||| | ||| || | |  | ||    | | |  ||||||||
6022 Qy AGCGTGAGGAGTACTGCCCGCCCCGGCTAATCCAGCCACGACGCGCCAAAGCACAAG 6074
```

RESULT  9

LOCUS       BGU73583     6096 bp    mRNA            INV       19-MAR-1997
DEFINITION  Blattella germanica para sodium channel mRNA, complete cds.
ACCESSION   U73583
NID         g1657983
KEYWORDS    .
SOURCE      German cockroach.
  ORGANISM  Blattella germanica
            Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;
            Tracheata; Hexapoda; Insecta; Pterygota; Orthopteroidea; Blattaria;
            Blattellidae; Blattellinae; Blattella.
REFERENCE   1  (bases 1 to 6096)
  AUTHORS   Dong,K.
  TITLE     A single amino acid change in the para sodium channel protein is
            associated with knockdown-resistance (kdr) to pyrethroid
            insecticides in German cockroach
  JOURNAL   Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)
  MEDLINE   97218696
REFERENCE   2  (bases 1 to 6096)
  AUTHORS   Dong,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1996) Entomology, Michigan State University, East
            Lansing, MI 48824, USA
FEATURES             Location/Qualifiers
     source          1..6096
                     /organism="Blattella germanica"
                     /strain="CSMA"
                     /note="insecticide-susceptible strain"
                     /db_xref="taxon:6973"
     CDS             1..6096
                     /codon_start=1
                     /product="para sodium channel"
                     /db_xref="PID:g1657984"
                     /translation="MSDDSSSISEEERSLRPFTRESLAAIEARIAEEYAKQKELEKK
                     RAEGEVRYDDEDEDGPQPDATLEQGAPIPVRMQGLFPPELASTPLEDIDPFYHNQRT
                     FVVSKGDIFRFSATDAMWLDPFNPIRRVAIYILVHPLFSLFIITTILTNCIFMIM"

Qy  690  GCTTTAGCTTATGTGACCATGGTATAGATTTAGGTAATCTAGCAGCCCTGCGAACGTTT  749
         ||||||||||  || |||| | || |  | |  |   ||| ||| ||||| ||||||||

Db  691  AGGGTGCTCGCAGCGTTGAGAGACTGTCGCTATTGTTCCAGGTTTGAAGACCATTGTGGC  750
         ||||| ||| |||||||| |||||||| | |||| ||||||||| ||||||| |||||||

Qy  750  AGGGTGCTGCGAGCCGCTTAAAACCGTAGCCATTGTGCCAGCTTGAAGACCATCGTCGGC  809
         |||||||| ||||| | ||||| |||| ||||||| | ||||||||||||||| || |||

Db  751  GCTGTGATTGAATCTGTAAAGAACCTGCGCGATGTGATAATCCTCACCATGTTCTCGCTC  810
         || ||| |||||||| ||| || | || |||||||| ||||||||||||||||| || ||

Qy  810  GCCGTCATCGAATCGGTGAAGAATCTGCCGCGATGTGATAATCCTGACCATGTTCTCCCTG  869
         ||||| |||||||| |||||| ||||| ||||||||| ||||||||| ||||||||| |||

Db  811  TCCGTGTTTGCCTAATGGGGCTCCAGATTTACATGGTGTCCTCACGCAGAAGTGCATC  870
         |||||||| || || ||||| ||||||||||| ||| |||| || ||||||||||||

Qy  870  TCCGTGTTCGCGTTGATGGGCCTACAGATCTATATGGGCGTGCTCACCGAGAAGTGCATC  929
         |||||||| ||| || |||| || ||| | || ||||| || || || |||||||||||

Db  871  AAAAACTTCCCATAAATGGTTCATGGGGGAATTGAATGATGGGAACTGGCATGCATTT  930
         |||| |||||| ||||| ||| |||| | | || ||| | ||| ||| ||||| |||

Qy  930  AAGAAGTTCCCGCTGACGGTTCCTGGGGCAATCTGACCGACGAGAACTGGGACTATCAC  989
         || |||||||| ||| ||| ||||||| || || |||| | || |||||| |||| ||

Db  931  TGCAGTAACACACGAACTGGTACTTTCCGGAAGTGCACCAGAAGTTCCACTGTGTGGG  990
         || || |||| || |||| |||| ||||| || | ||||||||||| ||||| ||

Qy  990  AATCGCCAATAGCTCCAATTGGTATTCCGAGGACGAGGGCATCTCATTTCCGTTATGCGGC  1049
         ||| || |||||||||||||| | || ||||| ||| ||||| || ||||| | |||||

Db  991  AATTCATCAGGAGCTGTACATGTCCACCTGATTACACATGTCTCCAGGGCTTTGGAGAA  1050
         ||| ||||||||||| |||||| || ||| |||| ||| ||| |||| |||| |||||

Qy  1050  AATATATCCGTGCGGGCAATGCGACGATTACGTGTCCTGCCTGCAGGGGTTTGGTCCG  1109
          |||| | ||||| ||||||| | |||| ||| || ||| ||||||||| |||| ||

Db  1051  AATCCCAACTATGGTTACACCAGTTCGATACGTTTGGTTGGGCATTCCTCCTGTCCGGCCTTC  1110
          ||| |||| ||| || |||||| |||| ||||| ||| ||||| |||| |||||||||

Qy  1110  AATCCGAATTATGGCTACACCAGCTTCGATTCGGTGGATGGGCTTTCCTCGTCCGGCCTTC  1169
          |||| ||| ||||| || |||||| | || ||| || |||||| |||| |||||||||

Db  1111  AGACTGATGACGACCAGGATTATTGGGAGAACCTTTATCAGCTGGTTTGAGATCTGCTGGG  1170
          ||| ||||| | || |||| | |  ||||||| |||||||||| ||| || |||| |||

Qy  1170  CGGCTGATGACGACCAGGATCCGTACCAGCTGGTGTTGCGCCGCCATCCTCGTGGG  1229
          ||||||||| ||||||||| ||| |||||||||| ||| | ||| || | |||||

Db  1171  CCCTGCGCATAGTCGTCTGTTCTTCATTGTCAATCGTTCTTAGGCTCATCCTATCTTGTGAAC  1230
          || ||| ||| |||| |||||||| || | ||| ||||| || |||| ||| |||||||||

Qy  1230  CCATGGCACATGCCATGTGGTCGTTCTTTATAGTCATCATCTTCCTAGGTTCATTCTATCTTGTGAAT  1289
          || |||| ||||| ||||| | || |||| || |||||||| |||| ||| |||| |||||||||

Db  1231  TTGATTTTGGCCATTGCTGCCCATGTCCTACGGATGAGTTCCACGATGAGTTGCAGAAAAGTGAGGAGGAA  1290
          |||||||||||| ||| || ||| || || ||| || || || ||| || | |||| ||||| || |||

Qy  1290  TTGATTTTGGCCATTGTTGCCCATGTGTCATCGTATGCCATGTCGTATGACGAATTGCAAAGGAGGCCGAAGAAGAAGA  1349
          ||||||||||||||| ||||||||| || ||| | |  ||  ||| || | || || || || || |||

Db  1291  GAAGCAGGCGGAAGAAGCGGTTGAGGAGAAGCGGAGCAGCTGGTTGGAAGAGGGCG  1350
          ||||||||||||||||||| || ||||| || || |||||||| |||||| || ||

Qy  1350  GAGGCTGCCGAAGAAGCGGATACGTGAAGCGGAAGAAGCTGCGCGCGGCCAAAGCCGGC  1409
          || || ||||||||||| | | | ||| || || ||||| || ||| || |||| ||

Db  1351  AAAAAATTAAGACAAGCGGATAAACTGGC--AG-CACAAGAATTAGCAGCAGCACAAGAA  1407
          |   ||| || ||| |||| || ||||    || |||||| | |||| || |||||||

Qy  1410  AAGCTGGAGGAGCGGCGGCCAATGCCGCAGGCTCAGGCAGCGATGCGGCTGCGCCGCCGAA  1469
          ||||| ||||| ||| || ||||| ||| || ||||| | ||| ||| |||| ||||||

Db  1408  CTAGCTGGCGCAAAATCTAGCAAAATCTCCCTCGG-GAAGT-TCGTCTCGT-AGTTATGAG  1464
          || ||| || ||| | |||| |||| |||| ||| ||| |   | |  || |||||||||

Qy  1470  GAGGCTGCACTGCATCCGGAAATGGCCAAGAGTCCCAAGAGTGGCCACGTTATTCAGCTATGAG  1529
          |||| ||| || || ||| | | ||| ||||| |  |||||  | || ||| ||| |||||||

Db  1465  TTGTTTTATAAATCAAAAGGACGACAATAATGACAACAAAGGAGAACATGAGCATCCGC  1524
          |  |||||   || |||  ||  ||| || |||| |||||| || | || ||||| ||

Qy  1530  CTATTTGTTGGCGGCGGAGAGGGCCAACGATGACAACAAAGAGAAGAATGTCCATTCGG  1589
          || |||||||| ||| |||||| |||||| |||| |||||| |  || || ||||| ||

Db  1525  AGCGA----AGGCGG-----GGACTCGATAAGGCA-ACACAAGG-AAG-AGTGGTGCAAAT  1575
          |||||    |||| |     |  ||  || | ||  |||| || ||| ||| || ||||

Qy  1590  AGCGTCGAGGTGGAGTCGGAGTCGGAGCTCGGTGAGCGTTATCAAAGACAACCAGCTACCACA  1649
          |||| ||||| ||| ||||| || || || || ||| ||| | ||| ||||| ||| ||||

Db  1576  GGT-ACG--GCGATCA--G---G-AAGGTGAGCGGCGGCAAGTTGAGTGTTCTACCAGGCTCA  1626
          ||| ||   ||||||   |    | ||| || ||||| ||| || ||||| ||| |||| ||

Qy  1650  GCACACCAGGTACCACAAAGTTCGTAAAGTGACGCACACCATCCTTAACCTTACCTGGTTCA  1709
          || |||| || ||||| |||| || ||| ||| ||||| || || |||| |||| ||| ||

Db  1627  CCTTTCAACCATCGCCGAGGTTCCAAGGTTCATCACTTTACAATTAGAAACCGGACGT  1686
          || ||||| ||| |||| ||||||||| ||||| ||| ||| |||| ||| ||||||

Qy  1710  CCGTTTAACATACGCAGGGGATCCATGGCTCGGACTTGCTGACTTCGTAGTAATA  1769
          || |||||| || ||| || ||||| ||| || |||| | || |||||| ||||

Db  1687  GGAAGGTTCGTGCGGCCACCTGGTGTGATCGAAAAACCCCTAGTACTTTCTACGTACCTC  1746
          || | || ||| ||||| |||| || | ||||| ||| |  ||  |   ||| || ||

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PTTPTIESEVIFTGIYTFESAVKVMARGFILQPFTYLRDANWLDFVVIALAYVTMG
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IHSRSPSVTVSRSTDV"

BASE     1615  a    1374  c    1532  g    1575  t
COUNT
ORIGIN

Query Match      29.3%;   Score 1910;  DB 15;  Length 6096;
Best Local Similarity 71.2%;  Pred. No. 0.00e+00;
Matches  4179;  Conservative  0;  Mismatches 1579;  Indels 115;  Gaps  74;

Db  151  CGTACGAGCGATGACGAGGAAGAGATGAAGAAGAGCCCTCAGCCGGATGCGACCTCGGAGCGACCAAGGG  210
         || |||||| || |||| ||||||||||||||||||| ||||  | |||| ||||| ||||||| |||

Qy  210  CGATATGAGTGACGAGGAGGAGGAGATGAAGAATGAAGGTCGTATGCCATGTCGTATGACGAATTGCAAAGGAGGAAGAA  269
         || || ||| || |||| ||||| |||||||| ||| |  ||| |||| || ||||| ||||| | ||

Db  211  GCGCCCCATCCGTCGCAAATGCAAGCCCTTTTCCCCGAGCTCGCCCTCTACCCCGCTC  270
         | ||| |||||| || ||||| ||| ||| || |||||| ||| ||| | || ||||

Qy  270  GTGCCAATACCGTTCGAATTGCAGGGCAGCTTCCCGGCCAGCTTCCCACTCCTCTC  329
         || ||||| |||| ||||||||||| ||||||||| || ||| |||  || || ||

Db  271  GAGGACATGACCCCTCTACCACCAGAGAACCATTGTGGTGGTGAGCAAAGGAAAG  330
         |||||| ||| ||| ||| |||||| |||| ||||||| ||||||||||||||

Qy  330  GAGGATGATCGATCCCTACTACAGCCATGTACTGACATTGCTGTAGTTGTAAGCAAAGGAAAA  389
         ||||| || | || ||| || |||| ||| |||| ||||||| | ||| ||||||||||

Db  331  GATATTTCCGGTTCGCATTGCCATCGATTTGAATCGGCCGTTAAGGTCGATGGCGAGGGGTTC  390
         |||||||| |||| ||||| |||| || || || ||||||||| |||| |||||| |||||

Qy  390  GATATTTTTCCGGTTTCGCTTTGCTGCCATCACACATTTGAATCGTTCGATGGCAGGAGGTTTC  449
         |||||||| |||| ||| ||||| |||| ||| || || || || ||||| ||||||| |||

Db  391  CGACGGGTTGCCATCGATGCAGGGATTACATTTTGGTTCACCCCGTGTTCTTCACCATTACCACC  450
         ||| ||||| ||||| ||||| | || ||||||||||| |||| | |||| |||||| |||||

Qy  450  GTGCGTGTGCCAATACCGTTCGATTGCAGGGCAGCTTCCCGGCGAATTGGCCTCCACTCCTCTC  509
         || ||| ||||| |||| || |||||||| ||||||||| |||| || ||||| ||| || ||

Db  451  ATTTAACAACTGGCCATCTCATGATCAACGCTACCAACCCACAATAGAGTCCACTGAA  510
         ||| ||||| || |||| || || ||| || || ||||| ||| |||| ||||||||

Qy  510  ATTCTCGTCAACTGACCATGATAATGCCGACAACGGCCCACGGTTGAGTCCACTGAG  569
         ||| || |||| ||||||| | ||| ||| || ||||| || ||||||||||||||

Db  511  GTAATTTTACTGGCATCTACACATTTGAATCGGCCGTTAAGGTCGATGGCGAGGGGTTC  570
         || |||| || ||||| | ||||| | ||| ||||||| ||| || ||||||||||||

Qy  570  GTGATTATTCACCGGAATCTACACACATTTGAATCGATGGCGTTAAAGTGATGGCGACGAGGTTTC  629
         || || || ||| ||||| |||| || || ||||| || ||||| ||| |||||| || ||||

Db  571  ATACTTCAGGCATTCACGTTAGGATGATCATGGAACTGGCTGGACTTCGTAGTAATA  630
         || ||||||||||| ||||| ||||| ||  || || |||| || |||||| ||||

Qy  630  ATTTTATGCCCGTTTACGTTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTAGTAATA  689
         || ||| |||||||||| ||| || || ||||| ||||||||| ||||| |||||| ||||

Db  631  GCTTTAGCTTATGTGACCATGGGGATAGATCTAGGAAACCTGGCCGCCCTTGCGAAACGTTC  690
         ||||||||| ||  |||| ||| |||||| |||| || ||||| || ||| ||||| |||||

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Qy  1770  GGCCGCTT--TGGTAT-ACCCGGTAGGCGATCGTAAGCCATTGGTATTGTCAACATATCAG  1826
Db  1747  GATGCACAAGAACATCTTCCTTATGCAGATGACTCGAATGCAGTCAGTAACACCTATGTCAGAG  1806

Qy  1827  GATGCCCAGCAGCACTTGCCCTATGCCGACGACTCGAATGCGTCACCCGATGTCCGAA  1886
Db  1807  GAGAATGGAGCAACATAGTTGTACCAGTTTATTACGGCCAGCCTCGGTTCCAGGCACTCATCC  1866

Qy  1887  GAGAATGGGGCCATCATAGTCCCCGTGTACTATGGCAATCTAGGCTCCGACACTCATCG  1946
Db  1867  TATACATCACACGGCATCCAGGATATCCTACACGTCTCATGGGGACCTCCTGGGTG-CA-G  1924

Qy  1947  TATACCTCCGATCAGTCCCGAATATCGTATACCTCACATGGCTATCGGCGGCGCCATG  2006
Db  1925  GCAA-CAAAT-C-TCAGACCAA-GATCAATCA-T-T--TGGCGAGCTCGTTCAGTGCGC  1974

Qy  2007  GCCGTGCATGGCGTCAGCAATGGCGGCCAATGCCGCACCACGCCAACACGC  2066
Db  1975  AA-CAACCCTT-----CAC--A-GGTG-C-CTAA-T-TCT--ACACCATACATGAATGC  2018

Qy  2067  AATCAATCAGTGGGGCCACCCAATGGCGGGCACCACCTGTCTCGGACCACCAATCACAAGCTC  2126
Db  2019  G-TCAGCA-GAC-A-GTGAT--GA-TGGAG-----CGGT-GAAA---GCAA-AGCA--CA-  2059

Qy  2127  GATCATCGCGACTACAGTCCCGTGACTACTGGCACGGACACCAAACGTGGTTGATATGAAGATGTG  2186
Db  2060  C-TGACAAATCCATTCATTGAACAAATGCAGCAAACTCTCTGGACAGCAGAGTCAGTGAACAT  2118

Qy  2187  CATGACAATCCTTTATCGAGCCCGTCCAGACACAAACGTGGTTGATATGAAGATGTG  2246
Db  2119  ATGGTGCTGAATGACATTCCGACTCTGGACAGCAGTCAGTAGAGCCAGTGAACAT  2178

Qy  2247  ATGGTCCTGAATGACATCATCGAACAGCGCGGGCCGCTGGGCACAGTCGGCCAAGGCATCGC  2306
Db  2179  GGAGTCCATCCATCTATTATTTCCCGACAGAGAAGTGACGAGGGTCCAAC-A-GTT-AAA  2235

Qy  2307  GGTGTCCGTTTACTATTCCCACAGAGGACGATGGGCCTGATGACGAGGACGTTCAAA  2366
Db  2236  GAGAAGGTGTTAGCTATATGCGGAGTCTCAAGGCATCGGATTGTTGC  2295

Qy  2367  GACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATTCGTGTTTGTGTGGGACTGTTGC  2426
Db  2296  TGGCTCTGGCTCAAGTTCAGGATGCCGTCATCTGGTTGGCCCTCGACCACCACGAC  2355

Qy  2427  TGGGTTTGGTTGGTTGAAATTTCAGGAGTGGTATCGGTCTCATCCGTTCGTCGCGAG  2486
Db  2356  TTGTTCATCATCCTTTGCATTGTGTCTCAATACACTGTTCATGGCCCTCGACCACCACGAC  2415

Qy  2487  CTCTTCATCACGCTGTGCATGTCTGCTCAACACGATGTTCAACACGATCACCACGAT  2546
Db  2416  ATGAATAAAGACATGGATAAGGCTCTCAAGAGTGGTCAATACACTCTTCTTCACAGCGACCTTT  2475

Qy  2547  TGGGTTTGGTTGGTTGAAATTTCAGGAGTGGTATCGGTCTCAAGGCATCTTCACAGCGACCTTT  2606
Db  2476  GCCATTGAGGCGACGCTCAAGTTGATAGCAATGAGCCCTAAGTACTACTATTTCCAGGAAGGA  2535

Qy  2607  GCCATCGAGGCGACGCCACCATGAACGTCAATGCCCTATCCAGCCCAAGTACTATTTCCAGGAGGGC  2666
Db  2536  TGGAACATTTGATTCATCATTGTTGCACTTCCTTCTGGCTGGAAGGTGGTCTTGGAAGGT  2595

Qy  2667  TGGAACATCTTCGACTTCGTGCTGCTGCGATCGTATTGCGTTATTGCGTTATCGCCTATGCGGGGT  2726
Db  2596  GTCCAAGGTCTGTCGCTGCGTTCCTTTCGTTCCGTTATCGGTATTCAAACTGGCCAAG  2655

Qy  2727  GTCCAGGGTCTGCCGAGCTGAATCGTGTGGTCGGTATTGCGTGCTGTCTATTCAAACTGGTGCTCTGGGT  2786
Db  2656  TCTTGGGCCGAGCCTGAATCTCCATCAGCATTCCATTTCATTTCGATTATATGAATGGCGTGTATGGACG  2715

Qy  2787  TCTTGGGCCCACCACTTAATTTACTTCGATTTCATTTTCATTTTCAATTACTTGCTTTTGTGCTTTGTCTTT  2846
Db  2716  AACCTGACTTTGTGCTTTGTACTTTGTATTATCATTGCCTTTGCTTTGCGTTTTGCATTGGGAATGGCAACTC  2775

Qy  2847  AATCTGACATTTGTACTTTGTACTTATCATCTTTCGATTGGAATGGCAACTG  2906
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Qy  2776  TTTGGCAAAAAAATTATTATGATAATGTTGAACGTTCCCTGACGGGGATATGCCGAGATGG  2835
Db  2907  TTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGATGGCGACCTGCCGCGGGGACTGG  2966

Qy  2836  AACTTTACGGACTTCATGCACTCATTCGATGATGTGTTCCGAGTGTGTTGCGGGGAGTGG  2895
Db  2967  AACTTCACCGACTTCATGCACAGCTTCCACGATCGCGTTTCCGGGTGTCTGCCGGAGAATGG  3026

Qy  2896  ATAGAGTCTATGTGGATTGTATGCTGTGTTGGAGACTGGTCCTGCATCCCGTTCTTCTTG  2955
Db  3027  ATCGAGTCCGATGTCCATGTGGGACTGCGATGTCTCCGTGCCATTCCCTTGCTGCTCAAGC  3086

Qy  2956  GCCACTGTCGTCATTGGAAACTTGGTTGTTGTTGGTACTTAACCTTTTCTTAGCCTTGCTTTTGTCC  3015
Db  3087  GCCACCCGTTGTCATCGGCAATCTTGTGGTACTTAACCTTTTCTTAGCGCAATGAAAACAAAATAGCC  3146

Qy  3016  AACTTTGGTTCATCCAATCGTGTCAGCCCCAACAGCTGACAATGAAACCTGACAATAAAATGCT  3075
Db  3147  AATTTTGGCTCATCTAGCTTATCAGCGCCGATTTAAAGTTGGGTTAAGCTAATATTGCTGATTGT  3206

Qy  3076  GAGGCATTTGAGCGTTCTCACGATTCTTAACTGGATAAAACGTAGCGC-GCTAAACGT  3134
Db  3207  GAGGCCTTCAATGAAATTGGCCAAATTAACCAATCCGATTCAGATATCCGATCAGACGCCGATGCGAG  3266

Qy  3135  GGCAAAAAATGTTGCGTCGCGCAAATTAACCAATCAGCAGAGCTGGCAACAAGTGTA  3193
Db  3267  TTCAAGT-TAATACGTAACAAATTGACAAATCAAATAAGTGATCAACCATCAGGTGCAAG  3325

Qy  3194  -ATGAGCGTGA-CAC--GGACCTTGACCTCACAGCG-GATGAAATC--CTGGC-C---G  3241
Db  3326  GACCAACCAGTCAGTTGGATTTGGAGCGCGAAGACCATGGTGCAACGAACTGGACTGGGG  3385

Qy  3242  --ATG--GA-ATCGT-GTATAGAG----A-CAAGAAGAGTCCAAAGGAGCAGACGCAGTT  3290
Db  3386  CCACGACGAGATCCTCGCCGACGGCCTCATCAAGAAGGGGATCAAGGAGCAGCAGCAACT  3445

Qy  3291  GGAGGTGGGGATAGGAGATGGGAATGACCGTGATCGGCAATCTTGAAAAAACAAGCT  3350
Db  3446  GGAGGTGGGCCATCGGGATCGGATGGAATTCACGACACGGCGACACTGGCAACTCAATTAACCACCA  3505

Qy  3351  GAAGAAGGACAAGCTGATGATGAACAGCACGAAGTGATCGGATCGGCAATTCTTGAATCATAA  3410
Db  3506  GCCGAAGAAATCCAAATATCTAAAATAACCATAGAGGTTTGTCCTTACACGACGACGACACACAA  3565

Qy  3411  AGACAATCGGATAGAA-A-GTGGTGA-CTATCTCACACAA-TCGG--CAGGACGAGGATAC  3464
Db  3566  AGACAATAGACTGGAACACGAGCTAAACCATATGGTAGCCATATGGGAGAAGAAAGATGCAAGGAGAGCGACAC  3625

Qy  3465  TTTGAGCACAGGGTGCATATGGAAGTGCACAAAAACCGTCCATACAAGGATGACAGAGGATAC  3524
Db  3626  TGCCAGCATTAACTCATATTCCGAATCCATCATGGTAGCCATATGGGAGGCGGCCAAGAGAGCCCACAA  3685

Qy  3525  GGGAAGTGCAGCGCCGCCCAGACTATGATGGGAGGAGGAAGATGCAAGCAAGAAATCTCGA  3584
Db  3686  GGGCAGCGCCGCCGCGATGGAGGGGCGGCCAGCAAGGCGCGACGCGCCAGCAAGGAGGATTTAGG  3745

Qy  3585  TCAAGAGGAGAAGGTGAAGAAGATGGAGAAGGTGGAAGAGGACCTCTGGAGGACCATGGT  3644
Db  3746  TCTCGACGAGGAGACTGACGAATCGGAGGAGGGCGAATCGGAGGAGGCCCCGCTGCGACGGTGATAT  3805

Qy  3645  ATTGGATGCAGGCACT-GAGGACGTGCTCATGATGTCAGAATGTCGATGCTGTCCTG  3703
Db  3806  CATT-ATTCATTGCACACGACGACGAGGATATCCCTTGCTGGACGGAAGACATCCAGCTGATTGCTGCCCCG  3864

Qy  3703  ATCATCGCTATATAAGGCGTTCCCCTTTCCTTCGGTCTTGGTGCTCTGGGT  3763
Db  3865  ATTTCGTACTATAGAAAATTTCCAGTCATCTTAGCCGGTGTCGACATCTTGCCGGTCTCGCAAG  3924

Qy  3763  GCTGGGGCAACCTCCGACTGAAAACCTTCCAACTCATTGAGACAACAAATACTTTGAAACGG  3823
Db  3925  GATGGGGCAATTTACGACTGAAAAACTTTTCAATTAATTAAATAATATTTTGAAACAG  3984
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Db   3824  CTGTGATCACCATGATCCTGCTCTAGCAGTCTCCGCCACTGGCCCTTGAGGATGTACAATCTGC   3883
                ||| |||| ||| ||   | |||| || ||| || | | ||  |||  | |||||||| ||
Qy   3985  CTGTTATCACTGATTTTAATGAGTAGCTTAGCTTGGCATTTGGCATCATCTGC               4044

Db   3884  CTCATCGACCAATTCTGCAGGACACTCTTATATATCAGTCGTATCTTCACTGTCATCT          3943
                |  |||||  ||||  || || | |||||| || || |||||| |||||||||
Qy   4045  CACAAAGACCCATACTGCAGGAATATTTATAACTATACAGAATATTTACGGTTATAT          4104

Db   3944  TCTTCATTGAGAGTGTGATCAAGTGGCTGGCTGGCCCTGGTTTCAAAAAATACTTCACAAATG   4003
                ||| ||||   ||||| ||| ||| || ||  | ||||| | |||||   | ||||
Qy   4105  TCTTCTTGGAAATGTTAATCAAGTGGCTTGGTCGGTTGGCGCTTCAAGTGTACTTCACCAACG   4164

Db   4004  CTTGGTGCTGGTTGGATTTCATCATGTCATGGTCTCCACTCATCTTCTCTGTCATCTTTGCCA   4063
                || ||||| ||| |||| || |   ||  || |  ||| |||||||| |||  ||| ||
Qy   4165  CGTGGTGTGGTCTGGCTCGATTTCGTGATGTGTCATGGTGTCTGTAATTTTTGGCTAATTTGCCA   4224

Db   4064  TGGTTGGCGGCCTGGAGGCCATTCAAGCCTCAAACATGAGGACACTCAGGGCCCTTAGGC     4123
                ||| ||| ||| ||| ||| |||||||| |||| |||| ||||| || ||||  |||
Qy   4225  TTGTTGGAGGCCTGGTGGCCCATCCGGCGCCTGCTGCGTGTGTGTGTACGTGTACAAG        4284

Db   4124  CTCTTAGGGCTATGTCTAGAAGTGCAGGGGATGAGGTGGTGGTGAACGCTTTGGTGCAAG      4183
                || ||||| || |||| || |||| || ||||  | |||||||  | ||||||||||
Qy   4285  CACTACGGTGTCCCATGGTCGTTAATGCGCTGGTCGTTGGTCGTTAATGCGCTGGTACAAG     4344

Db   4184  CCATCCCCAGTATCTTCAATGTGCTCCTCGTGTCTCATCTTCTGGCTCATCTTTGCCA        4243
                || || || ||| | ||||| || || |||| || ||||| ||||| ||||| ||||
Qy   4345  CTATACGGTCGTCATCTTCAATGTGCTCCATTGGTGTCTAATATTTTGGCTAATTTTGCCA     4404

Db   4244  TCATGGGTGTGCAGCTGTTTGCTGGGAAATCATTCTGTGGAAAATATCATAAATGTGGAT     4303
                ||||||||||| | ||||| ||||| |||| ||   |||| |||||| ||||| ||||
Qy   4405  TAATGGGTGTACAGCTTTTTGCTGGGAAATCTTTAAGTGGACAGCCGAGATCCGCAATGCCA   4464

Db   4304  CTTTGAGCCACGAAATCATTCCTGACACGTCGCAAAGCTTATCTCGCCTCCTTCCAAGTGG    4363
                ||| || ||||| || |||||| ||  ||| | || |||||| ||||  |||||||| ||
Qy   4465  AGCTCAGCCAGAGATCACATCATCAATCAAGGTCGCAAAGCGCTATCTCGCCTCCTTTCCAAGTGG  4524

Db   4364  AGAACTCGCCAATGAATTTTGATCACGTCGGCAAAGCTTATCTCGCCTCTTCCAAGTGG       4423
                || |||| ||||| ||| || ||| || || |  | | |||| | || |||||||||
Qy   4525  TGAATTCAGCAATGAATTTCACACTCAATCCAATCGTTCATTGGTGTTTCATTTTTCCAAGTGG   4584

Db   4424  CCCACTTCAAAGGATGGATTCAGATCATCAGAATGACCTATAGAGCTTCAGAGAGAAATAA      4483
                || || |||| ||| || ||||| ||||| |||   | |||| | |||| | |  |
Qy   4585  CCACCTTCAAAGGCTGGATCAGAATCATGAATGACGATCTGCTATGCTATCGGAGAGGTGGACA   4644

Db   4484  AGCAGCCAATCAGGGAAAGCAACAACATCTACAGTGACCTCTACTTTGTGTTCTTTATCATCT   4543
                ||||||||| |||| |||| ||| || |||||| ||| || ||  |||| || || |||||
Qy   4645  AGCAGCCAATTCGATCCGATCATCACGTACCATACGCTATGGATTCCGTATTTTTATTCATCATAT   4704

Db   4544  TTGGCTCATTTTCACTCTCCAACCTATTCCATTGGTGATCGACAACTTTAATGAGC        4603
                || || ||||| |  |||| ||| |||| || |||| ||| || ||| |||||||
Qy   4705  TGGGATCCTTTTTTTCACACTCAATCTGTTCATTGGTGTTATCAATTTTTAATGAGC        4764

Db   4604  AAAGAAAAGGCAGGAGTCGGTCAAGATGTTCATGACTGAAGATCAGAAGAAATACT        4663
                ||||||||||| ||  ||| | || |||| || || ||||  | ||| || ||
Qy   4765  AAAGAAAAGCAGGAGTTCGCGCCTGGGATCATGACCCTGGACCGGAAGATCAGAAAAGTACT      4824

Db   4664  ACAATGCTATGAAGAAATGGTTCGAAAAAAACCGTTAAAAGCCATCCCCAGGCCAAAGT     4723
                |||||||| | ||| ||||||||||| |||| ||| ||||||||||| ||||| |||||
Qy   4825  ATAATGCTATGAAGATGGGGCTCTAAAAAGAAGATAGAAAAGCCATTAAAAGCACCAAGGT    4884

Db   4724  TGGCTCATTTTCACTCTGTTGAAAATCTGACACGACAAGAAATTTGACATGATCATCA       4783
                || || ||||| |  | ||||||||||| ||| | |||||||| ||  ||| |||||
Qy   4885  GGCGACCACAGAACTCTTTGAAATGACTAACGATAGAGAAAATTCGATATAATCATTA      4944

Db   4784  TGTTGTTCATTGGCTTTAACATGTTTAACGATGTTCACTATCAACAGTCGAAGC        4843
                || ||||| || || || ||  || ||| ||||| ||| || |||||| |||||
Qy   4945  TGTTATTCATTGGTCTGAACATGTTCATCACCCTGACGATGCGTCGGACA             5004

Db   4844  AGTTCAGCGACGTTCTTGATTACTTGAACATCGTCATCGTCATCGTTCCAGTTCCGAGT    4903
                || || |  ||  | ||||| |||| ||||| ||||||| | | |||||||||||||
Qy   5005  CGTATAACGCGGTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTCGAGTTCCGAAT    5064

Db   4904  GTCTGATGAAGAGATATTCGCCCTCAGATACCACTACTTCAAGGACAACCATGGAACCTCTTTG   4963
                ||| ||||||| ||| ||||| |   |||| ||| ||||| || |  | ||||||||||||
Qy   5065  GTCTATTAAAAATATTCGCTTACTTTAGGATATCATCACTATTTATTGAGCCATGGAATTATTTG   5124
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Db   4964  ATTTCGTAGTTGTCATCCTATCATCATATATTGGGTCTGGTATTGGACTCATTGAGAAT     5023
                |  | || || ||  |  | | || |||| || | ||   ||  || ||  | ||
Qy   5125  ATGTAGTAGTGTCTCATTTTATTCCAATCTTAGGTCTTGTACTTGTACTAGGCGATATATCG    5184

Db   5024  ACTTGTGTCGCCTACACGTCTGCTTCGTCCAGTGGTGGAGTGAGTGGCGAAGGTGGTCGAGTCCTGC   5083
                ||| | || || || || || || || ||||||  | | ||||  |||| || || | | ||
Qy   5185  ACTTCGTGTCGCCGACCCTGCCGAGTGTGTGCGTGTGTGCGGGCGAAAGTGGGCCGTGTCCTTC   5244

Db   5084  GTCTGGTGAAGGTGCTAAGGGTATTCGGACATTCGGCCTATGCTGTTTGC       5143
                | |||||||| || ||  |||| || |||||| | ||||| | || ||
Qy   5245  GACTGGTGAAGGGAGCCAAGAGCATTCGGACACTGCACTCGTTGGGCCGTGC     5304

Db   5144  CAGGCTCTTCAATATCTGCCTACTACATTTTAGTCATGTTTATTTTGCCATCTCG       5203
                ||||| || ||| | || || |||| || | ||| |||  | | ||||| | |
Qy   5305  CGGCCCTGTCAACATCTGCTGCGTCTGTGTGTCATGTTCCATTTGCCATTTTTCG     5364

Db   5204  GCATGTCCTTCTTCATGCACAGTCCGGCTAAAAGTGGCCTTGATGACGTGTACAATTTCA      5263
                || |||  ||||| ||| |  |||| || |||||| ||  || || ||| ||||| ||
Qy   5365  GCATGTCGTTCTTCATGACGTTCAGGCACCGGTTGGAAGTCGACAGCTCTACAACTTCA       5424

Db   5264  AGACGTTTGGGCAGTCCATGATCCTCCTCGTCTTCCAGATGTCCACATCAGCTGGATGGGATG    5323
                || || |||| |||| ||||||| || ||  |||| |||||| | | ||| |||| ||
Qy   5425  AGACCTTTGGCCAGAGCATGATGCTCATTGGGCTGTTCAGATGTCAGGCGGTTCGCCGGATG   5484

Db   5324  GTGTGTTAGATGGGATCATGAATGAAGAGAGGACTGCAGGCATGGCAATAGCCAGAGATTGGCT    5383
                ||||| ||||  ||| ||| |||| |||| |  ||| |||| |  || || ||| |||| |
Qy   5485  GTGTACTGGACGGCCATTGTGGTTCAGGCGTCGAAGACCGTTGGAATTGCGGCGACAAAGGCT   5544

Db   5384  ACCCGGAGACTGGATCAGCATCAGCTACTGTCGGCGCATAGCTTCTTCTTGGAGAATTACTCCGTCA    5443
                |||| ||| |||| |   ||  |  |||| | ||| || |  |||| |||| ||  | |||
Qy   5545  ATCCGGCATTGGTTCAGCGACCGGTGGAATAACGTTCTCCTCATAACCTAGTTA           5604

Db   5444  TCAGTTCCTTATTGTTATTAACATGTTGTCGTCATTTGGAGAATTACTCCCAGG        5503
                |||| ||||| | ||| ||||  | | ||| || |||  ||| |||| |||
Qy   5605  TAAGCTTTTTGATAGTTATTAATATGTACTCATTCATTCTCGAGAACTATAGTCAGG      5664

Db   5504  CGACAGAGGATGTGCAGAAGGCTTGACGGATGATGAATACGATTACTATTGAAATTT      5563
                || | || |||| |||  || | | |||| | ||||| |||  |||||||| || |
Qy   5665  CCACCGGAGGACGTGCAAGAGGGTCGAAGATGGCGAAGCGTACGCTACTATATGAGATCT   5724

Db   5564  GGCAGCAGTTGACCCAGATGGGACGCCAATATAGTTCGCTATGACCCAGCTGTCGGATTTCC    5623
                || |||||| |||| ||| ||||| |||||||  | |||| ||  ||| |||| | ||||
Qy   5725  GGCAGCAATTCGATCCTGATGGGGCACCCAGTACGCTGATCATCAGCGTGTCCGAATTCC    5784

Db   5624  TCGACGTGCTGGAACCTCCGCTGACATCGCTATTAATCATCTGTTGCGAACAAGAGTCGCGA   5683
                |  | ||| ||| || |||| || |  | | ||||   ||   | || |||| || | ||
Qy   5785  TGGACGTACTGGAGCGCCCGCTGCAGATCGGTAACGGGCTATGAGGCTACGCTACAAGATCATATCGA  5844

Db   5684  TGGACATTCCGATCTGCAAGTGCCAAGTGGGCCTATAGCAAGATCAGAAGAAATACT       5743
                || ||| ||||| ||| |||| | | || ||| | ||||| ||||| | || ||||
Qy   5845  TGGACATACCCATCTGTCATGGCGTGACCATCAGCGTAGTACGCTAATCCAGCGCCCTTA     5904

Db   5744  CGAAGGACTTCTTTGCAAGGAAAAGGCAATCCTATAGAAGAGTCTCCGAGAGTGTGGAAG   5803
                || | |||| | || | ||||| | || ||  ||||| |   | | ||||| | || ||
Qy   5905  CGAAAGACTTCTTTGCGGAAGGCAATCCGATACGGAGGGCTATGAGACGCACGCAGGTGAGA    5964

Db   5804  TGCAACCAGGGCGGCGGCCTATGGTGGGCTAGGGTGTATGAGCCTATGGATGCTTTGA    5863
                ||  || |||| || | || ||  | | || || ||||| |||   |||| | |||||
Qy   5965  T--AGCGGCCGCCCCGGATACGGAGGGCTACGAGCCCGTCTCATCAACCGTCGTGGCGTC   6021

Db   5864  AGCGGAGAAGAATATTGTGCGCGACAATTGTGCGCTGATACAGATGCATGGCGCAAGCACAG    5916
                || |||||| | || |||||   || ||||||| || |  ||||| ||| |||||||||
Qy   6022  AGCGGTGAGGTAGTACGCGCCCGGCTAATCCAGCGCCTGGCGAAAGCACAG           6074
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RESULT      10
LOCUS       DVU26343      2144 bp      mRNA      INV      10-DEC-1995
DEFINITION  Drosophila virilis sodium channel protein (para) mRNA, partial cds.
ACCESSION   U26343
NID         g1110461

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KEYWORDS   .
SOURCE     Drosophila virilis.
ORGANISM   Drosophila virilis
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
           Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 2144)
AUTHORS    Thackeray,J.R. and Ganetzky,B.
TITLE      Conserved alternative splicing patterns and splicing signals in the
           Drosophila sodium channel gene para
JOURNAL    Unpublished (1995)
REFERENCE  2 (bases 1 to 2144)
AUTHORS    Thackeray,J.R. and Ganetzky,B.
TITLE      Developmentally regulated alternative splicing generates a complex
           array of Drosophila para sodium channel isoforms
JOURNAL    J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)
MEDLINE    94238327
REFERENCE  3 (bases 1 to 2144)
AUTHORS    Thackeray,J.R. and Ganetzky,B.
TITLE      Direct Submission
JOURNAL    Submitted (04-MAY-1995) Justin R. Thackeray, Biology, Yale
           University, 266 Whitney Avenue, New Haven, CT 06520, USA
FEATURES             Location/Qualifiers
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                     /note="cDNA was derived by RT-PCR; sequence compiled from
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Qy  1897  CCATCATAGTGCCGCCCGTGCTACTATGCAATCTAGAGCTCTAGACACTCGTCGTATACCTCGC  1956
                                                         DNDTNKIAEAFNRIGRFKSWVKRNVADCFKLIRNKLTNQISDQPSGKGVCRCISAEHG
Db   301  ACCAGTCCCGTATATCGTATACCTCCTT||||||CACATGGCGATCTGCTTGGCGGCATGGCCGTCATGG    360
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Qy  1957  ATCAGTCCCGAATATCGTATACCTCCTT||||||CACATGGCGATCTGCTTGGCGGCATGGCCGTCATGG   2016
                                                         DNELELGHDEILADGLIKKGIKEQTQLEVAIGDGMEFTIHGDMKNKPKKSKYLNNAT
Db   361  GCGTCAGCAACAATGACCAAGGAGAGCAAGTGCGCAATGCAATACACCGAATCAATCAG    420
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Qy  2017  GCGTCAGCAACAATGACCAAGGAGAGCAAATGCGCAAATTGCGCAATCAACACACGAATCAATCAG   2076
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Db   601  ATGATATTATTGAGCAAGCCGCTGGCCATAGTCGAGCAAGTGATCGCGGTGTCTCCG    660
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Db   721  TCGAAGTGATACTCAAAGGCATCGATGTGTTTGTGTCTGGGACTGCTGCTGGGTTTGGT    780
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Db   961  CCACGGATGAAACTGATGGCCAGAGTCCCAAATACTATTTCCAGGAGGATGGAACATCT   1020
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Note: remainder of annotations omitted.

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Best Local Similarity  90.6%;    Pred. No. 0.00e+00;
Matches 1943;  Conservative   0;  Mismatches 171;  Indels 30;  Gaps  12;
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Qy  2677  TCGACTTCATTATCGTGGCCCTATCGTGGCCTATTCGAAACTGGAACTGGACTCGAGGGTGTCCAGGGTC   2736
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Db  1081  TATCCGTATTGCGTTCGTTGCTCGCGTGATTCGATTATGGCCCGCCAAATCTTGGCCAA   1140
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Db    61  ACATACGCAGGAGGGATCACGTAGTTCTCACAAGTACACGACGATACGCGTGCGTT    120
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Qy  2797  CACTTAATTTACTTACTCATTCGATTATGGGACGCACCATGGCGCTTTGGGAATCTGACAT   2856
Db   121  TCGGGATACCTGGCAGCGATCGCAAGCCTTGGTATTGTCAACATATCAGGATGCACAAC   1260
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Db   181  AACACTTGCCATACGCCCATGACTCGAATCGCTGCTGGTATGCCTGACGCCAAATGTCTGACGGAGAATGGAG   1320
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MEDLINE    96397510
REFERENCE  2 (bases 1 to 5068)
AUTHORS    Miyazaki,M., Ohyama,K., Dunlap,D.Y. and Matsumura,F.
TITLE      Direct Submission
JOURNAL    Submitted (17-SEP-1996) Environmental Toxicology, University of
           California at Davis/ITEH, Davis, CA 95616, USA
FEATURES             Location/Qualifiers
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mutation        2355
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BASE COUNT   1363 a   1104 c   1252 g   1349 t
ORIGIN
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Query Match             22.1%;  Score 1441;  DB 15;  Length 5068;
Best Local Similarity   70.4%;  Pred. No. 0.00e+00;
Matches   3659;  Conservative    0;  Mismatches 1402;  Indels 136;  Gaps 81;
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Db     1 GCGTGGAACTGGCTGGACTTCGTAGTAATAGCTTTAGCTTACGTAACCATGGGGATAGAT 60
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Qy   660 GCATGGAATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGGTATAGAT 719

Db    61 CTAGGAAACCTGGCCGCCTTGCGAACGTTCAGGGTGCTCCGGGCTTTGAGAGACTTGCGCTT 120
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Qy   720 TTAGGTAATCTAGCAGCCCTGCGAACGTTCAGGGTGCTGCGGGCGCTTAAAACCGTAGCC 779

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Qy   780 ATTGTTCCAGGCTTGAAGACCATATCGTCGCCGCGTCATCGAATCGGTGAAGAATCTGCGC 839

Db   181 GATGTGATAATCCTCACCATGTTCTCGCTCTCCGTGCTTGCCTTAATGGGGCTCCAGATT 240
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Qy   840 GATGTGATTATCCTGACCATGTTCTCCCTGTCCGTGCTTGCGTTGGCGTTGATGGGGCTACAGATC 899

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RESULT      11
LOCUS       BGU71083      5068 bp    mRNA              INV    28-OCT-1997
DEFINITION  Blattella germanica para-type sodium channel mRNA, partial cds.
ACCESSION   U71083
NID         g1633647
KEYWORDS    .
SOURCE      German cockroach.
ORGANISM    Blattella germanica
            Eukaryotae; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Orthopteroidea; Dictyoptera; Blattellidae; Blattellinae;
            Blattella.
REFERENCE   1 (bases 1 to 5068)
AUTHORS     Miyazaki,M., Ohyama,K., Dunlap,D.Y. and Matsumura,F.
TITLE       Cloning and sequencing of the para-type sodium channel gene from
            susceptible and kdr-resistant German cockroaches (Blattella
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JOURNAL     Mol. Gen. Genet. 252 (1-2), 61-68 (1996)
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Db  1381 TGTGGGACTGCATGCTGGTCGGCGACGTCCGTCCATTCCATTCTTCCTTGGCCACCGTTG 1440
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Qy  3037 TGTGGGACTGCATGTACGTGGGCGATGTCCGTGCATTCCCTTTCTTCTTGGCCACCGTTG 3096

Db  1441 TCATCGGCCAATCTGTGTCGGTTCTTAACCTTTCTTAGCCTTGCTTTTGTGTCAAATTTGGCT 1500
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Qy  3097 TCATCGGCCAATCTGTGTCGGTACTTAACCTTTCTTAGCCTTGCTTTGTCCAATTTTGGCT 3156

Db  1501 CATCTAGTTTATCAGCACCGACTGCCGACAATGATACCAACAAAATAGCCGAGGCCTTTA 1560
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Qy  3157 CATCTAGCTTATCAGCACCGACTGCCGATAACGATACGAATAAAATAGCCGAGGCCTTCA 3216

Db  1561 ATCGTATCCGTCGTTTAAAAGTTGGGTTAAGCGTAAGCTAATGTTGCTGATTGTTTCAAGTTAA 1620
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Qy  3217 ATCGGAATTGGCCGATTTAAAAGTTGGGTTAAGCGTAATATTGCTGATTGTTTCAAGTTAA 3276

Db  1621 TACGTAACAAATTGACAAATCAAATAAGTGATCAACCTTCAGGTGAGAGGATCAACCAGA 1680
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Qy  3277 TACGTAACAAATTGACAAATCAAATAAGTGATCAACCATCAGGTGAGAGGACCAACCAGA 3336

Db  1681 TCAGTTGGATTTGGAGCGGAAGGCAAGGCGGTTGTCGTTGTATATCTGCAGAGCCATGGTG 1740
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Qy  3337 TCAGTTGGATTTGGAGCGGAAG---AG--CAT--G--GT-G---A----CA-A-C-----G 3372

Db  1741 ACAACGAGTTGGAACTGGACACGACGAGATTCTCGCCGACGCGCTTGATCAAGAAAGGGA 1800
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Qy  3373 A--AC-----TGGAGCTGGGCCACGACGACGACGAGTCCTCGCCGACGCCCTCATCAAGAAGGGGA 3426

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Db  1861 GCGACATGAAGAACAATAGCCGAGAAATCCAAATATCTAAATAATGCAACGATGATGATG 1920
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Qy  3487 GCGACATGAAGAACAACAAGCCGAGAAATCCAAATATCTAAATAACGACGATGATTG 3546

Db  1921 GCAACTCAATTAACCACCACCAAGAGCAAGAGCAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGT 1980
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Qy  3547 GCAACTCAATTAACCACCACCAAGAGCCAAGAGCAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGT 3606

Db  1981 CCTTCAGGACGACGACACTGCCAGCATTAACTCACATAATGTAGCCATTAAGAATCGACCAT 2040
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Qy  3607 CCTTACAGGACGACGACACTGCCAGCATTAACTCACATAATGTAGCCATTAAGAATCGACCAT 3666

Db  2041 TCAAGGACGAAAGCCACAAGGTAGCGCCGAAACGATGGAGGGCCGGAGGAAGCCCGACG 2100
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DNA sequence alignment (Db / Qy), positions 2362–5274 / 3410–5274.

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                 /db_xref="PID:g2231547"
                 /translation="EGWNIFDFIIVALSLLELGVQGLSVLRSFRLLRVFKLAKSW
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                 LSNFGSSSLSAPTADNDNKMAEAFNRISRFKNWVKRNIADCFKLIRNKLTNQISDQP
                 SGERINQISWIWSEEHGDNLEGELEHDDIMGDGLIKKGMKEQTQLEVAIGDGMEFIHG
                 DMKNNKPKKSKFLNNTTMIGNSINHQDNRLEHELNHRGLSIQDDDTASINSYG"

BASE COUNT       285 a          186 c          221 g          294 t
ORIGIN

Query Match      10.7%;   Score 696;   DB 15;   Length 986;
Best Local Similarity 85.3%;  Pred. No. 0.00e+00;
Matches 841;   Conservative   0;   Mismatches 145;   Indels   0;   Gaps   0;

Db     1 GAGGGCTGGAATATTTCGATTCATTATCGTTGCCTGTCTTACTGGAATTGGGCCTG   60
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Qy  2661 GAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATCTGGAACTGGGACTC 2720

Db    61 GAAGGTGTCCAGGGCTTGTCCGTGTTAAGAAGTTTTCGTTTGCTTCGTGTATTCAAATTG  120
         || ||||||| ||||||| ||| || ||  |||| || ||||| |||||||||| ||||
Qy  2721 GAGGGTGTCCAGGGCTGTCCGTATTGCGTGTTCCTTTGCGATTGCTGCGTGTATTCAAACTG 2780

Db   121 GCAAAATCTTGGCCACCCTGGAACTACTCATTCAATTATGGGCCGGACAATGGGTGCA  180
         || || |||||||||| ||||| || |  ||||||||||||| |||||||||| ||
Qy  2781 GCCAAGTCTTGGCCCACAGTTAATTTACTCATTCGATTATGGGACGCACCATGGGCGCT 2840

Db   181 TTGGGTAATCTAACATTGTACTTTGCATTATCATCTTCATTGGCGTATGGGAATG  240
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Qy  2841 TTGGGTAATCTGACATTTGCACTTTGCATTATCATCTTCATCTTGCGGTGATGGGAATG 2900

Db   241 CAACTTTGTGGAAAGAACTATATTGATCACAAGGACAAATTCAAAGATCAAAATTACCT  300
         ||||||||||||||||| |||||| || |||||||||| |||||| ||||||| |||
Qy  2901 CAACTGTTCTGGAAAGAATTATCATGATCACAAGGACCGCTTCCGAGATGCGGACCTGCCG 2960

Db   301 CGATGGAATTCACCGATTCATGCACTCCTTTATGATTGTGTTCCGAGTGTTATGTGGT  360
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Qy  2961 CGCTGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTGTTCCGGGTGCTCTGCGGA 3020

Db   361 GAATGGATTGAATCCATGTGGGACATGATGTGGGACATGATGTCCTGTATACCATTC  420
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Qy  3021 GAATGGATCGAGTCCATGTGGGACTGCATGGTGGGCATGACGTTCGTCGTTCATCCCCTTC 3080

Db   421 TTCTTGGCTACTGTTGTCATCGGCAATCTGTGTGGTTCTTAATCTTTTCTTAGCTTTGCTT  480
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Qy  3081 TTCTTGGCCACCGTTGTCATCGGCAATCTGTGGTGGACTTAACCTTTTCTTAACCTTTGCTT 3140

Db   481 TTGTCCAATTCGGTTCATCTAGTTATCAGCAACAATGATACCAATAACAATAA  540
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Qy  3141 TTGTCCAATTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAATAA 3200

Db   541 ATGGCGGAGGCCTTCAATCGTATTCTCGTTTAAGAACTGGTGAAACGTAATATTGCC  600
         || || ||||||||||||  ||||||| ||| | ||| ||| | |||| |||||||||
Qy  3201 ATAGCCGAGGCCTTCAATCGAATTGCCGATTAAAAGTTGGGTTAAGCGTAATATTGCT 3260

Db   601 GATTGTTTAAGTTAATACGTAATAAATTGACAATCAAATAAGTGACCAACCATCAGGT  660
         ||||||||||||| |||||||||||||| |||||||||||||||| |||||||||||||
Qy  3261 GATTGTTTCAAGTTATACGTAACAAATTGACAAATCAAATAAGTGATCAACCACCACAGGT 3320

Db   661 GAGAGGATCAACCAGATCAGTTGGATTTGGAGCGAAGAACATGGCGATAATGAACTGGAG  720
         |||||||| || || |||||||| ||| |||||||| ||||||| |  || ||||||||||
Qy  3321 GAGAGGACCAACCAGATCAGTTGGATTTGGAGCGAAGAGCATGGTGACCAACCTGGGGAG 3380

Db   721 TTGGGTCATGACATCATGGCCGATGGCCGTGATCAAGAAGGAATGAAAGAGCAAACC  780
         ||||| | || | || || || ||| ||  |||||||||  || ||||  || ||
Qy  3381 CTGGGCCACGACGACGAGATCCTCGCCGCCTCATCAAGAAGGGATCAAGGAGCAGACG 3440

Db   781 CAACTGGAGTGGCCATTGGCGATGGCATGGCATGGAGTTCACCATACGATATGAAGAAC  840
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Qy  5275 CACTGCTCTTCGGCGTTGGGCCATGTCCGTGCCTGGCCGGCCCTGTCAACATCTTCGACTCCTGCTGCTGT  5334

Db  4550 TTTAGTCATGTTATTTTTGCCATCTTCGGCATGTCCTTCTTCATGGCCGTCCGCGATA  4609

Qy  5335 TCCTGGTCATGTCATCTTCGGCATGTCCATTTTCGGCATGTCGTTCTTCATGGCACGTGAAGGAGA  5394

Db  4610 AAGGTGGCCTGACGTGTACAATTCAAGACGTTGGGCAGTCCATGATCCTGCTCT  4669

Qy  5395 AGAGCGGCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGACGATCATCCTGCTCT  5454

Db  4670 TCCAGATGTCCACATCAGCTGGATGGGATGCGTGTTAGATGGAGTCATGAATGAAGAGG  4729

Qy  5455 TTCAGATGTCGACGTCAGCCGGTTGGGATGGTACTGGGACGCGCCATTATCAATGAGGAAG  5514

Db  4730 ACTGCAACAAACCAAATAGCGAGATTGGCTACCCGGGAGACTGTGGATCAGCTACTGTCG  4789

Qy  5515 CATGGCGATCCACCCGACAGCGCACAAAAGGCTATCCGGCAATTGTGGTTCAGCGCGACCGTTG  5574

Db  4790 GCATAGCTTTCTTGCTGCTCATACACCTCGTCATCAGTTCCTTATTGTTATTAAACATGTACA  4849

Qy  5575 GAATAACGTTCTCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACA  5634

Db  4850 TTGCTGTCATTTGGAGAATTACTCCCAGGCGCACAGAGGATGTGCAGAAGCCTTGACGG  4909

Qy  5635 TTGCTGTCATTTCTGAGAATTCTGAGAATATAGTCAGGACCACCGAGAGCGTCAAGAGGGTCTAACCG  5694

Db  4910 ATGATGACTACGATATGTTACTATGAAAATTTGGCAGCAGTTGACCCAGATGGGACGGCAAT  4969

Qy  5695 ACGACGACTACGACGTACTATGAGATCGTGGCACCAATTCGATCCGGAGGGCCACCCAGT  5754

Db  4970 ATATTCGCTATGACCAGCGTCGCGGATTCCTGCCGACGTGCTGGAACCTCCGCTGCAGATAC  5029

Qy  5755 ACATACGCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGACGTACTGGAGGATCC  5814

Db  5030 ATAAGCCGAACAAGTACAAGAGATAGTGTCGATGGACAT  5066

Qy  5815 ACAAACCGAACAAGTACAAGATCATATCGATGGACAT  5851
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RESULT     12
LOCUS      U83872          986 bp    mRNA              INV        07-APR-1998
DEFINITION Haematobia irritans para-like sodium channel (HF-para-b) mRNA,
           alternatively spliced, partial cds.
ACCESSION  U83872
NID        g2231546
KEYWORDS   .
SOURCE     horn fly.
ORGANISM   Haematobia irritans
           Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;
           Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
           Muscomorpha; Muscoidea; Muscidae; Haematobia.
REFERENCE  1  (bases 1 to 986)
AUTHORS    Guerrero,F.D., Janroz,R.C., Kammlah,D. and Kunz,S.E.
TITLE      Toxicological and molecular characterization of
           pyrethroid-resistant horn flies; Haematobia irritans:
           identification of kdr and super-kdr point mutations
JOURNAL    Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)
MEDLINE    98105586
REFERENCE  2  (bases 1 to 986)
AUTHORS    Guerrero,F.D., Janroz,R.C. and Kunz,S.E.
TITLE      Direct Submission
JOURNAL    Submitted (06-JAN-1997) USDA-ARS, Knipling-Bushland Livestock
           Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,
           TX 78028, USA
FEATURES             Location/Qualifiers
     source          1..986
                     /organism="Haematobia irritans"
                     /strain="pyrethroid susceptible"
                     /note="propagated on citrated bovine blood; DNA designated
                     'sus**'"
                     /db_xref="taxon:7368"
     gene            1..986

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Db    3441  ||||||||  ||||||||||  ||  ||  |||||  ||||  |||||||  |||||||
Qy    3441  CAACTGGAGTGGCCATCGGGGATCGGATGGGAATTCACGATACACGGGGACATGAAGAAC 3500

Db     841  AACAAGCCCAAGAAATCAAAATTCTTAAATAACACAACGATGATTGGAAACTCAATAAAC 900
            ||||||| |||||||  |||   |||||||  |  |||||||||||||||||||||| |||
Qy    3501  AACAAGCCGAAGAAATCCAAATATCTAAATAACCGAACGATGATTGGCAACTCAATTAAC 3560

Db     901  CACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGAGGTTTGTCCATACAGGACGAT 960
            ||||||||||||| |||||||  |||  |||| |||||||||||||||||||||||| |||
Qy    3561  CACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAGAGGTTTGTCCTTACAGGACGAC 3620

Db     961  GACACTGCCAGCATTAACTCATATGG 986
            ||||||||||||||||||||||||||
Qy    3621  GACACTGCCAGCATTAACTCATATGG 3646
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RESULT  13

LOCUS        U83874         986 bp       mRNA         INV        07-APR-1998
DEFINITION   Haematobia irritans para-like sodium channel (HF-para-like) mRNA,
             alternatively spliced, partial cds.
ACCESSION    U83874
NID          g2231550
KEYWORDS     .
SOURCE       horn fly.
  ORGANISM   Haematobia irritans
             Eukaryote; mitochondrial eukaryotes; Metazoa; Arthropoda;
             Tracheata; Hexapoda; Insecta: Pterygota; Diptera; Brachycera;
             Muscomorpha; Muscoidea; Muscidae; Haematobia.
REFERENCE    1  (bases 1 to 986)
  AUTHORS    Guerrero,F.D., Jamroz,R.C., Kammlah,D. and Kunz,S.E.
  TITLE      Toxicological and molecular characterization of
             pyrethroid-resistant horn flies, Haematobia irritans:
             identification of kdr and super-kdr point mutations
  JOURNAL    Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)
  MEDLINE    98105586
REFERENCE    2  (bases 1 to 986)
  AUTHORS    Guerrero,F.D., Jamroz,R.C. and Kunz,S.E.
  TITLE      Direct Submission
  JOURNAL    Submitted (06-JAN-1997) USDA-ARS, Knipling-Bushland Livestock
             Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,
             TX 78028, USA
FEATURES             Location/Qualifiers
     source          1..986
                     /organism="Haematobia irritans"
                     /strain="untreated pyrethroid-resistant"
                     /note="propagated on a steer without pyrethroid
                     applications; DNA designated 'Super Res**'"
                     /db_xref="taxon:7368"
     gene            1..986
                     /gene="HF-para-like"
     CDS             <1..>986
                     /gene="HF-para-like"
                     /note="similar to Drosophila para; splice variant B"
                     /codon_start=1
                     /product="para-like sodium channel"
                     /db_xref="PID:g2231551"
                     /translation="EGWNIFDFIIVALSLLELGLEGVQGLSVLRSFRLLRVFKLAKSW
                     PTLNLLISIYGRTMGALGNLTFVLCIIIFIFAVMGMQLFGKNYIDHKDFKPDHELPRW
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                     LSNFGSSLSAPTADNDTNKIAEAFNRISRFKNWVKRNIADCFKLIRNKLTNQISDQP
                     SGERINQISWIWSEEHGDNELELGHDDIMGDGSLIKKGMKEQTOLEVAIGDGMEFTIHG
                     DMKNNRPKKSKFLNNTMIGNSINHQDNRLEHELNHRGLSIQDDDTASINSYG"
BASE COUNT   287 a   186 c   219 g   294 t
ORIGIN
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Qy    2721  GAGGGTGTCCAGGGTCGTCGTCCGTATTGCGTTCCTTTCGGATTCGTGCGTGTATTCAAACTG 2780
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Query Match      10.7%;   Score 694;   DB 15;   Length 986;
Best Local Similarity  85.2%;   Pred. No. 0.00e+00;
Matches    840;  Conservative    0;  Mismatches 146;   Indels   0;   Gaps   0;

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Db       1  GAGGGCTGGAATATTTCGATTTCATTATCGTTGCCTTGTCTTTACTGGAATTGGGCCTG 60
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Qy    2661  GAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATCCGCTATTGGAACTGGGACTC 2720
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RESULT  14

LOCUS        DMU26715        1840 bp       DNA          INV        30-APR-1996
DEFINITION   Drosophila melanogaster sodium channel protein (para) gene,
             optional segments f and h, partial cds.
ACCESSION    U26715
NID          g1110473
KEYWORDS     .
SOURCE       fruit fly.

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ORGANISM   Drosophila melanogaster
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
           Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1  (bases 1 to 1840)
AUTHORS    Thackeray,J.R. and Ganetzky,B.
TITLE      Developmentally regulated alternative splicing generates a complex
           array of Drosophila para sodium channel isoforms
JOURNAL    J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)
MEDLINE    9423837
REFERENCE  2  (bases 1 to 1840)
AUTHORS    Thackeray,J.R. and Ganetzky,B.
TITLE      Conserved alternative splicing patterns and splicing signals in the
           Drosophila sodium channel gene para
JOURNAL    Genetics 141 (1), 203-214 (1995)
MEDLINE    96042905
REFERENCE  3  (bases 1 to 1840)
AUTHORS    Thackeray,J.R. and Ganetzky,B.
TITLE      Direct Submission
JOURNAL    Submitted (10-MAY-1995) Justin R. Thackeray, Biology, Yale
           University, 266 Whitney Avenue, New Haven, CT 06520, USA
FEATURES            Location/Qualifiers
    source          1..1840
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                    /db_xref="taxon:7227"
                    /map="X; 14C7-8"
                    /chromosome="X"
    gene            405..1674
                    /note="paralytic"
                    /gene="para"
                    /allele=""
                    /db_xref="FlyBase:FBgn0003036"
    CDS             join(<405..623,1267..>1674)
                    /gene="para"
                    /standard_name="paralytic"
                    /codon_start=1
                    /product="sodium channel protein"
                    /db_xref="PID:g1110474"
                    /translation="TKGKGVCRCISAEHGDNELELGHDEILADGLIKKGIKEQTQLEV
                    AIGDGMEFTIHGDMKNNKPKKSKYLNNATDDDTASINSYGSHKNRPFKDESHKGSAET
                    MEGEEKRDASKEDLGLDEELDEEGECEEGPLDGDIIIHAHDEDILDEYPADCCPDSYY
                    KKFPILAGDDDSPFWQGWGNLRLKTFQLIENKYFETAVITMILMSSLAL"
BASE COUNT    673 a    374 c    305 g    488 t
ORIGIN

Query Match      7.4%;  Score 485;  DB 15;  Length 1840;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches   48;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0:

Db  1191  GATGATTGGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAG  1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3539  GATGATTGGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAG  3598

Db  1251  AGGTTGTCCTTACAGGACGACGACGACTGCCAGCATTAACTACATGGTAGCCATAAGAA  1310
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3599  AGGTTGTCCTTACAGGACGACGACGACTGCCAGCATTAACTACATGGTAGCCATAAGAA  3658

Db  1311  TCGACCATTCAAGGACGACGAGACGCCACAAGGGCAGCCGCGAGACGATGGAGGGCGAGGAGAA  1370
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3659  TCGACCATTCAAGGACGACGAGACGCCACAAGGGCAGCCGCGAGACGATGGAGGGCGAGGAGAA  3718

Db  1371  GCGGCACGGCCAGCAAGGAGGATTTAGGTCTCGACGACGAGAACTGGACGAGAGGCGAATG  1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3719  GCGGCACGGCCAGCAAGGAGGATTTAGGTCTCGACGACGAGAACTGGACGAGAGGCGAATG  3778

Db  1431  CGAGGAGGGCCCGCTCGACGGTGATATCATTATTCATGCACACGACGAGGATATACTCGA  1490
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3779  CGAGGAGGGCCCGCTCGACGGTGATATCATTATTCATGCACACGACGAGGATATACTCGA  3838

Db  1491  TGAATATCCAGCTGATTGCTGCCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGG  1550
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3839  TGAATATCCAGCTGATTGCTGCCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGG  3898
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Db  1551  TGACGATGACTCGCCGTTCTCGGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATT  1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3899  TGACGATGACTCGCCGTTCTCGGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATT  3958

Db  1611  AATTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGC  1670
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Qy  3959  AATTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGC  4018

Db  1671  TTTGG  1675
          |||||
Qy  4019  TTTGG  4023

RESULT  15
LOCUS       U83871        947 bp    mRNA            INV    07-APR-1998
DEFINITION  Haematobia irritans para-like sodium channel (HF-para) mRNA,
            alternatively spliced, partial cds.
ACCESSION   U83871
NID         g2231544
KEYWORDS    .
SOURCE      horn fly.
ORGANISM    Haematobia irritans
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
            Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
            Muscomorpha; Muscoidea; Muscidae; Haematobia.
REFERENCE   1  (bases 1 to 947)
AUTHORS     Guerrero,F.D., Jamroz,R.C., Kammlah,D. and Kunz,S.E.
TITLE       Toxicological and molecular characterization of
            pyrethroid-resistant horn flies: Haematobia irritans:
            identification of kdr and super-kdr point mutations
JOURNAL     Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)
MEDLINE     98105586
REFERENCE   2  (bases 1 to 947)
AUTHORS     Guerrero,F.D., Jamroz,R.C. and Kunz,S.E.
TITLE       Direct Submission
JOURNAL     Submitted (06-JAN-1997) USDA-ARS, Knipling-Bushland Livestock
            Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,
            TX 78028, USA
FEATURES            Location/Qualifiers
    source          1..947
                    /organism="Haematobia irritans"
                    /strain="pyrethroid-susceptible"
                    /note="propagated on citrated bovine blood; DNA designated
                    'sus*'"
                    /db_xref="taxon:7368"
    gene            1..947
                    /gene="HF-para"
                    <1..>947
                    /gene="HF-para"
    CDS             /note="similar to Drosophila para; splice variant A"
                    /codon_start=1
                    /product="para-like sodium channel"
                    /db_xref="PID:g2231545"
                    /translation="EGWNIFDFIVALSLLELGEVQGLSVLRSFRLLRVFKLAKSW
                    PTLNLLISIMGRTMGALGNLTFVLCIIIFIFAVMGMQLFGKNYIDHKDRFKDHELPRW
                    NFTDFMHSFMIVFRVLCGEWIESMWDCMYVGDVSCIPFFLATVVIGNLVVLFLALL
                    LSNFGSSSLSAPTADNDTNKMAEAFNRISRFKNWVKRNIADCFKLIRNKLTNQISDQP
                    SEHGDNELELGHDDIMGDGLIKKGMKEQTQLEVAIGDGMEFTIHGDMKNNKPKKSKFL
                    NNTIMIGNSINHQDNRLEHELNHRGLSIQDDDTASINSYG"
BASE COUNT    273 a    181 c    207 g    286 t
ORIGIN

Query Match      6.9%;  Score 448;  DB 15;  Length 947;
Best Local Similarity 84.0%;  Pred. No. 0.00e+00;
Matches  553;  Conservative    0;  Mismatches 105;  Indels    0;  Gaps    0:

Db     1  GAGGGCTGGAATATTTCCATTTCATTATCGTTGCCTTGTCTTTACTGGAATTGGGCCTG   60
          |||||||| || |||||| ||||| |||||||||||| || |||| |||||||||||||
Qy  2661  GAGGGCTGGAACATCTTGACTTCATTATCGTGGCCCTATCGCTATTGGAACTGGGACTC  2720

Db    61  GAAGGTGTCCAGGGCTTGTCCGTGTTAAGAAGTTTTCGTTGCTTCGTGTATTCAAATTG  120
          || |||||||||||| ||| || ||| |||||| | |||| || || || ||| |||||
Qy  2721  GAGGGTGTCCAGGGTCGTCCCGTATTGCGTTCCTTCGATTGCTGCGCGTGATTCAAACTG  2780
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Db   121  GCAAAATCTTGGGCCACCCTGAACTTACTCATTCATTCAATTATGGGCCGACAATGGGTCA  180
               || || |||||||||| || || ||||||||| ||||||| || || ||||| ||
Qy  2781  GCCAAGTCTTGGCCCACACTTAATTACTCATTTCGATTATGGGGACGCACCCATGGGCGCT  2840

Db   181  TTGGGTAATCTAACATTTGTACTTTGCATTATCATCTTCATCTTGCCGTTATGGGAATG  240
               |||||||| |||||||||||||||||||||||||||| || |||||||||||
Qy  2841  TTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTGCCGTGATGGGAATG  2900

Db   241  CAACTTTTCGGAAAGAACTATATTGATCACAAGGACAAATTCAAAGATCATGAATTACCT  300
               ||||| |||||||||| ||| |||||||||| || || || |||
Qy  2901  CAACTGTTCGGAAAGAATTATCATCACAAGGACCCGCTTTCCGGATGGGCGACCTGCCG  2960

Db   301  CGATGGAATTCACCGATTTCATGCACTCCTTATGATTGCGTTCCGAGTGTTATGTGGT  360
               || ||||| ||||||| || ||||| ||| |||||| ||||||| ||| || ||
Qy  2961  CGCTGGAACTTCACCGACTTTATGCACAGCTTCATGATCCGTGTTCCGGGTGCTGCGGA  3020

Db   361  GAATGGATTGAATCCATGTGGGACTGCATGTATGTGGGCGATGTCTCCTGTATACCATTC  420
               ||||||| || ||||||||||||||||| |||||||| || || |||
Qy  3021  GAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCTCGTGCATTCCCTTC  3080

Db   421  TTCTTGGCTACTGTTGTCATCGGCAATCTTGTGGTTCTTAATCTTTCTTAGCTTTGCTT  480
               |||||||| |||||||||||||||||| || ||||||| ||||||||||| || ||||
Qy  3081  TTCTTGGCCACCGTGTCATCGGCAATCTGTGTGTACTTAACCTTTCTTAGCCTTGCTT  3140

Db   481  TTGTCCAATTCGGTTCATCTAGTTTATCAGCACCGACTGCCGACAATGATACCAATAAA  540
               |||||||||| || |||||||||||| || ||||||||||| || || |||||||||
Qy  3141  TTGTCCAATTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGATAACGATACGAAATAAA  3200

Db   541  ATGGCGGAGGCCTTCAATCGTATTTCTCGTTTTAAGAACTGGGTGAAACGTAATATTGCC  600
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Qy  3201  ATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTTGGGTTAAGCGTAATATTGCT  3260

Db   601  GATTGTTTTAAGTAATAATACGTAATAAAATGACAAAATCAAATAAGTGACCAACCATCAG  658
               ||||||||| ||||||||||||||||||||| |||||||||||| |||||||||
Qy  3261  GATTGTTTCAAGTTAATACGTAACAAATCAACAAATCAAATAAGTGATCAACCATCAG  3318
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